



Query Match 100.0%; Score 1047; DB 3; Length 202;  
Best Local Similarity 100.0%; Pred. No. 3e-89;  
Matches 202; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MATGSRSTSLLAAGLLCLPWLQEGSAPPTIPLSRLFDNASTRAHRLHQLAFDTYQEFNPQ 60  
DB 1 MATGSRSTSLLAAGLLCLPWLQEGSAPPTIPLSRLFDNASTRAHRLHQLAFDTYQEFNPQ 60  
QY 61 TSLCFSESIPTPPSNRRETOOKSNLELRISLLIQSWLEBPQFLRSVFANSIYVGSADSN 120  
DB 61 TSLCFSESIPTPPSNRRETOOKSNLELRISLLIQSWLEBPQFLRSVFANSIYVGSADSN 120  
QY 121 VYDLKDLERGIQTLWMLRLEDPSPRTQIFKQYASKPDTSNHDALLKNYGLLYCFERKD 180  
DB 121 VYDLKDLERGIQTLWMLRLEDPSPRTQIFKQYASKPDTSNHDALLKNYGLLYCFERKD 180  
QY 181 MDKVEFLRIYQCRSVESGCGF 202  
DB 181 MDKVEFLRIYQCRSVESGCGF 202

RESULT 2  
ADQ39295 ADQ39295 standard; protein; 202 AA.

AC ADQ39295;

DT 18-NOV-2004 (first entry)

DE Human myocardial infarction-associated gene derived protein, SEQ ID 958.

XX Myocardial infarction; detection; single nucleotide polymorphism; SNP;

KW cardiact; gene therapy; human.

OS Homo sapiens.

PN WO2004058052-A2.

PD 15-JUL-2004.

PF 22-DEC-2003; 2003WO-US040978.

XX 20-DEC-2002; 2002US-0434778P.

PR 10-MAR-2003; 2003US-0453135P.

PR 30-APR-2003; 2003US-0466412P.

PR 23-SEP-2003; 2003US-0504955P.

PA (APPL-) APPLERA CORP.

PI Cargill M, Devlin J, Takubova O;

DR N-PSDB; ADQ38467.

PT Identifying an individual who has an altered risk for developing myocardial infarction by detecting a single nucleotide polymorphism in the individual's nucleic acids.

PS Claim 10; SEQ ID NO 958; 145bp; English.

XX The invention relates to a novel method for identifying an individual who  
XX has an altered risk for developing myocardial infarction. The method  
XX comprises detecting a single nucleotide polymorphism (SNP) in any one of  
XX the nucleotide sequences given in the specification in the individual's  
XX nucleic acids, where the presence of the SNP is correlated with an  
XX altered risk for myocardial infarction in the individual. The invention  
XX further comprises: an isolated nucleic acid molecule comprising at least  
XX 8 contiguous nucleotides where one of the nucleotides is an SNP given in  
XX the specification or its complement and encoding any one of the amino  
XX acid sequences given in the specification; an isolated polypeptide  
XX comprising an amino acid sequence given in the specification; an antibody  
XX that specifically binds to the polypeptide or its antigen-binding

CC fragment; an amplified polynucleotide containing an SNP given in the  
CC specification and which is between about 16 and 1000 nucleotides in  
CC length; a kit for detecting an SNP in a nucleic acid, comprising the  
CC polynucleotide, a buffer and an enzyme; a method of detecting an SNP in a  
CC nucleic acid molecule; a method of detecting a variant polypeptide; and a  
CC method for identifying an agent useful in treating or preventing  
CC myocardial infarction. The novel detection method has cardiact activity.  
CC The nucleic acids of the invention may be used in gene therapy. The  
CC method is useful in identifying an individual who has an increased or  
CC decreased risk for developing myocardial infarction and for preparing a  
CC composition for treating or preventing myocardial infarction. This  
CC sequence represents the protein of a human myocardial infarction-  
CC associated gene containing one or more SNPs of the invention. Note: This  
CC sequence was not shown in the specification. The sequence has come from  
CC an electronic sequence listing downloaded from the WIPO website.

Sequence 202 AA;

Query Match 99.5%; Score 1042; DB 8; Length 202;  
Best Local Similarity 99.5%; Pred. No. 8.6e-89;  
Matches 201; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 MATGSRSTSLLAAGLLCLPWLQEGSAPPTIPLSRLFDNASTRAHRLHQLAFDTYQEFNPQ 60  
DB 1 MATGSRSTSLLAAGLLCLPWLQEGSAPPTIPLSRLFDNASTRAHRLHQLAFDTYQEFNPQ 60  
QY 61 TSLCFSESIPTPPSNRRETOOKSNLELRISLLIQSWLEBPQFLRSVFANSIYVGSADSN 120  
DB 61 TSLCFSESIPTPPSNRRETOOKSNLELRISLLIQSWLEBPQFLRSVFANSIYVGSADSN 120  
QY 121 VYDLKDLERGIQTLWMLRLEDPSPRTQIFKQYASKPDTSNHDALLKNYGLLYCFERKD 180  
DB 121 VYDLKDLERGIQTLWMLRLEDPSPRTQIFKQYASKPDTSNHDALLKNYGLLYCFERKD 180  
QY 181 MDKVEFLRIYQCRSVESGCGF 202  
DB 181 MDKVEFLRIYQCRSVESGCGF 202

RESULT 3  
ADQ39284 ADQ39284 standard; protein; 202 AA.

AC ADQ39284;

DT 18-NOV-2004 (first entry)

DE Human myocardial infarction-associated gene derived protein, SEQ ID 947.

XX Myocardial infarction; detection; single nucleotide polymorphism; SNP;

KW cardiact; gene therapy; human.

OS Homo sapiens.

PN WO2004058052-A2.

PD 15-JUL-2004.

PF 22-DEC-2003; 2003WO-US040978.

XX 20-DEC-2002; 2002US-0434778P.

PR 10-MAR-2003; 2003US-0453135P.

PR 30-APR-2003; 2003US-0466412P.

PR 23-SEP-2003; 2003US-0504955P.

PA (APPL-) APPLERA CORP.

PI Cargill M, Devlin J, Takubova O;

DR N-PSDB; ADQ38456.

PT Identifying an individual who has an altered risk for developing

PT myocardial infarction by detecting a single nucleotide polymorphism in  
PT the individual's nucleic acids.

PS Claim 10; SEQ ID NO 947; 145bp; English.

CC The invention relates to a novel method for identifying an individual who  
CC has an altered risk for developing myocardial infarction. The method  
CC comprises detecting a single nucleotide polymorphism (SNP) in any one of  
CC the nucleotide sequences given in the specification in the individual's  
CC nucleic acids, where the presence of the SNP is correlated with an  
CC altered risk for myocardial infarction in the individual. The invention  
CC further comprises: an isolated nucleic acid molecule comprising at least  
CC 8 contiguous nucleotides where one of the nucleotides is an SNP given in  
CC the specification or its complement and encoding any one of the amino  
CC acid sequences given in the specification; an isolated polypeptide  
CC comprising an amino acid sequence given in the specification; an antibody  
CC that specifically binds to the polypeptide or its antigen-binding  
CC fragment; an amplified polynucleotide containing an SNP given in the  
CC specification and which is between about 16 and 1000 nucleotides in  
CC length; a kit for detecting an SNP in a nucleic acid, comprising the  
CC polynucleotide, a buffer and an enzyme; a method of detecting an SNP in a  
CC nucleic acid molecule; a method of detecting a variant polypeptide; and a  
CC method for identifying an agent useful in treating or preventing  
CC myocardial infarction. The novel detection method has candidate activity.  
CC The nucleic acids of the invention may be used in gene therapy. The  
CC method is useful in identifying an individual who has an increased or  
CC decreased risk for developing myocardial infarction and for preparing a  
CC composition for treating or preventing myocardial infarction. This  
CC sequence represents the protein of a human myocardial infarction. Note: This  
CC associated gene containing one or more SNPs of the invention. Note: This  
CC sequence was not shown in the specification. The sequence has come from  
CC an electronic sequence listing downloaded from the WIPO website.

XX Sequence 202 AA;

Query Match 99.5%; Score 1042; DB 8; Length 202;  
Best Local Similarity 99.5%; Pred. No. 8.6e-89;

Matches 201; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 MATGSRSTLLAAGLCLPWLQEGSAFPTPLSRFPNALSRAHRLHQLAFDTYQEFNPQ 60  
DB 1 MATGSRSTLLAAGLCLPWLQEGSAFPTPLSRFPNALSRAHRLHQLAFDTYQEFNPQ 60  
QY 61 TSLCFSESIPTPSNRETOQKSNLELRISLLIQSWLEPVOFLRSVFANSIYVGASDSN 120  
DB 61 TSLCFSESIPTPSNRETOQKSNLELRISLLIQSWLEPVOFLRSVFANSIYVGASDSN 120  
QY 121 VVDLLADLEBGIQTLMGRLSDGSPRTGQIFKQTSKPDTSNNDALLKNYGLLYCPRKD 180  
DB 121 VVDLLADLEBGIQTLMGRLSDGSPRTGQIFKQTSKPDTSNNDALLKNYGLLYCPRKD 180  
QY 181 MKKVFETLRIVQCRSVGSGCF 202  
DB 181 MKKVFETLRIVQCRSVGSGCF 202

RESULT 4

AAR60516  
ID AAR60516 standard; protein; 217 AA.

XX AAR60516;

AC 25-MAR-2003 (revised)

DT 22-MAR-1995 (first entry)

DE Human somatotropin.

KW Serine protease; Factor-Xa; recognition site; fusion protein cleavage;  
KW protein folding; growth hormone; somatotropin; primer;  
KW polymerase chain reaction; amplification.

XX Homo sapiens.

XX

PN W09418227-A2.

XX 18-AUG-1994.

PF 04-FEB-1994; 94WO-DK000054.

XX 04-FEB-1993; 93DK-00000130.

PR 05-FEB-1993; 93DK-00000139.

PR 03-DEC-1993; 93WO-GB002492.

XX (DENZ-) DENZYME APS.

XX Thogersen HC, Holtet TL, Etzerodt M;

DR WPI; 1994-279681/34.

PT Refolding of polypeptide molecules - using a cyclic process involving  
PT denaturing and renaturing conditions to produce a correctly folded prod.  
PS Disclosure; Page 129-30; 202pp; English.

CC cDNA encoding human somatotropin (aa sequence given in AAR60516) was PCR  
CC amplified using primers given in AA071248-49. Amplified cDNA was linked  
CC to a sequence encoding the Factor-Xa cleavage site (given in AAR60503),  
CC subcloned in vector pTH6 so that it was N-terminally linked to a  
CC hexahistidine-encoding sequence and expressed in E. coli BL21. The  
CC resulting fusion protein included an affinity tag (AAR60513) that  
CC facilitating fusion protein purification on Ni2+-activated NTA-agarose. A cyclic  
CC procedure was used to obtain correctly folded recombinant protein.  
CC (Updated on 25-MAR-2003 to correct PN field.)

XX Sequence 217 AA;

Query Match 98.3%; Score 1029.5; DB 2; Length 217;  
Best Local Similarity 93.1%; Pred. No. 1.4e-87;

Matches 202; Conservative 0; Mismatches 0; Indels 15; Gaps 1;

QY 1 MATGSRSTLLAAGLCLPWLQEGSAFPTPLSRFPNALSRAHRLHQLAFDTYQEFNPQ 57  
DB 1 MATGSRSTLLAAGLCLPWLQEGSAFPTPLSRFPNALSRAHRLHQLAFDTYQEFNPQ 57  
QY 58 -----NPQTSLSFSESIPTPSNRETOQKSNLELRISLLIQSWLEPVOFLR 105  
DB 61 YIPKEQKYSFLQNPQTSLSFSESIPTPSNRETOQKSNLELRISLLIQSWLEPVOFLR 120  
QY 106 SVFANSIYVGASDSNVDLLKDLKEBGIQTLMGRLSDGSPRTGQIFKQTSKPDTSNND 165  
DB 121 SVFANSIYVGASDSNVDLLKDLKEBGIQTLMGRLSDGSPRTGQIFKQTSKPDTSNND 180  
QY 166 ALLKNYGLLYCPRKMDKVFETLRIVQCRSVGSGCF 202  
DB 181 ALLKNYGLLYCPRKMDKVFETLRIVQCRSVGSGCF 217

RESULT 5

AAU11731  
ID AAU11731 standard; protein; 217 AA.

XX AAU11731;

DT 12-MAR-2002 (first entry)

DE Growth hormone 1 gene (GH1), 569L mutant.

KW Growth hormone 1; GH1; osteopathic; gene therapy; protein therapy;  
KW diabetes; obesity; infection; acromegaly; gigantism; sodium retention;  
KW water retention; metabolic syndrome; mood disorder; sleep disorder;  
KW Growth hormone dysfunction; familial growth hormone deficiency;  
KW short stature; pituitary storage defect; human; mutant; mutein.

XX Homo sapiens.

XX Synthetic.

XX

Db 181 AALKNYGLYCFERKMDXVETPLRIYQCRSVESGSCF 217

RESULT 6  
ID AAU11719  
AAU11719 standard; protein; 217 AA.  
XX AAU11719;  
DT 12-MAR-2002 (first entry)  
XX  
DE Growth hormone 1 gene (GH1), major isoform.  
XX  
KW Growth hormone 1; GH1; osteopathic; gene therapy; protein therapy;  
diabetes; obesity; infection; acromegaly; gigantism; sodium retention;  
water retention; metabolic syndrome; mood disorder; sleep disorder;  
RW Growth hormone dysfunction; familial growth hormone deficiency;  
short stature; pituitary storage defect; human; chromosome 17q23.  
XX  
OS Homo sapiens.  
PN WO200185993-A2.  
XX  
PD 15-NOV-2001.  
XX  
PF 14-MAY-2001; 2001WO-GB002126.  
XX  
PR 12-MAY-2000; 2000GB-00011459.  
PR 14-JUL-2000; 2000EP-00306004.  
XX  
PA (UYWA-) UNIV WALES COLLEGE OF MEDICINE.  
XX  
FI Cooper DN, Procter AM, Gregory J, Millar DS;  
PI WPI; 2002-089798/12.  
DR N-PSDB; AAS18887.  
PT  
PT Detecting growth hormone variants (GH1), useful in screening patients for  
growth hormone irregularities, comprises comparing the nucleotide  
sequence of a GH1 gene from a test sample with that of a standard  
sequence of the human GH1.

Disclosure; Fig 6; 95pp; English.

The invention described a method of detecting variation in growth hormone  
1 (GH1), and therefore GH dysfunction in an individual. The method  
comprises comparing the nucleotide sequence of GH1 gene obtained from the  
test sample with a standard human GH1 gene sequence, in order to identify  
variation (GH1 variant). The method is useful in screening patients for  
growth hormone irregularities or producing variant proteins for treating  
irregularities, and for the early detection and appropriate clinical  
management of familial GH deficiency. The GH1 variants are useful in  
therapeutic, diagnostic or detection method, particularly for determining  
binding defects and susceptibility to a disease such as diabetes, obesity  
or infection; for treating acromegaly or gigantism conditions associated  
with Iacogenic, diabetogenic, lipolytic and protein anabolic effects,  
conditions associated with sodium and water retention, metabolic  
syndromes, mood and sleep disorders; diagnosing GH dysfunction and  
determining pituitary storage defects. The GH1 variants are especially  
useful in gene therapy or protein therapy. The GH1 or GH variant may also  
be used in the preparation of a medicament, diagnostics composition or  
kit, or detection kit. The method has the advantage of: expanding the  
known spectrum of GH1 gene mutations; evaluating the role of GH1 gene  
mutations in the etiology of short stature; identifying of the mode of  
inheritance of novel lesions; evaluation the effects of GH1 mutations on  
the structure and function of the GH molecule and development of rapid  
diagnostic tests for inherited GH deficiency. This is the amino acid  
sequence of the major isoform of human growth hormone 1 (GH1), located on  
chromosome 17q23), used as a reference sequence for creating the mutants  
(AAU11721-AAU11750 and AAU11901) described in the method of the invention

Sequence 217 AA:



Query Match 98.3%; Score 1029.5; DB 5; Length 217;  
 Best Local Similarity 93.1%; Pred. No. 1.4e-87;  
 Matches 202; Conservative 0; Mismatches 0; Indels 15; Gaps 1;

QY 1 MATGRTSLILAFGLICLPWLQGSAPFTIPISRLFDNLSLAHRHQAFTYQGF--- 57  
 DB 1 MATGRTSLILAFGLICLPWLQGSAPFTIPISRLFDNLSLAHRHQAFTYQGF--- 57  
 QY 58 -----NPOTSLCFSESIPTPSNREBTQOKSNIELIRISILLIQSWLEPVQFLR 105  
 DB 61 YIPKOKSYFLONPOTSLCFSSSIPTPSNREBTQOKSNIELIRISILLIQSWLEPVQFLR 120  
 QY 106 SVFANSLVYGASDSNVYDLKDLREGIOTLMGRLEDSPRTGOIFKQYTSKPDNNSHND 165  
 DB 121 SVFANSLVYGASDSNVYDLKDLREGIOTLMGRLEDSPRTGOIFKQYTSKPDNNSHND 180  
 QY 166 ALKNYGLLYCFERKMDKVEFTFLRIYQCRSVGSGCF 202  
 DB 181 ALKNYGLLYCFERKMDKVEFTFLRIYQCRSVGSGCF 217

## RESULT 7

AAU11720  
 ID AAU11720 standard; protein; 217 AA.

AC AAU11720;  
 DT 12-MAR-2002 (first entry)  
 XX

DE Growth hormone 1 gene (GH1), E56G mutant.

KW Growth hormone 1; GH1, osteopathic; gene therapy; protein therapy;  
 KW diabetes; obesity; infection; acromegaly; gigantism; sodium retention;  
 KW water retention; metabolic syndrome; mood disorder; sleep disorder;  
 KW Growth hormone dysfunction; familial growth hormone deficiency;  
 KW short stature; pituitary storage defect; human; mutant; mutein.

OS Homo sapiens.  
 OS Synthetic.

FT Key Location/Qualifiers  
 FT Misc-difference 56 /note= "Wild type Glu substituted by Gly"

FN WO200185993-A2.  
 XX  
 PD 15-NOV-2001.  
 XX  
 PF 14-MAY-2001; 2001WO-GB002126.  
 XX  
 PR 12-MAY-2000; 2000GB-00011459.  
 PR 14-JUL-2000; 2000EP-00306004.

XX (UYMA-) UNIV WALES COLLEGE OF MEDICINE.  
 PA  
 XX  
 PI Cooper DN, Procter AM, Gregory J, Millar DS;  
 DR WPI; 2002-089798/12.  
 DR N-PSDB; AAS18888.  
 XX

PT Detecting growth hormone variants (GH1), useful in screening patients for  
 PT growth hormone irregularities, comprises comparing the nucleotide  
 PT sequence of a GH1 gene from a test sample with that of a standard  
 PT sequence of the human GH1.  
 XX  
 PS  
 XX

Claim 20; Fig 7; 95pp; English.

CC The invention described a method of detecting variation in growth hormone  
 CC 1 (GH1), and therefore GH dysfunction in an individual. The method  
 CC comprises comparing the nucleotide sequence of GH1 gene obtained from the  
 CC test sample with a standard human GH1 gene sequence, in order to identify  
 CC variation (GH1 variant). The method is useful in screening patients for

CC growth hormone irregularities or producing variant proteins for treating  
 CC irregularities, and for the early detection and appropriate clinical  
 CC management of familial GH deficiency. The GH1 variants are useful in  
 CC therapeutic, diagnostic or detection method, particularly for determining  
 CC binding defects and susceptibility to a disease such as diabetes, obesity  
 CC or infection; for treating acromegaly or gigantism conditions associated  
 CC with lactogenic, diabetogenic, lipolytic and protein anabolic effects,  
 CC conditions associated with sodium and water retention, metabolic  
 CC syndromes, mood and sleep disorders; diagnosing GH dysfunction and  
 CC determining pituitary storage defects. The GH1 variants are especially  
 CC useful in gene therapy or protein therapy. The GH1 or GH variant may also  
 CC be used in the preparation of a medicament, diagnostics composition or  
 CC kit, or detection kit. The method has the advantage of: expanding the  
 CC known spectrum of GH1 gene mutations; evaluating the role of GH1 gene  
 CC mutations in the etiology of short stature; identifying of the mode of  
 CC inheritance of novel lesions; evaluation of the effects of GH1 mutations on  
 CC the structure and function of the GH molecule and development of rapid  
 CC diagnostic tests for inherited GH deficiency. This sequence is a variant  
 CC of human growth hormone 1 (GH1), created from the GH1 wild type sequence  
 CC (AAU11719) given in figure 6 and one of many variations of the gene  
 CC discussed in the method of the invention  
 XX

SQ Sequence 217 AA;

Query Match 98.3%; Score 1029.5; DB 5; Length 217;  
 Best Local Similarity 93.1%; Pred. No. 1.4e-87;  
 Matches 202; Conservative 0; Mismatches 0; Indels 15; Gaps 1;

QY 1 MATGRTSLILAFGLICLPWLQGSAPFTIPISRLFDNLSLAHRHQAFTYQGF--- 57  
 DB 1 MATGRTSLILAFGLICLPWLQGSAPFTIPISRLFDNLSLAHRHQAFTYQGF--- 57  
 QY 58 -----NPOTSLCFSESIPTPSNREBTQOKSNIELIRISILLIQSWLEPVQFLR 105  
 DB 61 YIPKOKSYFLONPOTSLCFSSSIPTPSNREBTQOKSNIELIRISILLIQSWLEPVQFLR 120  
 QY 106 SVFANSLVYGASDSNVYDLKDLREGIOTLMGRLEDSPRTGOIFKQYTSKPDNNSHND 165  
 DB 121 SVFANSLVYGASDSNVYDLKDLREGIOTLMGRLEDSPRTGOIFKQYTSKPDNNSHND 180  
 QY 166 ALKNYGLLYCFERKMDKVEFTFLRIYQCRSVGSGCF 202  
 DB 181 ALKNYGLLYCFERKMDKVEFTFLRIYQCRSVGSGCF 217

## RESULT 8

AAU11730  
 ID AAU11730 standard; protein; 217 AA.

AC AAU11730;  
 DT 12-MAR-2002 (first entry)  
 XX

DE Growth hormone 1 gene (GH1), K67R mutant.

KW Growth hormone 1; GH1, osteopathic; gene therapy; protein therapy;  
 KW diabetes; obesity; infection; acromegaly; gigantism; sodium retention;  
 KW water retention; metabolic syndrome; mood disorder; sleep disorder;  
 KW Growth hormone dysfunction; familial growth hormone deficiency;  
 KW short stature; pituitary storage defect; human; mutant; mutein.

OS Homo sapiens.  
 OS Synthetic.

FT Key Location/Qualifiers  
 FT Misc-difference 67 /note= "Wild type Lys substituted by Arg"

FN WO200185993-A2.  
 XX  
 PD 15-NOV-2001.  
 XX  
 PF 14-MAY-2001; 2001WO-GB002126.

us-09-856-796b-2.rag

XX	13-AUG-2002 (first entry)
DT	
XX	
XX	Human growth hormone (hGH).
DE	
XX	
KW	Transcellular transport; transcytotic transport; paracellular transport
KW	respiratory system disorder; lung cancer; tumour; asthma;
KW	pathogenic infection; allergy-related disorder;
KW	gastrointestinal tract disorder; gastrointestinal hormone disorder;
KW	Chron's disease; eating disorder; polyimmunoglobulin receptor; pIgR.
XX	

AA Homo sapiens.  
OS  
XX  
XX W0200228408-A2.  
PN  
XX  
PD 11-APR-2002.

XX  
PF 02-OCT-2001; 2001WO-US030832.

02-OCT-2000; 2000US-0237929P.  
PR 13-NOV-2000; 2000US-0248478P.  
PR 14-NOV-2000; 2000US-0248819P.  
PR 09-FEB-2001; 2001US-0267601P.  
XX (ARIZ-) ARIZKEE PHARM INC.  
XX  
XX  
PI Houston IL, Sheridan PJ, Hawley S, Glynn JM, Chapin S, Basu A;  
XX  
XX WPI; 2002-416628/44.  
XX  
XX N-PSDB; ABR81192.  
XX  
PT Complex useful for transporting active agent through epithelial barrier,  
PT has biologically active portion and target element directed to ligand  
PT that confers e.g. transcytotic properties to agent specific to ligand.  
XX  
XX  
XX Disclosure; Fig 22; 379pp; English.  
XX  
XX The invention described a complex or compound (I) comprising a  
CC biologically active portion and a target element (II) directed to a  
CC ligand that confers transcellular, transcytotic or paracellular  
CC transporting properties to an agent specifically bound to the ligand,  
CC where (II) is not an antibody. Alternatively, (I) comprises two or  
CC (II) directed to one or more ligands. (I) is useful for delivering a  
CC biologically active agent to an animal, for transporting an active agent  
CC through an epithelial or mucosal barrier, and for treating or identifying  
CC a disease in an animal e.g. diseases of the respiratory system including

20

00

CC disease or disorder involving polymorphisms in a gene  
CC displaying cells. This is the amino acid sequence of a protein associated  
CC with the transport of biologically active agents across cellular barriers

50. b

•

Db 181 ALKKNVGLYCFRRMDKVFPLRIYVCRSVESGCGF 217

RESULT 10

AAU11742 standard; protein; 217 AA.

AAU11742;

12-MAR-2002 (first entry)

Growth hormone 1 gene (GH1), V1361 mutant.

Growth hormone 1; GH1; osteopathic; gene therapy; protein therapy; diabetes; obesity; infection; acromegaly; gigantism; sodium retention; water retention; metabolic syndrome; mood disorder; sleep disorder; Growth hormone dysfunction; familial growth hormone deficiency; short stature; pituitary storage defect; human; mutant; mutain.

OS Homo sapiens.

OS Synthetic.

Key Location/Qualifiers

Misc-difference 136

/note= "wild type Val substituted by Ile"

MO200185993-A2.

15-NOV-2001.

14-MAY-2001; 2001WO-GB002126.

12-MAY-2000; 2000GB-00011459.

14-JUL-2000; 2000EP-00306004.

(UYMA-) UNIV WALES COLLEGE OF MEDICINE.

Cooper DN, Procter AM, Gregory J, Millar DS;

WPI; 2002-089798/12.

Detecting growth hormone variants (GH1), useful in screening patients for sequence of a GH1 gene from a test sample with that of a standard sequence of the human GH1.

Claim 18; Page; 95pp; English.

The invention described a method of detecting variation in growth hormone 1 (GH1), and therefore GH dysfunction in an individual. The method comprises comparing the nucleotide sequence of GH1 gene obtained from the test sample with a standard human GH1 gene sequence, in order to identify variation (GH1 variant). The method is useful in screening patients for growth hormone irregularities or producing variant proteins for treating irregularities, and for the early detection and appropriate clinical management of familial GH deficiency. The GH1 variants are useful in binding defects and susceptibility to a disease such as diabetes, obesity with lactogenic, diabetogenic, lipolytic and protein anabolic associated conditions associated with sodium and water retention, metabolic syndromes, mood and sleep disorders; diagnosing GH dysfunction and determining pituitary storage defects. The GH1 variants are especially useful in gene therapy or protein therapy. The GH1 or GH variant may also be used in the preparation of a medicament, diagnostics composition or kit, or detection kit. The method has the advantage of: expanding the know spectrum of GH1 gene mutations; evaluating the role of GH1 gene mutations in the etiology of short stature; identifying the mode of inheritance of novel lesions; evaluation of the effects of GH1 mutations on the structure and function of the GH molecule and development of rapid diagnostic tests for inherited GH deficiency. This sequence is a variant of human growth hormone 1 (GH1), one of many variations of the gene discussed in the method of the invention. Note: This sequence does not.

CC appear in the specification but has been created from the GH1 wild type  
CC sequence (AAU11719) given in figure 6  
XX  
SQ Sequence 217 AA;

Query Match 98.2%; Score 1028.5; DB 5; Length 217;  
Best Local Similarity 92.6%; Pred. No. 1.7e-87;  
Matches 201; Conservative 1; Mismatches 0; Indels 15; Gaps 1;

1 MATGRTSLAFAGLCTPWLQESAFPTIPISRLFDNALSRAHRLQALPDTYGEF--- 57

1 MATGRTSLAFAGLCTPWLQESAFPTIPISRLFDNALSRAHRLQALPDTYGEFBEA 60

58 -----NPQTSICFSESIPTPENREETQKSNLELRISLLLIQSWLEPVQPLR 105

61 YIPKQKYSPLQNPQTSICFSESIPTPENREETQKSNLELRISLLLIQSWLEPVQPLR 120

106 SVFANSIYVYGASDSNVYDLDKLEBGIQTLMLGRLEDSPTGQIFKQTSKPTDND 165

121 SVFANSIYVYGASDSNVYDLDKLEBGIQTLMLGRLEDSPTGQIFKQTSKPTDND 180

166 ALKKNVGLYCFRRMDKVFPLRIYVCRSVESGCGF 202

181 ALKKNVGLYCFRRMDKVFPLRIYVCRSVESGCGF 217

RESULT 11

AAU11726 standard; protein; 217 AA.

AAU11726;

12-MAR-2002 (first entry)

Growth hormone 1 gene (GH1), 130V mutant.

Growth hormone 1; GH1; osteopathic; gene therapy; protein therapy; diabetes; obesity; infection; acromegaly; gigantism; sodium retention; water retention; metabolic syndrome; mood disorder; sleep disorder; Growth hormone dysfunction; familial growth hormone deficiency; short stature; pituitary storage defect; human; mutant; mutain.

OS Homo sapiens.

OS Synthetic.

Key Location/Qualifiers

Misc-difference 30

/note= "wild type Ile substituted by Val"

MO200185993-A2.

15-NOV-2001.

14-MAY-2001; 2001WO-GB002126.

12-MAY-2000; 2000GB-00011459.

14-JUL-2000; 2000EP-00306004.

(UYMA-) UNIV WALES COLLEGE OF MEDICINE.

Cooper DN, Procter AM, Gregory J, Millar DS;

WPI; 2002-089798/12.

Detecting growth hormone variants (GH1), useful in screening patients for growth hormone irregularities, comprises comparing the nucleotide sequence of a GH1 gene from a test sample with that of a standard sequence of the human GH1.

Claim 18; Page; 95pp; English.

The invention described a method of detecting variation in growth hormone 1 (GH1), and therefore GH dysfunction in an individual. The method

comprises comparing the nucleotide sequence of GH1 gene obtained from the test sample with a standard human GH1 gene sequence, in order to identify variation (GH1 variant). The method is useful in screening patients for growth hormone irregularities or producing variant proteins for treating irregularities, and for the early detection and appropriate clinical management of familial GH deficiency. The GH1 variants are useful in therapeutic, diagnostic or detection method, particularly for determining binding defects and susceptibility to a disease such as diabetes, obesity or infection; for treating acromegaly or gigantism conditions associated with lactogenic, diabetogenic, lipolytic and protein anabolic effects, conditions associated with sodium and water retention, metabolic syndromes, mood and sleep disorders; diagnosing GH dysfunction and determining pituitary storage defects. The GH1 variants are especially useful in gene therapy or protein therapy. The GH1 or GH variant may also be used in the preparation of a medicament, diagnostic composition or kit, or detection kit. The method has the advantage of: expanding the know spectrum of GH1 gene mutations; evaluating the role of GH1 gene mutations in the etiology of short stature; identifying of the mode of inheritance of novel lesions; evaluation the effects of GH1 mutations on the structure and function of the GH molecule and development of rapid diagnostic tests for inherited GH deficiency. This sequence is a variant of human growth hormone 1 (GH1), one of many variations of the gene discussed in the method of the invention. Note: This sequence does not appear in the specification but has been created from the GH1 wild type sequence (AAU11719) given in figure 6

Sequence 217 AA:

Query Match 98.2%; Score 1028.5; DB 5; Length 217;  
Best Local Similarity 92.6%; Pred. No. 1.7e-87;  
Matches 201; Conservative 1; Mismatches 0; Indels 15; Gaps 1;

1 MATGSRSTLLAFGLCLPWLQEGSAFPTPLSRFDNASLRARHLHQAADPTYOEF-- 57  
1 MATGSRSTLLAFGLCLPWLQEGSAFPTPLSRFDNASLRARHLHQAADPTYOEFBEA 60  
58 -----NPQTSICFSESIPTPSNRETOOKSNLELRISLLIQSWLEVPQFLR 105  
61 YIPKQKYSFLQNPQTSICFSESIPTPSNRETOOKSNLELRISLLIQSWLEVPQFLR 120  
106 SVFANSLLVYGASDSNVYDLKDLBEGIQTLMRLEBDSRPTQGIKQYTSKPTDTSND 165  
121 SVFANSLLVYGASDSNVYDLKDLBEGIQTLMRLEBDSRPTQGIKQYTSKPTDTSND 180  
166 ALKNYGLLYCPRKMDKVFELRIVQCRSVEGSCGF 202  
181 ALKNYGLLYCPRKMDKVFELRIVQCRSVEGSCGF 217

RESULT 12

AAU11746 standard; protein; 217 AA.

AAU11746;

12-MAR-2002 (first entry)

Growth hormone 1 gene (GH1), K194R mutant.

Growth hormone 1; GH1; osteopathic; gene therapy; protein therapy;  
diabetes; obesity; infection; acromegaly; gigantism; sodium retention;  
water retention; metabolic syndrome; mood disorder; sleep disorder;  
growth hormone dysfunction; familial growth hormone deficiency;  
short stature; pituitary storage defect; human; mutant; mutein.

Homo sapiens.

Synthetic.

Location/Qualifiers

Key MISC-difference 194 /note= "Wild type Lys substituted by Arg"

MO200185993-A2.

15-NOV-2001.  
14-MAY-2001; 2001WO-GB002126.  
12-MAY-2000; 2000GB-00011459.  
14-JUL-2000; 2000EP-00306004.  
(UYWA-) UNIV WALES COLLEGE OF MEDICINE.  
Cooper DN, Procter AM, Gregory J, Miller DS;  
WPI; 2002-089798/12.

Detecting growth hormone variants (GH1), useful in screening patients for growth hormone irregularities, comprises comparing the nucleotide sequence of a GH1 gene from a test sample with that of a standard sequence of the human GH1.

Claim 18; Page; 95pp; English.

The invention described a method of detecting variation in growth hormone 1 (GH1), and therefore GH dysfunction in an individual. The method comprises comparing the nucleotide sequence of GH1 gene obtained from the test sample with a standard human GH1 gene sequence, in order to identify variation (GH1 variant). The method is useful in screening patients for growth hormone irregularities or producing variant proteins for treating irregularities, and for the early detection and appropriate clinical management of familial GH deficiency. The GH1 variants are useful in therapeutic, diagnostic or detection method, particularly for determining binding defects and susceptibility to a disease such as diabetes, obesity or infection; for treating acromegaly or gigantism conditions associated with lactogenic, diabetogenic, lipolytic and protein anabolic effects, conditions associated with sodium and water retention, metabolic syndromes, mood and sleep disorders; diagnosing GH dysfunction and determining pituitary storage defects. The GH1 variants are especially useful in gene therapy or protein therapy. The GH1 or GH variant may also be used in the preparation of a medicament, diagnostic composition or kit, or detection kit. The method has the advantage of: expanding the know spectrum of GH1 gene mutations; evaluating the role of GH1 gene mutations in the etiology of short stature; identifying of the mode of inheritance of novel lesions; evaluation the effects of GH1 mutations on the structure and function of the GH molecule and development of rapid diagnostic tests for inherited GH deficiency. This sequence is a variant of human growth hormone 1 (GH1), one of many variations of the gene discussed in the method of the invention. Note: This sequence does not appear in the specification but has been created from the GH1 wild type sequence (AAU11719) given in figure 6

Sequence 217 AA:

Query Match 98.0%; Score 1026.5; DB 5; Length 217;  
Best Local Similarity 92.6%; Pred. No. 2.6e-87;  
Matches 201; Conservative 1; Mismatches 0; Indels 15; Gaps 1;

1 MATGSRSTLLAFGLCLPWLQEGSAFPTPLSRFDNASLRARHLHQAADPTYOEF-- 57  
1 MATGSRSTLLAFGLCLPWLQEGSAFPTPLSRFDNASLRARHLHQAADPTYOEFBEA 60  
58 -----NPQTSICFSESIPTPSNRETOOKSNLELRISLLIQSWLEVPQFLR 105  
61 YIPKQKYSFLQNPQTSICFSESIPTPSNRETOOKSNLELRISLLIQSWLEVPQFLR 120  
106 SVFANSLLVYGASDSNVYDLKDLBEGIQTLMRLEBDSRPTQGIKQYTSKPTDTSND 165  
121 SVFANSLLVYGASDSNVYDLKDLBEGIQTLMRLEBDSRPTQGIKQYTSKPTDTSND 180  
166 ALKNYGLLYCPRKMDKVFELRIVQCRSVEGSCGF 202  
181 ALKNYGLLYCPRKMDKVFELRIVQCRSVEGSCGF 217

RESULT 13

Query Match	97.9%	Score 1025.5	DB 5	Length 217
Best local similarity	92.6%	Pred. No. 3.3e-87		
Matches 201	Conservative 1	Mismatches 0	Indels 15	Gaps 1
QY	1	MATSSRSLIAEGLCLPWLQSGSAPPTPLSRLEFDNASTLRHRLHQAFLDPTYOER---	57	
DB	1	MATSSRSLIAEGLCLPWLQSGSAPPTPLSRLEFDNASTLRHRLHQAFLDPTYOER	60	
QY	58	-----NPQSLCSSESIPPPSNEETQOKSNLELRISLLIQSWLEPVQFLR	105	
DB	61	YIPEOKYSPLQNPQSLCSSESIPPPSNEETQOKSNLELRISLLIQSWLEPVQFLR	120	
QY	106	SVPANSIVYGASDSNNYDILKLQEEGIQTLMGRLDGSPRTQGIKQIYSKFDYNSHND	165	
DB	121	SVPANSIVYGASDSNNYDILKLQEEGIQTLMGRLDGSPRTQGIKQIYSKFDYNSHND	180	
QY	166	ALKKNYGLYCERKMDKVEYELFRIVQCSVSGSGCF	202	
DB	181	ALKKNYGLYCERKMDKVEYELFRIVQCSVSGSGCF	217	
RESULT 14				
ID	AAU11735			
XX	AAU11735	standard; protein; 217 AA.		
AC	AAU11735;			
XX				
DT	12-MAR-2002	(first entry)		
XX				
DE	Growth hormone 1 gene (GH1), E100K mutant.			
XX				
KW	Growth hormone 1; GH1; osteopathic; gene therapy; protein therapy;			
KW	diabetes; obesity; infection; acromegaly; gigantism; sodium retention;			
KW	water retention; metabolic syndrome; mood disorder; sleep disorder;			
KW	Growth hormone dysfunction; familial growth hormone deficiency;			
KW	short stature; pituitary storage defect; human; mutant; mutein.			
XX				
OS	Homo sapiens.			
OS	Synthetic.			
XX				
FH	Key	Location/Qualifiers		
FT	Misc-difference 100			
FT	/note= "Wild type Glu substituted by Lys"			
XX	W0200185993-A2.			
XX				
PD	15-NOV-2001.			
XX				
PF	14-MAY-2001; 2001WO-GB002126.			
XX				
PR	12-MAY-2000; 2000GB-00011459.			
XX	14-JUL-2000; 2000EP-00306004.			
XX				
PA	(UYMA-) UNITV WALES COLLEGE OF MEDICINE.			
XX				
PI	Cooper DN, Procter AM, Gregory J, Millar DS;			
XX				
DR	WPI; 2002-089798/12.			
XX				
PT	Detecting growth hormone variants (GH1), useful in screening patients for			
PT	growth hormone irregularities, comprises comparing the nucleotide			
PT	sequence of a GH1 gene from a test sample with that of a standard			
PT	sequence of the human GH1.			
XX				
PS	Claim 18; Page; 95pp; English.			
XX				
CC	The invention described a method of detecting variation in growth hormone			
CC	1 (GH1), and therefore GH dysfunction in an individual. The method			
CC	comprises comparing the nucleotide sequence of GH1 gene obtained from the			
CC	test sample with a standard human GH1 gene sequence.			

14-MAY-2001; 2001WO-GB002126.

. Job time : 167 Secs

Search completed: February 6, 2005, 13:01:28  
Job time : 167 secs

GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: February 6, 2005, 12:45:33 ; Search time 174 Seconds

(without alignments)  
594.483 Million cell updates/sec

Title: US-09-856-796B-2

Perfect score: 1047

Sequence: 1 MATGSRITSLIAFGILCLPW.....KMTFLRIVQCRSEVSGSGF 202

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 1612378 segs, 512079187 residues

Total number of hits satisfying chosen parameters: 1612378

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database: 1: uniprot\_sprot:\*  
2: uniprot\_trembl:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1024.5	97.9	217	1	SOMA_HUMAN
2	1020.5	97.5	217	1	O61YE1
3	1018.5	97.3	217	1	SOMA_PANTR
4	1016.5	97.1	217	2	O61YF0
5	981.5	93.7	217	1	SOMA_MACMU
6	957	91.4	202	2	O14643
7	955.5	91.3	217	1	SOMA_PANTR
8	945.5	90.3	217	2	O6FH54
9	939.5	89.7	217	1	SOMA_HUMAN
10	939.5	89.7	217	2	O6FH32
11	908.5	86.8	217	2	O8WNE0
12	904.5	86.4	217	1	SOMA_SALIB
13	895.5	85.5	217	1	SOMA_CALJA
14	882.5	84.3	217	2	O866U1
15	872.5	83.3	217	1	CSH_HUMAN
16	870.5	83.1	217	2	O6PF11
17	866.5	82.8	217	2	O07369
18	855.5	81.7	217	2	O866T8
19	853.5	81.5	217	2	O866U0
20	850.5	81.2	217	2	O07367
21	831.5	79.4	212	2	O07368
22	829.5	79.2	217	1	SOMA_MACMU
23	779.5	74.5	199	2	O14406
24	754.5	72.1	217	2	O8WNE0
25	751.5	71.8	217	2	O8WNE0
26	728.5	63.6	217	2	O8WNE0
27	726.5	63.4	217	2	O866T9
28	702	67.0	216	1	SOMA_BALPH
29	670	67.0	216	2	O7YOB8
30	701	67.0	216	2	O7YOB8
31	696	66.5	216	2	O7YRR6

32	694	66.3	216	1	SOMA_PIG
33	693	66.2	216	1	SOMA_HORSE
34	688	65.7	216	2	O70615
35	687	65.6	216	1	SOMA_CANPA
36	687	65.6	216	1	SOMA_FELCA
37	682	65.1	216	1	SOMA_MESAU
38	682	65.1	216	1	SOMA_RABIT
39	681	65.0	217	2	O28957
40	679	64.9	216	1	SOMA_MOUSE
41	679	64.9	217	1	SOMA_CEREL
42	678	64.8	217	2	O7YQD2
43	677	64.7	217	1	SOMA_BOVIN
44	677	64.7	217	2	O864S7
45	673.5	64.3	167	2	P78451

## ALIGNMENTS

RESULT 1	ID	STANDARD	PRT	217 AA
AC	SOMA_HUMAN			
AD	P01241; Q14405; Q16531; Q9HBZ1; Q9UMJ7; Q9UNL5;			
DT	21-JUL-1986 (Rel. 01, Created)			
DT	01-MAR-1992 (Rel. 21, Last sequence update)			
DT	25-OCT-2004 (Rel. 45, Last annotation update)			
DE	Somatotropin precursor (Growth hormone) (GH) (GH-N) (Pituitary growth hormone) (Growth hormone 1).			
GN	Name=GH1;			
OS	Homo sapiens (Human).			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.			
OX	NCBI_Taxid=9606;			
RN	[1]			
RP	SEQUENCE FROM N.A. (ISOFORM 1).			
RX	MEDLINE=80034477; PubMed=386281;			
RA	Roskam W., Rougeon F.;			
RT	"Molecular cloning and nucleotide sequence of the human growth hormone structural gene.";			
RL	Nucleic Acids Res. 7:305-320(1979).			
RN	[2]			
RP	SEQUENCE FROM N.A. (ISOFORM 1).			
RX	MEDLINE=79203293; PubMed=377496;			
RA	Martini J.A., Halliwell R.A., Baxter J.D., Goodman H.M.;			
RT	"Human growth hormone: complementary DNA cloning and expression in bacteria.";			
RL	Science 205:602-607(1979).			
RN	[3]			
RP	SEQUENCE FROM N.A. (ISOFORM 1), AND POSSIBLE ALTERNATIVE SPLICING.			
RX	MEDLINE=82014939; PubMed=6269091;			
RA	Danoto F.M., Moore D.D., Goodman H.M.;			
RT	"Human growth hormone DNA sequence and mRNA structure: possible alternative splicing.";			
RL	Nucleic Acids Res. 9:3719-3730(1981).			
RN	[4]			
RP	SEQUENCE FROM N.A.			
RX	MEDLINE=83182010; PubMed=7169009;			
RA	Seeburg P.H.;			
RT	"The human growth hormone gene family: nucleotide sequences show recent divergence and predict a new polypeptide hormone.";			
RL	DNA 1:239-249(1982).			
RN	[5]			
RP	SEQUENCE FROM N.A.			
RX	MEDLINE=89307277; PubMed=2744760;			
RA	Chen E.Y., Liao Y.C., Smith D.H., Barrera-Saldana H.A., Gelinas R.E., Seeburg P.H.;			
RT	"The human growth hormone locus: nucleotide sequence, biology, and evolution.";			
RL	Genomics 4:479-497(1989).			
RN	[6]			
RP	SEQUENCE FROM N.A. (ISOFORM 3).			
RT	TISSUE=Pituitary;			
RA	Gu J., Huang Q.-H., Li N., Xu S.-H., Han Z.-G., Fu G., Chen Z.;			

RT "A novel gene expressed in human pituitary.";  
 RL Submitted (SEP-1999) to the EMBL/GenBank/DBJ databases.  
 RN [17]  
 RP SEQUENCE FROM N.A. (ISOFORM 4).  
 RC TISSUE=Pituitary;  
 RL MEDLINE=20402571; PubMed=10931946; DOI=10.1073/pnas.160270997;  
 RA Hu R.-M., Han Z.-G., Song H.-D., Peng Y.-D., Huang Q.-H., Ren S.-X.,  
 RA Gu Y.-J., Huang C.-H., Li Y.-B., Jiang C.-L., Fu G., Zhang Q.-H.,  
 RA Gu B.-W., Dai M., Mao Y.-F., Gao G.-F., Rong R., Ye M., Zhou J.,  
 RA Huang G.-Y., Chen Z., Chen M.-D., Chen J.-L.,  
 RA "Gene expression profiling in the human hypothalamus-pituitary-adrenal  
 RT axis and full-length cDNA cloning.";  
 RL Proc. Natl. Acad. Sci. U.S.A. 97:9543-9548(2000).  
 RN [8]  
 RP SEQUENCE OF 1-26 FROM N.A.  
 RC MEDLINE=86137393; PubMed=3912261; DOI=10.1016/0378-1119(85)90319-1;  
 RA Gray G.L., Baldrige J.S., McKean K.S., Heyneker H.L., Chang C.N.,  
 RT "Periplasmic production of correctly processed human growth hormone in  
 RT Escherichia coli: natural and bacterial signal sequences are  
 RT interchangeable.";  
 RL Gene 39:247-254(1985).  
 RN [9]  
 RP SEQUENCE OF 27-217.  
 RC MEDLINE=69289202; PubMed=5810834;  
 RA Li C.H., Dixon J.S., Liu W.-K.,  
 RT "Human pituitary growth hormone. XIX. The primary structure of the  
 RT hormone.";  
 RL Arch. Biochem. Biophys. 133:70-91(1969).  
 RN [10]  
 RP SEQUENCE OF 27-217, AND REVISIONS.  
 RC MEDLINE=72143935; PubMed=5144027;  
 RA Li C.H., Dixon J.S.,  
 RT "Human pituitary growth hormone. 32. The primary structure of the  
 RT hormone: revision.";  
 RL Arch. Biochem. Biophys. 146:233-236(1971).  
 RN [11]  
 RP REVISION.  
 RC MEDLINE=73092028; PubMed=4675454;  
 RA Bewley T.A., Dixon J.S., Li C.H.,  
 RT "Sequence comparison of human pituitary growth hormone, human  
 RT chorionic somatomammotropin, and ovine pituitary growth and lactogenic  
 RT hormones.";  
 RL Int. J. Pept. Protein Res. 4:281-287(1972).  
 RN [12]  
 RP SEQUENCE OF 27-61 AND 102-124.  
 RC MEDLINE=71139765; PubMed=5279046;  
 RA Niall H.D.,  
 RT "Revised primary structure for human growth hormone.";  
 RL Nature New Biol. 230:90-91(1971).  
 RN [13]  
 RP REVISIONS TO 119-120 AND 157-159.  
 RC MEDLINE=71153968; PubMed=5279528;  
 RA Niall H.D., Hogan M.L., Sauer R., Rosenblum I.Y., Greenwood F.C.,  
 RT "Sequences of pituitary and placental lactogenic and growth hormones:  
 RT evolution from a primordial peptide by gene reduplication.";  
 RL Proc. Natl. Acad. Sci. U.S.A. 68:866-869(1971).  
 RN [14]  
 RP REVISION.  
 RC MEDLINE=81117361; PubMed=7462247;  
 RA Niall H.D.,  
 RT "The chemistry of the human lactogenic hormones.";  
 RL (in) Griffiths K. (eds.), Proc. fourth tenous workshop prolactin,  
 RL prolactin and carcinogenesis, Proc. fourth tenous workshop prolactin,  
 RL pp.13-20, Alpha Omega Alpha Press, Cardiff (1972).  
 RN [15]  
 RP SEQUENCE OF 27-79 (ISOFORM 2).  
 RC MEDLINE=81117361; PubMed=7462247;  
 RA Chapman G.E., Rogers K.M., Brittain T., Bradshaw R.A., Bates O.J.,  
 RT "The 20,000 molecular weight variant of human growth hormone.  
 RT Preparation and some physical and chemical properties.";  
 RL J. Biol. Chem. 256:2395-2401(1981).  
 RN [16]

RP SEQUENCE OF 46-80 (ISOFORM 2).  
 RX MEDLINE=80130196; PubMed=7356479;  
 RA Lewis U.J., Bonewald L.F., Lewis L.J.,  
 RT "The 20,000-dalton variant of human growth hormone: location of the  
 RT amino acid deletions.";  
 RL Biochem. Biophys. Res. Commun. 92:511-516(1980).  
 RN [17]  
 RP DEMINATION OF GLN-163 AND ASN-178.  
 RC MEDLINE=82052997; PubMed=7028740;  
 RA Lewis U.J., Singh R.N., Bonewald L.F., Seavey B.K.,  
 RT "Altered proteolytic cleavage of human growth hormone as a result of  
 RT deamidation.";  
 RL J. Biol. Chem. 256:11645-11650(1981).  
 RN [18]  
 RP PHOSPHORYLATION SITES SER-132 AND SER-176.  
 RC TISSUE=Pituitary;  
 RL MEDLINE=14997482; DOI=10.1002/pmic.200300584;  
 RA Giorgianni F., Beranova-Giorgianni S., Desiderio D.M.,  
 RT "Identification and characterization of phosphorylated proteins in the  
 RT human pituitary.";  
 RL Proteomics 4:587-598(2004).  
 RN [19]  
 RP REVIEW.  
 RC MEDLINE=99321812; PubMed=10393484; DOI=10.1159/000053128;  
 RA Baumann G.,  
 RT "Growth hormone heterogeneity in human pituitary and plasma.";  
 RL Horm. Res. 51 Suppl. 1:2-6(1999).  
 RN [20]  
 RP 3D-STRUCTURE MODELING.  
 RC MEDLINE=88190073; PubMed=3447173;  
 RA Cohen F.B., Kuntz I.D.,  
 RT "Prediction of the three-dimensional structure of human growth  
 RT hormone.";  
 RL Proteins 2:162-166(1987).  
 RN [21]  
 RP X-RAY CRYSTALLOGRAPHY (2.8 ANGSTROMS).  
 RC MEDLINE=92196577; PubMed=1549776;  
 RA de Vos A.M., Ultsch M., Kossiakoff A.A.,  
 RT "Human growth hormone and extracellular domain of its receptor:  
 RT crystal structure of the complex.";  
 RL Science 255:306-312(1992).  
 RN [22]  
 RP X-RAY CRYSTALLOGRAPHY (2.9 ANGSTROMS).  
 RC MEDLINE=95075462; PubMed=7984244; DOI=10.1038/372478a0;  
 RA Somers W., Ultsch M., de Vos A.M., Kossiakoff A.A.,  
 RT "The X-ray structure of a growth hormone-prolactin receptor complex.";  
 RL Nature 372:478-481(1994).  
 RN [23]  
 RP X-RAY CRYSTALLOGRAPHY (2.5 ANGSTROMS).  
 RC MEDLINE=96150232; PubMed=8552145; DOI=10.1074/jbc.271.50.32197;  
 RA Chantalat L., Chirgadze N.Y., Jones N., Korber F., Navaza J.,  
 RT "The crystal-structure of wild-type growth-hormone at 2.5-A  
 RT resolution.";  
 RL Protein Pept. Lett. 2:333-340(1995).  
 RN [24]  
 RP X-RAY CRYSTALLOGRAPHY (2.5 ANGSTROMS).  
 RC MEDLINE=97113023; PubMed=8943276; DOI=10.1074/jbc.271.50.32197;  
 RA Sundstroem M., Lundqvist T., Roedin J., Giebel L.B., Milligan D.,  
 RT "Crystal structure of an antagonist mutant of human growth hormone,  
 RT G120R, in complex with its receptor at 2.9-A resolution.";  
 RL J. Biol. Chem. 271:32197-32203(1996).  
 RN [25]  
 RP VARIANT KOWARSKI SYNDROME CYS-103.  
 RC MEDLINE=96150232; PubMed=8552145; DOI=10.1056/NEJM199602153340704;  
 RA Takahashi Y., Kaji H., Okimura Y., Goji K., Abe H., Chihara K.,  
 RT "Short stature caused by a mutant growth hormone.";  
 RL N. Engl. J. Med. 334:432-436(1996).  
 RN [26]  
 RP ERRATUM.  
 RA Takahashi Y., Kaji H., Okimura Y., Goji K., Abe H., Chihara K.,  
 RL N. Engl. J. Med. 334:1207-1207(1996).  
 RN [27]



RP VARIANT KOMARSKI SYNDROME GUY-138.  
RX MEDLINE=97426478; PubMed=9276733;

Query Match 97.9%; Score 1024.5; DB 1; Length 217;  
Best Local Similarity 92.6%; Pred. No. 8.2e-85;  
Matches 201; Conservative 0; Mismatches 1; Indels 15; Gaps 1;

QY 1 MATGSRSTLLAFGLICLPMLOEGSAFPTIPLSRLFDNASLRARHLHOLAFPTYOEF--- 57  
DB 1 MATGSRSTLLAFGLICLPMLOEGSAFPTIPLSRLFDNASLRARHLHOLAFPTYOEFEEA 60  
QY 58 -----NPTSICFSESIPTPSNRETOOKSNLELRISLLIQSWLEVPQFLR 105  
DB 61 YIPKQKXSPFONPOTSLCFSESIPTPSNRETOOKSNLELRISLLIQSWLEVPQFLR 120  
QY 106 SVFANSILVYGASDSNVVDLLKDLLEGIGIOTLMGRLEDGSPRTGQIFKQYTSKFDTNSHND 165  
DB 121 SVFANSILVYGASDSNVVDLLKDLLEGIGIOTLMGRLEDGSPRTGQIFKQYTSKFDTNSHND 180  
QY 166 ALLKNYGLLYCFRDMKVETFLRIVQCRSVGSGCF 202  
DB 181 ALLKNYGLLYCFRDMKVETFLRIVQCRSVGSGCF 217

## RESULT 2

Q61YF1 PRELIMINARY; PRT; 217 AA.  
AC 061YF1; (Tremblrel. 27, Created)  
DT 05-JUL-2004 (Tremblrel. 27, Last sequence update)  
DT 05-JUL-2004 (Tremblrel. 27, Last annotation update)  
DE Growth hormone 1 variant 1.  
GN Name=GH1;  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
OX NCBI\_Taxid=9606;  
RN [1]  
RP SEQUENCE FROM N.A.  
RA Jorge A.A.L., Arnold I.J.P., Mendonca B.B.;  
RL Submitted (APR-2004) to the EMBL/GenBank/DBJ databases.  
DR HSSP; A613431; AAT11508.1; -  
DR HSSP; P01241; IA22.  
DR GO; GO:0005576; C:extracellular; IEA.  
DR GO; GO:0005179; F:hormone activity; IEA.  
DR InterPro; IPR009079; 4 helix cytokine.  
DR InterPro; IPR001400; Somatotropin.  
DR Pfam; PF00103; Hormone\_1; 1.  
DR PRINTS; PR00836; SOMATOTROPIN.  
DR PROSITE; PS00266; SOMATOTROPIN\_1; 1.  
DR PROSITE; PS00338; SOMATOTROPIN\_2; 1.  
SQ SEQUENCE 217 AA; 24875 MW; 12DB1B92F63934D8 CRC64;

Query Match 97.5%; Score 1020.5; DB 2; Length 217;  
Best Local Similarity 92.2%; Pred. No. 1.9e-84;  
Matches 200; Conservative 0; Mismatches 2; Indels 15; Gaps 1;

QY 1 MATGSRSTLLAFGLICLPMLOEGSAFPTIPLSRLFDNASLRARHLHOLAFPTYOEF--- 57  
DB 1 MATGSRSTLLAFGLICLPMLOEGSAFPTIPLSRLFDNASLRARHLHOLAFPTYOEFEEA 60  
QY 58 -----NPTSICFSESIPTPSNRETOOKSNLELRISLLIQSWLEVPQFLR 105  
DB 61 YIPKQKXSPFONPOTSLCFSESIPTPSNRETOOKSNLELRISLLIQSWLEVPQFLR 120  
QY 106 SVFANSILVYGASDSNVVDLLKDLLEGIGIOTLMGRLEDGSPRTGQIFKQYTSKFDTNSHND 165  
DB 121 SVFANSILVYGASDSNVVDLLKDLLEGIGIOTLMGRLEDGSPRTGQIFKQYTSKFDTNSHND 180  
QY 166 ALLKNYGLLYCFRDMKVETFLRIVQCRSVGSGCF 202  
DB 181 ALLKNYGLLYCFRDMKVETFLRIVQCRSVGSGCF 217

## RESULT 3

SOMA\_PANTR STANDARD; PRT; 217 AA.  
ID SOMA\_PANTR  
AC P58756;  
DT 28-FEB-2003 (Rel. 41, Created)  
DT 28-FEB-2003 (Rel. 41, Last sequence update)  
DT 05-JUL-2004 (Rel. 44, Last annotation update)  
DE Somatotropin precursor (Growth hormone) (GH) (GH-N) (Pituitary growth hormone) (Growth hormone 1).  
GN Name=GH1;  
OS Pan troglodytes (Chimpanzee).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Pan.  
OX NCBI\_Taxid=9598;  
RN [1]  
RP SEQUENCE FROM N.A.  
RA Revol A., Seguel D., Santiago D., Barrera-Saldana H.;  
RT "Independent duplication of the growth hormone gene in three Anthropoid lineages."  
RL Submitted (APR-2001) to the EMBL/GenBank/DBJ databases.  
CC -1- FUNCTION: Plays an important role in growth control. Its major role in stimulating body growth is to stimulate the liver and other tissues to secrete IGF-1. It stimulates both the differentiation and proliferation of myoblasts. It also stimulates amino acid uptake and protein synthesis in muscle and other tissues (By similarity).  
CC -1- SUBCELLULAR LOCATION: Secreted.  
CC -1- SIMILARITY: Belongs to the somatotropin/prolactin family.  
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CC

DR EMBL; AF374232; AAL72284.1; -  
DR HSSP; P01241; IHMG.  
DR InterPro; IPR009079; 4 helix cytokine.  
DR InterPro; IPR001400; Somatotropin.  
DR Pfam; PF00103; Hormone\_1; 1.  
DR PRINTS; PR00836; SOMATOTROPIN.  
DR PROSITE; PS00266; SOMATOTROPIN\_1; 1.  
DR PROSITE; PS00338; SOMATOTROPIN\_2; 1.  
KW Hormone; Pituitary; Signal.  
FT SIGNAL 1 26 By similarity.  
FT CHAIN 27 217 Somatotropin.  
FT DISULFID 79 191 By similarity.  
FT DISULFID 208 215 By similarity.  
SQ SEQUENCE 217 AA; 24843 MW; FEA295DEB0518674 CRC64;

Query Match 97.3%; Score 1018.5; DB 1; Length 217;  
Best Local Similarity 92.2%; Pred. No. 2.9e-84;  
Matches 200; Conservative 0; Mismatches 2; Indels 15; Gaps 1;

QY 1 MATGSRSTLLAFGLICLPMLOEGSAFPTIPLSRLFDNASLRARHLHOLAFPTYOEF--- 57  
DB 1 MATGSRSTLLAFGLICLPMLOEGSAFPTIPLSRLFDNASLRARHLHOLAFPTYOEFEEA 60  
QY 58 -----NPTSICFSESIPTPSNRETOOKSNLELRISLLIQSWLEVPQFLR 105  
DB 61 YIPKQKXSPFONPOTSLCFSESIPTPSNRETOOKSNLELRISLLIQSWLEVPQFLR 120  
QY 106 SVFANSILVYGASDSNVVDLLKDLLEGIGIOTLMGRLEDGSPRTGQIFKQYTSKFDTNSHND 165  
DB 121 SVFANSILVYGASDSNVVDLLKDLLEGIGIOTLMGRLEDGSPRTGQIFKQYTSKFDTNSHND 180  
QY 166 ALLKNYGLLYCFRDMKVETFLRIVQCRSVGSGCF 202  
DB 181 ALLKNYGLLYCFRDMKVETFLRIVQCRSVGSGCF 217

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RESULT 4
Q61YFO PRELIMINARY; PRT; 217 AA.
ID Q61YFO
AC Q61YFO
DT 05-JUL-2004 (TREMBLrel. 27, Created)
DT 05-JUL-2004 (TREMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TREMBLrel. 27, Last annotation update)
DE Growth hormone 1 variant 2.
GN Name=GHI;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OC NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Jorje A.A.L., Arnold I.J.P., Mendonca B.B.;
RL Submitted (Apr-2004) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY613432; AAT1509.1; -
DR HSSP; P01241; IAXI.
DR GO; GO:0005576; C:extracellular; IEA.
DR GO; GO:0005179; F:hormone activity; IEA.
DR InterPro; IPR009079; 4_helix_cytokine.
DR InterPro; IPR001400; Somatotropin.
DR Pfam; PF00103; Hormone_1; 1.
DR PRINTS; PR00836; SOMATOTROPIN.
DR PROSITE; PS00266; SOMATOTROPIN_1; 1.
DR PROSITE; PS00338; SOMATOTROPIN_2; 1.
SQ SEQUENCE 217 AA; 24946 MW; 72D079D52BD51A CRC64;

Query Match 97.1%; Score 1016.5; DB 2; Length 217;
Best Local Similarity 92.2%; Pred. No. 4.4e-84;
Matches 200; Conservative 0; Mismatches 2; Indels 15; Gaps 1;

QY 1 MATGSRSTLLAFGLCLPMLQSGSAFPTIPLSRLFDNASLRARHLQLAFTYQEF--- 57
DB 1 MATGSRSTLLAFGLCLPMLQSGSAFPTIPLSRLFDNASLRARHLQLAFTYQEFBEA 60
QY 58 -----NPQTSLCFSSESIPTPSNREETOQKSNLELRISLLIQSWLEPVQFLR 105
DB 61 YIPKEQKYSFLQNPQTSLCFSSESIPTPSNREETOQKSNLELRISLLIQSWLEPVQFLR 120
QY 106 SVFANSLVYGASDSNVYDLKDLKEGIIQTLKGRLEDSGSRITQIFKQYTSKPTDTHSHND 165
DB 121 SVFANSLVYGASDSNVYDLKDLKEGIIQTLKGRLEDSGSRITQIFKQYTSKPTDTHSHND 180
QY 166 ALIKNYGLYCFRKMDKVFETFLRIYQCRSVESGCGF 202
DB 181 ALIKNYGLYCFRKMDKVFETFLRIYQCRSVESGCGF 217

RESULT 5
SOWA MACMU STANDARD; PRT; 217 AA.
ID SOWA MACMU
AC P33053;
DT 01-OCT-1993 (Rel. 27, Created)
DT 01-OCT-1994 (Rel. 30, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Somatotropin precursor (Growth hormone) (GH) (GH-N) (Pituitary growth hormone) (Growth hormone 1).
GN Name=GHI;
OS Macaca mulatta (Rhesus macaque).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Cercopitheciidae;
OC Cercopitheciidae; Macaca.
OC NCBI_TaxID=9544;
RN [1]
RP SEQUENCE FROM N.A.
RA MEDLINE=94008724; PubMed=8404617; DOI=10.1210/en.133.4.1744;
RA Golos T.G., Durning M., Fisher J.M., Fowler P.D.;
DE "Cloning of four growth hormone/chorionic somatomotropin-related complementary deoxyribonucleic acids differentially expressed during pregnancy in the rhesus monkey placenta.";

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RL Endocrinology 133:1744-1752 (1993).
RN [2]
RP SEQUENCE OF 27-217.
RX MEDLINE=86129460; PubMed=3080959;
RA Li C.H., Chung D., Lahm H.W., Stein S.;
RT "The primary structure of monkey pituitary growth hormone.";
RL Arch. Biochem. Biophys. 245:287-291(1986).
CC -1- FUNCTION: Plays an important role in growth control. Its major role in stimulating body growth is to stimulate the liver and other tissues to secrete IGF-1. It stimulates both the differentiation and proliferation of myoblasts. It also stimulates amino acid uptake and protein synthesis in muscle and other tissues.
CC -1- SUBCELLULAR LOCATION: Secreted.
CC -1- SIMILARITY: Belongs to the somatotropin/prolactin family.
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CC EMBL; L16556; AAA18842.1; -
CC PIR; I67410; I67410.
CC HSSP; P01241; IAXI.
CC InterPro; IPR009079; 4_helix_cytokine.
CC InterPro; IPR001400; Somatotropin.
CC Pfam; PF00103; Hormone_1; 1.
CC PRINTS; PR00836; SOMATOTROPIN.
CC PROSITE; PS00266; SOMATOTROPIN_1; 1.
CC PROSITE; PS00338; SOMATOTROPIN_2; 1.
CC Direct protein sequencing; Hormone; Pituitary; Signal.
CC KW SIGNAL 1 26
CC CHAIN 27 217 Somatotropin.
CC DISULFID 79 191 By similarity.
CC DISULFID 208 215 By similarity.
CC CONFLICT 100 100 E -> Q (in Ref. 2).
CC CONFLICT 179 179 N -> D (in Ref. 2).
SQ SEQUENCE 217 AA; 24913 MW; 2C5180341ECC46D0 CRC64;

Query Match 93.7%; Score 981.5; DB 1; Length 217;
Best Local Similarity 88.9%; Pred. No. 6.6e-81;
Matches 193; Conservative 3; Mismatches 6; Indels 15; Gaps 1;

QY 1 MATGSRSTLLAFGLCLPMLQSGSAFPTIPLSRLFDNASLRARHLQLAFTYQEF--- 57
DB 1 MATGSRSTLLAFGLCLPMLQSGSAFPTIPLSRLFDNASLRARHLQLAFTYQEFBEA 60
QY 58 -----NPQTSLCFSSESIPTPSNREETOQKSNLELRISLLIQSWLEPVQFLR 105
DB 61 YIPKEQKYSFLQNPQTSLCFSSESIPTPSNREETOQKSNLELRISLLIQSWLEPVQFLR 120
QY 106 SVFANSLVYGASDSNVYDLKDLKEGIIQTLKGRLEDSGSRITQIFKQYTSKPTDTHSHND 165
DB 121 SVFANSLVYGASDSNVYDLKDLKEGIIQTLKGRLEDSGSRITQIFKQYTSKPTDTHSHND 180
QY 166 ALIKNYGLYCFRKMDKVFETFLRIYQCRSVESGCGF 202
DB 181 ALIKNYGLYCFRKMDKVFETFLRIYQCRSVESGCGF 217

RESULT 6
ID O14643 PRELIMINARY; PRT; 202 AA.
AC O14643;
DT 01-JAN-1998 (TREMBLrel. 05, Created)
DT 01-JAN-1998 (TREMBLrel. 05, Last sequence update)
DT 01-MAR-2004 (TREMBLrel. 26, Last annotation update)
DE Placental growth hormone 20kDa isoform precursor.
GN Name=HG-V;
OS Homo sapiens (Human).

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CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
CC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
CC NCB1_TaxID=9606;
CC [1]
CC SEQUENCE FROM N.A.
CC TISSUE=full-term placenta;
CC MEDLINE=9837337; PubMed=9709963; DOI=10.1210/jc.83.8.2878;
CC Boguszewski C.L., Svensson P.A., Jansson T., Clark R.,
CC Carlsson L.M.S., Carlsson B.,
CC "Cloning of two novel growth hormone transcripts expressed in human
CC placenta."
CC J. Clin. Endocrinol. Metab. 83:2878-2885 (1998).
CC EMBL; AF006060; AAB71828.1;
CC HSSP; P01241; 1A22.
CC GO; GO:0005576; C:extracellular; IEA.
CC GO; GO:0005179; F:hormone activity; IEA.
CC InterPro; IPR009079; 4_helix_cytokine.
CC Pfam; PF00103; Hormone_1; 1.
CC PRINTS; PR00836; SOMATOTROPIN.
CC PROSITE; PS00266; SOMATOTROPIN_1; 1.
CC PROSITE; PS00338; SOMATOTROPIN_2; 1.
CC SIGNAL.
CC FT SIGNAL.
CC FT CHAIN.
CC FT DISULFID.
CC FT DISULFID.
CC SEQUENCE 202 AA; 23128 MW; 38B64D011A9197C6 CRC64;

Query Match 91.4%; Score 957; DB 2; Length 202;
Best Local Similarity 92.6%; Pred. No. 1e-78;
Matches 187; Conservative 4; Mismatches 11; Indels 0; Gaps 0;

QY 1 MATGSRRTSLIAFGLCLPWLQEGSAPPTPLSLRFPNASLRARHLQLAFTDYQEFNPQ 60
DB 1 MAAGSRRTSLIAFGLCLPWLQEGSAPPTPLSLRFPNASLRARHLQLAFTDYQEFNPQ 60
QY 61 TSLCFSSISIPSPSNEETQOKSNELRLISILLIQSWLEPVQFLRSVPANSLVYGASDSN 120
DB 61 TSLCFSSISIPSPSNEETQOKSNELRLISILLIQSWLEPVQFLRSVPANSLVYGASDSN 120
QY 121 VYDLKDLREGIQTLMGRLEDSGSPRTGQIFKQYTSKEDPTNSHNDALKNYGLLYCRKO 180
DB 121 VYDLKDLREGIQTLMGRLEDSGSPRTGQIFKQYTSKEDPTNSHNDALKNYGLLYCRKO 180
QY 121 VYHLKDLREGIQTLMGRLEDSGSPRTGQIFKQYTSKEDPTNSHNDALKNYGLLYCRKO 180
DB 121 VYHLKDLREGIQTLMGRLEDSGSPRTGQIFKQYTSKEDPTNSHNDALKNYGLLYCRKO 180
QY 181 MDKVFETFLRIVQCRSVGSGCF 202
DB 181 MDKVFETFLRIVQCRSVGSGCF 202
QY 181 MDKVFETFLRIVQCRSVGSGCF 202
DB 181 MDKVFETFLRIVQCRSVGSGCF 202

RESULT 7
SOM2_PANTR
ID SOM2_PANTR STANDARD; PRT; 217 AA.
AC P58757;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Growth hormone variant precursor (GH-V) (Placenta-specific growth
DE hormone) (growth hormone 2).
GN Name=GH2;
OS Pan troglodytes (Chimpanzee).
CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
CC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Pan.
CC NCB1_TaxID=9598;
CC [1]
CC SEQUENCE FROM N.A.
CC Revol A., Esquivel D., Santiago D., Barrera-Saldana H.;
CC "Independent duplication of the growth hormone gene in three
CC Antropoidcan lineages."
CC Submitted (Apr-2001) to the EMBL/GenBank/DBJ databases.
CC -i- FUNCTION: Plays an important role in growth control. Its major
CC role in stimulating body growth is to stimulate the liver and
CC other tissues to secrete IGF-1. It stimulates both the
CC differentiation and proliferation of myoblasts. It also stimulates
CC amino acid uptake and protein synthesis in muscle and other
CC tissues.

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CC -i- SUBCELLULAR LOCATION: Secreted.
CC -i- TISSUE SPECIFICITY: Expressed in the placenta.
CC -i- SIMILARITY: Belongs to the somatotropin/prolactin family.
CC -----
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CC -----
CC EMBL; AF374233; AAL72285.1;
CC HSSP; P01241; 1A22.
CC InterPro; IPR009079; 4_helix_cytokine.
CC InterPro; IPR001400; Somatotropin.
CC Pfam; PF00103; Hormone_1; 1.
CC PRINTS; PR00836; SOMATOTROPIN.
CC PROSITE; PS00266; SOMATOTROPIN_1; 1.
CC PROSITE; PS00338; SOMATOTROPIN_2; 1.
CC Glycoprotein; Hormone; Placenta; Signal.
CC SIGNAL.
CC FT CHAIN.
CC FT DISULFID.
CC FT DISULFID.
CC SEQUENCE 217 AA; 24990 MW; 1592A429075677DE CRC64;

Query Match 91.3%; Score 955.5; DB 1; Length 217;
Best Local Similarity 87.1%; Pred. No. 1.5e-78;
Matches 189; Conservative 4; Mismatches 9; Indels 15; Gaps 1;

QY 1 MATGSRRTSLIAFGLCLPWLQEGSAPPTPLSLRFPNASLRARHLQLAFTDYQEF--- 57
DB 1 MAAGSRRTSLIAFGLCLPWLQEGSAPPTPLSLRFPNASLRARHLQLAFTDYQEFBEA 60
QY 58 -----NPOISLCSSESIPTPSNEETQOKSNELRLISILLIQSWLEPVQFLR 105
DB 61 YILKEQKSYFLQNPQISLCSSESIPTPSNWKVQOKSNELRLISILLIQSWLEPVQFLR 120
QY 106 SVFANSLVYGASDSNVDLKLDEGEGITLMGRLEDSGSPRTGQIFKQYTSKEDPTNSHND 165
DB 121 SVFANSLVYGASDSNVDLKLDEGEGITLMGRLEDSGSPRTGQIFKQYTSKEDPTNSHND 180
QY 166 ALLKNYGLLYCPRKMDKVFETFLRIVQCRSVGSGCF 202
DB 181 ALLKNYGLLYCPRKMDKVFETFLRIVQCRSVGSGCF 217

RESULT 8
O6FH54
ID O6FH54 PRELIMINARY; PRT; 217 AA.
AC O6FH54;
DT 05-JUL-2004 (TREMBLrel. 27, Created)
DT 05-JUL-2004 (TREMBLrel. 27, Last sequence update)
DE Growth hormone variant precursor (GH-V) (Placenta-specific growth
DE hormone) (growth hormone 2).
GN Name=GH2;
OS Homo sapiens (Human).
CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
CC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
CC NCB1_TaxID=9606;
CC [1]
CC SEQUENCE FROM N.A.
CC Hallack A., Ebert L., Moundinya M., Schick M., Eisenstein S.,
CC Neubert P., Kistrang K., Schatten R., Shen B., Henze S., Mar W.,
CC Korn B., Zuo D., Hu Y., Labaer J.;
CC Submitted (JUN-2004) to the EMBL/GenBank/DBJ databases.
CC EMBL; CR541902; CAG46700.1;
CC GO; GO:0005576; C:extracellular; IEA.
CC GO; GO:0005179; F:hormone activity; IEA.
CC InterPro; IPR009079; 4_helix_cytokine.
CC InterPro; IPR001400; Somatotropin.
CC Pfam; PF00103; Hormone_1; 1.

```

RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,  
RA Klausner R.D., Collins F.S., Wagner L., Shemmen C.M., Schuler G.D.,  
RA Altschul S.F., Ziegler B., Buetow K.H., Schaefer C.F., Bhat N.K.,  
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang Y., Hsieh P.,  
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,  
RA Stupliscion M., Soares M.B., Bonaldi M.F., Casavant T.L., Scheetz T.E.,  
RA Brownstein M.U., Ueda T.B., Toshiyuki S., Carinci P., Prange C.,  
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,  
RA Bosak S.A., McKernan P.J., McKernan K.J., Malek J.A., Gnatratie P.H.,  
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Huliy S.W.,  
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,  
RA Fahy J., Helton E., Kettelman M., Madan A., Rodrigues S., Sanchez A.,  
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,  
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,  
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,  
RA Buttefield Y.S.N., Krzyzanski M.I., Skalka U., Smalhus D.E.,  
RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.,  
RA "Generation and initial analysis of more than 15,000 full-length human  
RA and mouse cDNA sequences." ;  
RA Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).  
RL [6]  
RN REVIEW  
RP MEDLINE=99321812; PubMed=10393484; DOI=10.1159/000053128;  
RX Baumann G.;  
RL "Growth hormone heterogeneity in human pituitary and plasma." ;  
RL Horm. Res. 51 Suppl. 1:2-6(1999).  
CC -I- FUNCTION: plays an important role in growth control. Its major  
CC role in stimulating body growth is to stimulate the liver and  
CC other tissues to secrete IGF-1. It stimulates both the  
CC differentiation and proliferation of myoblasts. It also stimulates  
CC amino acid uptake and protein synthesis in muscle and other  
CC tissues.  
CC -I- SUBUNIT: Monomer, dimer, trimer, tetramer and pentamer, disulfide-  
CC linked or non-covalently associated, in homopolymeric and  
CC heteropolymeric combinations. Can also form a complex either with  
CC GHBP or with the alpha2-macroglobulin complex.  
CC -I- SUBCELLULAR LOCATION: Secreted.  
CC -I- ALTERNATIVE PRODUCTS:  
CC Event=Alternative splicing; Named isoforms=2;  
CC Name=1; Synonyms=GH-V1;  
CC IsoId=P01242-1; Sequence=Displayed;  
CC Name=2; Synonyms=GH-V2;  
CC IsoId=P01242-2; Sequence=VSP\_006203;  
CC IsoId=P01242-2; Sequence=VSP\_006203;  
CC Note=No experimental confirmation available;  
CC -I- TISSUE SPECIFICITY: Expressed in the placenta.  
CC -I- SIMILARITY: Belongs to the somatotropin/prolactin family.  
CC -----  
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CC -----  
CC EMBL; J00470; AAA98619.1; -  
CC EMBL; J03756; AAB59547.1; -  
CC EMBL; J03756; AAB59548.1; -  
CC EMBL; M38451; AAA55891.1; -  
CC EMBL; J03071; AAA52552.1; -  
CC EMBL; BC020760; AAH20760.1; -  
CC PIR; A28072; STHU2.  
CC PIR; D32435; STHUV.  
CC HSSP; P01241; 1A22.  
CC Genew; HGNC:4262; GH2.  
CC H-invDB; HIX0014071; -  
CC MIM; 139240; -  
CC GO; GO:0005179; F: hormone activity; TAS.  
CC InterPro; IPR009079; 4\_helix\_cytokine.  
CC InterPro; IPR001400; Somatotropin.  
CC Pfam; PF00103; Hormone 1; 1.  
CC PRINTS; PR00836; SOMATOTROPIN.  
CC PROSITE; PS00266; SOMATOTROPIN\_1; 1.  
CC -----

	Query Match	89.7%	Score 930.5	DB 1	Length 217
	Best Local Similarity	86.2%	Pred. 4.3e-77		
	Matches 187	Conservative 4	Mismatches 11	Indels 15	Gaps 1
Qy	1	MATGSRISLLA	FGILCLPWLQSGSAPFTIPLSRLEFDNANLRAHLOHQAFTTYQGF---	57	
Db	1	MAAGSRISLLA	FGILCLSWLQSGSAPFTIPLSRLEFDNANLRAHLYQALAYTYQGFEBEA	60	
Qy	58	-----NOTSLCFSEBSITPTPSNRBEETQOKSNIELLIRISLLIQSWLEBQVQFLR		105	
Db	61	YILKEQKYSFLQNTQSTLCFSEBSIPTPSNRVYTOOKSNIELLIRISLLIQSWLEBQVQLLR		120	
Qy	106	SVPANSLVYGASDSNVVDLLKDLBEGITLWGLREDGSPRTGOIKQKQYKSFDTNSHND		165	
Db	121	SVPANSLVYGASDSNVYRHLKDLBEGITLWRLLEDGSPRTGOIFNOSYSKFTYKSHND		180	
Qy	166	ALLKNYVLLCFRRDMNKVETFLAIRIVQCRSVESGCGF	202		
Db	181	ALLKNYVLLCFRRDMNKVETFLAIRIVQCRSVESGCGF	217		

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RESULT 10
06FH32 ID 06FH32 PRELIMINARY; PRT; 217 AA.
AC 06FH32;
DT 05-JUL-2004 (TREMblrel. 27, Created)
DT 05-JUL-2004 (TREMblrel. 27, Last sequence update)
DE CH2 protein (TREMblrel. 27, Last annotation update)
GN Name=CH2;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Halleck A., Ebert L., Moundinya M., Schick M., Eisenstein S.
RA Neubert P., Ketrang K., Schacten R., Shen B., Henze S., Mar V
RA Korn B., Zhu D., Hu Y., Labaer J.;
RL Submitted (JUN-2004) to the EMBL/GenBank/DBJ databases.
DR EMBL; C5541924; CAG46722.1; -
DR GO; GO:0005576; Cxetracellular; IEA.
DR GO; GO:0005179; Fhormone activity; IEA.
DR InterPro; IPR009079; Fhormone cyclif.
DR InterPro; IPR001400; Somatotropin.
DR Pfam; PF00103; Hormone 1; 1.
DR PRINTS; PR00836; SOMATOTROPIN.
DR PROSITE; PS00266; SOMATOTROPIN_1; 1.
DR PROSITE; PS00338; SOMATOTROPIN_2; 1.
FT NON TER 217
SQ SEQUENCE 217 AA; 25010 MW; 075C0EF63C15A85 CRC64;
Query Match 89.7%; Score 939.5; DB 2; Length 217;
Best Local Similarity 86.2%; P-Val. No. 4.3e-77;

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RESULT 11
ORNNED0
ID Q8WNE0 PRELIMINARY; PR7; 217 AA.
AC Q8WNE0;
DT 01-MAR-2002 (TREMBLrel. 20, Created)
DT 01-MAR-2002 (TREMBLrel. 20, Last sequence update)
DT 01-MAR-2004 (TREMBLrel. 26, Last annotation update)
DE Growth hormone.
GN Name=GH-N;
OS Ateles geoffroyi (Black-handed spider monkey).
OC Eumaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Platyrrhini; Cebidae; Ateleinae; Ateles
OX NCBI_TaxID=9509;
RN [1]
RP SEQUENCE FROM N.A.
R1 Revol A., Baquivel D., Santiago D., Barrera-Saldana H.,
RL Submitted (APR-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL: AB74234; AAL72286.1; -.
DR HSSP: P01241; IA22.
GO GO:0005576; C:extracellular; IEA.
GO GO:0005179; F:hormone activity; IEA.
DR Pfam: PF00103; Hormone_1; 1.
DR PRINTS: PR00836; SOMATOTROPIN.
DR PROSITE: PS00266; SOMATOTROPIN_1; 1.
DR PROSITE: PS00387; SOMATOTROPIN_2; 1.
SQ 217 AA; 24894 MM; 425829PF41EEAA6 CRC64;

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Query Match	Best Local Similarity	86.8%;	Score 908.5;	DB 2;	Length 217;
Matches 178;	Conservative 11;	Mismatches 13;	Indels 15;	Gaps 1	
Qy	1	MATGASTLLAFAGLCLPMLQEGSAFPITTPLSRLFDNNLSRAHRLHQLAFDTYQEF---	57		
Db	1	MAGSRTSLLLAFTLLCLPQLQEGAGAFPITPSRLLDNMLRAHRLHQLAFDTYQEEEA	60		
Qy	58	-----NPQSLCFSESIPPSNRRETSQKSNELLRLISLLLIQSWLEPVOFLR	105		
Db	61	YIPKQKTSFLONPQTSICFSESIPTPASKKETQKSNELLRLISLLLIQSWMEPQFLR	120		
Qy	106	SVFANSLVYGASDSNVVYDLKDLREGIQTLMLRELDGSPRTQIQFYQTSKEDPTNSHND	165		
Db	121	SVFANSLLVYGSDSDVYEYKLDLKEGIIQTLMLRELDGSPQTGEIFRQYTRKEDINSQND	180		
Qy	166	ALLKNYGLLYCPRKMDKVEFELRLVQCRSVGSGCGF	202		
Db	181	ALLKNYGLLYCPRKMDKVEFELRLVQCRSVGSGCGF	217		

DT 05-JUL-2004 (Rel. 44, last annotation update)  
 DE Somatotropin precursor (Growth hormone).  
 GN Name=GHI;  
 OS Saimiri boliviensis boliviensis (Bolivian squirrel monkey).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 CC Mammalia; Eutheria; Primates; Platyrrhini; Cebidae; Cebinae; Saimiri.  
 NCBI\_TaxID=9483;  
 RX [1]  
 RN SEQUENCE FROM N.A.  
 RA MEDLINE=21265430; PubMed=11371582;  
 RT Liu J.C., Makova K.D., Adkins R.M., Gibson S., Li W.H.;  
 RL "Episodic evolution of growth hormone in primates and emergence of the  
 species specificity of human growth hormone receptor";  
 Mol. Biol. Evol. 18:945-953(2001).  
 CC -1- FUNCTION: Plays an important role in growth control. Its major  
 CC role in stimulating body growth is to stimulate the liver and  
 CC other tissues to secrete IGF-1. It stimulates both the  
 CC differentiation and proliferation of myoblasts. It also stimulates  
 CC amino acid uptake and protein synthesis in muscle and other  
 CC tissues (By similarity).  
 CC -1- SUBCELLULAR LOCATION: Secreted.  
 CC -1- SIMILARITY: Belongs to the somatotropin/prolactin family.  
 CC  
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 CC or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).  
 CC  
 CC EMBL; AF339060; AAK62287.1; -  
 CC HSSP; P01241; I422.  
 CC InterPro; IPR009079; 4 helix cytokine.  
 CC InterPro; IPR001400; Somatotropin.  
 CC Pfam; PF00103; Hormone\_1.1.  
 CC PRINTS; PR00836; SOMATOTROPIN.  
 CC PROSITE; PS00266; SOMATOTROPIN\_1; 1.  
 CC PROSITE; PS00338; SOMATOTROPIN\_2; 1.  
 CC Hormone; Pituitary; Signal.  
 CC KW Hormone; Pituitary; Signal.  
 CC FT SIGNAL 1 26 By similarity.  
 CC FT CHAIN 27 217 Somatotropin.  
 CC FT DISULFID 79 191 By similarity.  
 CC FT DISULFID 208 215 By similarity.  
 CC SQ SEQUENCE 217 AA; 24864 MW; 9515289992C529F7 CRC64;  
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 CC Query Match 86.4%; Score 904.5; DB 1; Length 217;  
 CC Best Local Similarity 82.0%; Pred. No. 6,4e-74;  
 CC Matches 178; Conservative 10; Mismatches 14; Indels 15; Gaps 1;  
 CC  
 CC QY 1 MATGSRSTLLAAGLCLPWLQEGSAPPTIPLSRLFDNASLRARHLHQLAFTTYOEF-- 57  
 CC DB 1 MATGSRSTLLAAGLCLPWLQEGSAPPTIPLSRLFDNASLRARHLHQLAFTTYOEFBEA 60  
 CC QY 58 -----NPQSLCFSESIPTPSNRETOOKSNLELRISLLILIQSWLEPVQFLR 105  
 CC DB 61 YIPKQKYSFLQNPQSLCFSESIPTPSKKETOOKSNLELRISLLILIQSWLEPVQFLR 120  
 CC QY 106 SVFANSLVYGASDSNVYDLKDLBEGIQTLWRLEDSGSPRTGQIFKQYTSKPDYNSHND 165  
 CC DB 121 SVFANSLLYGASDSNVYDLKDLBEGIQTLWRLEDSGSPRTGAIKQYTSKPDYNSHND 180  
 CC QY 166 ALIKNYGLLYCFRKMDKVFETFLRIYQCRSVGSGCGF 202  
 CC DB 181 ALIKNYGLLYCFRKMDKVFETFLRIYQCRSVGSGCGF 217  
 CC  
 CC RESULT 13  
 CC SOMA\_CALJA STANDARD; PRT; 217 AA.  
 CC AC Q9GMB3; 28-FEB-2003 (Rel. 41, Created)  
 CC DT 28-FEB-2003 (Rel. 41, Last sequence update)

DT 05-JUL-2004 (Rel. 44, last annotation update)  
 DE Somatotropin precursor (Growth hormone).  
 GN Name=GHI;  
 OS Callithrix jacchus (Common marmoset).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 CC Mammalia; Eutheria; Primates; Platyrrhini; Callitrichidae; Callitrix.  
 NCBI\_TaxID=9483;  
 RX [1]  
 RN SEQUENCE FROM N.A.  
 RA Wallis O.C., Wallis M.;  
 RT "Cloning and characterization of a putative growth hormone encoding  
 gene from the marmoset (Callithrix jacchus).";  
 RL Submitted (Aug-2000) to the EMBL/GenBank/DBJ databases.  
 CC -1- FUNCTION: Plays an important role in growth control. Its major  
 CC role in stimulating body growth is to stimulate the liver and  
 CC other tissues to secrete IGF-1. It stimulates both the  
 CC differentiation and proliferation of myoblasts. It also stimulates  
 CC amino acid uptake and protein synthesis in muscle and other  
 CC tissues (By similarity).  
 CC -1- SUBCELLULAR LOCATION: Secreted.  
 CC -1- SIMILARITY: Belongs to the somatotropin/prolactin family.  
 CC  
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 CC or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).  
 CC  
 CC EMBL; AJ297563; CAC03481.1; -  
 CC HSSP; P01241; I422.  
 CC InterPro; IPR009079; 4 helix cytokine.  
 CC InterPro; IPR001400; Somatotropin.  
 CC Pfam; PF00103; Hormone\_1.1.  
 CC PRINTS; PR00836; SOMATOTROPIN.  
 CC PROSITE; PS00266; SOMATOTROPIN\_1; 1.  
 CC PROSITE; PS00338; SOMATOTROPIN\_2; 1.  
 CC KW Hormone; Pituitary; Signal.  
 CC FT SIGNAL 1 26 By similarity.  
 CC FT CHAIN 27 217 Somatotropin.  
 CC FT DISULFID 79 191 By similarity.  
 CC FT DISULFID 208 215 By similarity.  
 CC SQ SEQUENCE 217 AA; 24959 MW; E102151A12CB192 CRC64;  
 CC  
 CC Query Match 85.5%; Score 895.5; DB 1; Length 217;  
 CC Best Local Similarity 81.1%; Pred. No. 4,2e-73;  
 CC Matches 176; Conservative 11; Mismatches 15; Indels 15; Gaps 1;  
 CC  
 CC QY 1 MATGSRSTLLAAGLCLPWLQEGSAPPTIPLSRLFDNASLRARHLHQLAFTTYOEF-- 57  
 CC DB 1 MATGSRSTLLAAGLCLPWLQEGSAPPTIPLSRLFDNASLRARHLHQLAFTTYOEFBEA 60  
 CC QY 58 -----NPQSLCFSESIPTPSNRETOOKSNLELRISLLILIQSWLEPVQFLR 105  
 CC DB 61 YIPKQKYSFLQNPQSLCFSESIPTPSKKETOOKSNLELRISLLILIQSWLEPVQFLR 120  
 CC QY 106 SVFANSLVYGASDSNVYDLKDLBEGIQTLWRLEDSGSPRTGQIFKQYTSKPDYNSHND 165  
 CC DB 121 SVFANSLLYGASDSNVYDLKDLBEGIQTLWRLEDSGSPRTGAIKQYTSKPDYNSHND 180  
 CC QY 166 ALIKNYGLLYCFRKMDKVFETFLRIYQCRSVGSGCGF 202  
 CC DB 181 ALIKNYGLLYCFRKMDKVFETFLRIYQCRSVGSGCGF 217  
 CC  
 CC RESULT 14  
 CC Q866U1 PRELIMINARY; PRT; 217 AA.  
 CC AC Q866U1; 01-JUN-2003 (T-EMBLrel. 24, Created)  
 CC DT 01-JUN-2003 (T-EMBLrel. 24, Last sequence update)  
 CC DT 01-MAR-2004 (T-EMBLrel. 26, Last annotation update)

DE Placental lactogen PL-A.  
 OS Pan troglodytes (Chimpanzee).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Pan.  
 OX NCBI\_TaxID=9598;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RA PubMed=15246530; DOI=10.1016/j.gene.2004.03.034;  
 RX Revol De Mendoza A., Esquivel Escobedo D., Martinez Davila I.,  
 RA Saldana H.;  
 RT "Expansion and divergence of the GH locus between spider monkey and  
 chimpanzee.";  
 RL Gene 336:185-193 (2004).  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RA Revol A., Esquivel D.E., Barrera H.S.;  
 RT "The GH-PL locus a hot-point between human and chimpanzee genomes.";  
 RL Submitted (AUG-2002) to the EMBL/GenBank/DBS databases.  
 DR HSSP; P01241; 1A22.  
 DR GO; GO:0005576; C:extracellular; IEA.  
 DR GO; GO:0005179; F:hormone activity; IEA.  
 DR InterPro; IPR009079; 4 helix cytokine.  
 DR InterPro; IPR01400; Somatotropin.  
 DR Pfam; PF00103; Hormone\_1; 1.  
 DR PRINTS; PR00836; SOMATOTROPIN.  
 DR PROSITE; PS00266; SOMATOTROPIN\_1; 1.  
 DR PROSITE; PS00338; SOMATOTROPIN\_2; 1.  
 SQ SEQUENCE 217 AA; 25081 MW; C74B6262D8A3060 CRC64;  
 Query Match 84.3%; Score 882.5; DB 2; Length 217;  
 Best Local Similarity 80.6%; Pred. No. 6,4e-72;  
 Matches 175; Conservative 9; Mismatches 18; Indels 15; Gaps 1;  
 QY 1 MATGSRSLIAEGLCLPMLQEGSAPPTPLSLFLPNASIRARHLQALADTYQEF-- 57  
 DB 1 MAAGSRSLIAEGLCLPMLQEGSAPPTPLSLFLPNASIRARHLQALADTYQEF-- 60  
 QY 58 -----NPTSLCFSESPTPSNRETOOKNLELRSLILISWLEPVQFLR 105  
 DB 61 YILKEQKVSFLQNPQSLCFSESPTPSNRETOOKNLELRSLILISWLEPVQFLR 120  
 QY 106 SVFASLVVYASDSNVYDLKLEEGIQTMGRLEDSPTGQIFKQTSKEPTNSND 165  
 DB 121 SMFANLVVDTSDSDYHLKLEEGIQTMGRLEDSPTGQILKQTSKEPTNSND 180  
 QY 166 ALLKNTGLLYCPKMDKVFETFLRIYQCRSVESGCGF 202  
 DB 181 ALLKNTGLLYCPKMDKVFETFLRIYQCRSVESGCGF 217  
 Db  
 RESULT 15  
 CSH\_HUMAN STANDARD; PRT; 217 AA.  
 ID CSH\_HUMAN  
 AC P01243; Q14407;  
 DT 21-JUL-1986 (Rel. 01, Created)  
 DT 01-APR-1988 (Rel. 07, Last sequence update)  
 DT 25-OCT-2004 (Rel. 45, Last annotation update)  
 DE Chorionic somatomammotropin hormone precursor (choriomammotropin)  
 DE (Lactogen).  
 GN Name=CSH1;  
 GN and  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
 OX NCBI\_TaxID=9606;  
 RN [1]  
 RP SEQUENCE FROM N.A. (GENE CSH1).  
 RA MEDLINE=85030426; PubMed=6208192;  
 RA Selby M.J., Barta A., Baxter J.D., Bell G.I., Eberhardt N.L.;  
 RT "Analysis of a major human chorionic somatomammotropin gene. Evidence  
 for two functional promoter elements.";

RL J. Biol. Chem. 259:13131-13138 (1984).  
 RN [2]  
 RP SEQUENCE FROM N.A. (GENE CSH2).  
 RX MEDLINE=87161235; PubMed=3030680;  
 RA Hirt H., Kimmelman J., Birnbaum M.J., Chen E.Y., Seeburg P.H.,  
 RA Eberhardt N.L., Barta A.;  
 RT "The human growth hormone gene locus: structure, evolution, and  
 allelic variations.";  
 RL DNA 6:59-70 (1987).  
 RN [3]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=83160916; PubMed=6300056;  
 RA Barrera-Saldana H.A., Seeburg P.H., Saunders G.F.;  
 RT "Two structurally different genes produce the same secreted human  
 placental lactogen hormone.";  
 RL J. Biol. Chem. 258:3787-3793 (1983).  
 RN [4]  
 RP SEQUENCE FROM N.A. (GENES CSH1 AND CSH2).  
 RX MEDLINE=89307277; PubMed=2744760;  
 RA Chen E.Y., Liao Y.C., Smith D.H., Barrera-Saldana H.A., Gelinas R.E.,  
 RA Seeburg P.H.;  
 RT "The human growth hormone locus: nucleotide sequence, biology, and  
 evolution.";  
 RL Genomics 4:479-497 (1989).  
 RN [5]  
 RP SEQUENCE.  
 RX MEDLINE=83182010; PubMed=7169009;  
 RA Seeburg P.H.;  
 RT "The human growth hormone gene family: nucleotide sequences show  
 recent divergence and predict a new polypeptide hormone.";  
 RL DNA 1:239-249 (1982).  
 RN [6]  
 RP SEQUENCE FROM N.A.  
 RX TISSUE=Placenta, and Uterus;  
 RA MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;  
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,  
 RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,  
 RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,  
 RA Hopkins R.F., Jordan H., Moore T., Max S.T., Wang J., Hsieh F.,  
 RA Diatchenko L., Marusik A., Farmer A.A., Rubin G.M., Hong L.,  
 RA Scapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,  
 RA Brownstein M.J., Ustin T.B., Toshiyuki S., Carninci P., Prange C.,  
 RA Bha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mulhally S.J.,  
 RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,  
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,  
 RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,  
 RA Fahy J., Helton E., Kettelman M., Madan A.C., Rodigues S., Sanchez A.,  
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,  
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,  
 RA Butterfield Y.S.N., Krzywicki M.I., Skalska U., Smalhus D.E.,  
 RA Scherch A., Schein J.E., Jones S.J.M., Marra M.A.;  
 RT "Generation and initial analysis of more than 15,000 full-length human  
 Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).  
 RN [7]  
 RP SEQUENCE OF 50-217 FROM N.A.  
 RX MEDLINE=78071761; PubMed=593368;  
 RA Shine J., Seeburg P.H., Martial J.A., Baxter J.D., Goodman H.M.;  
 RT "Construction and analysis of recombinant DNA for human chorionic  
 somatomammotropin.";  
 RL Nature 270:494-499 (1977).  
 RN [8]  
 RP SEQUENCE OF 27-217.  
 RX MEDLINE=73201971; PubMed=4712450;  
 RA Li C.H., Dixon J.S., Chung D.;  
 RT "Amino acid sequence of human chorionic somatomammotropin.";  
 RL Arch. Biochem. Biophys. 155:95-110 (1973).  
 RN [9]  
 RP SEQUENCE OF 27-117.  
 RX MEDLINE=72016313; PubMed=5286363;  
 RA Sherwood L.M., Handwerker S., McLaurin W.D., Lanner M.;  
 RT "Amino-acid sequence of human placental lactogen.";

RL Nature New Biol. 233:59-61 (1971).  
 RN [10]  
 RP ERRATUM.  
 RA Sherwood L.M., Handwerker S., McLaurin W.D., Lanner M.;  
 RL Nature New Biol. 235:64-64 (1972).  
 RN [11]  
 RP INTERCHAIN DISULFIDE BONDS.  
 RX MEDLINE=79173081; PubMed=438159;  
 RA Schneider A.B., Kowalski K., Russell J., Sherwood L.M.;  
 RT "Identification of the interchain disulfide bonds of dimeric human  
 placental lactogen."  
 RL J. Biol. Chem. 254:3782-3787 (1979).  
 CC - FUNCTION: Similar to that of somatotropin.  
 CC - SUBCELLULAR LOCATION: Secreted.  
 CC - MISCELLANEOUS: The sequence of CSH1 is shown.  
 CC - SIMILARITY: Belongs to the somatotropin/prolactin family.  
 CC -----  
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 CC or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).  
 CC -----  
 CC  
 CC EMBL: V00573; CAA23836.1; -  
 CC EMBL: J00289; AAA98747.1; -  
 CC EMBL: K02401; AAA52115.1; -  
 CC EMBL: M15894; AAA52116.1; -  
 CC EMBL: J03071; AAA52551.1; -  
 CC EMBL: J03071; AAA52553.1; -  
 CC EMBL: J00118; AAA98621.1; -  
 CC EMBL: BC002717; AAH02717.1; -  
 CC EMBL: BC005921; AAH05921.1; -  
 CC EMBL: BC020756; AAH20756.1; -  
 CC EMBL: BC022044; AAH22044.1; -  
 CC EMBL: BC035965; AAH35965.1; -  
 CC PIR: A26449; A26449.  
 CC PIR: A26449; A26449.  
 CC PIR: C32435; LCHUC.  
 CC HSSP: P01241; 1A22.  
 CC Genew; HGNC:2440; CSH1.  
 CC Genew; HGNC:2441; CSH2.  
 CC H-InVDB: HIX0014076; -  
 CC MIM: 118820; -  
 CC MIM: 150200; -  
 CC GO: GO:007565; P:pregnancy; TAS.  
 CC InterPro: IPR009079; 4\_helix\_cytokine.  
 CC InterPro: IPR001400; Somatotropin.  
 CC Pfam: PF00103; Hormone\_1; 1.  
 CC PRINTS: PR00836; SOMATOTROPIN.  
 CC PROSITE: PS00286; SOMATOTROPIN\_1; 1.  
 CC PROSITE: PS00338; SOMATOTROPIN\_2; 1.  
 KW Direct protein sequencing; Hormone; Multigene family; Placenta;  
 KW Signal.  
 FT SIGNAL 1 26  
 FT CHAIN 27 217 Choriionic somatomammotropin hormone.  
 FT DISULFID 79 191  
 FT DISULFID 208 215  
 FT DISULFID 208 208  
 FT DISULFID 215 215 Interchain (with C-215 in a dimer).  
 FT VARIANT 3 3 Interchain (with C-208 in a dimer).  
 FT VARIANT 3 3 P -> A (in CSH2; dbSNP:1805274).  
 FT VARIANT 3 3 /FTID=VAR 007166.  
 FT VARIANT 104 105 IS -> L (in CSH2).  
 FT VARIANT 104 105 /FTID=VAR 007167.  
 FT CONFLICT 84 84 I -> T (in Ref. 9).  
 FT CONFLICT 95 95 Missing (in Ref. 9).  
 FT CONFLICT 116 116 Missing (in Ref. 9).  
 FT CONFLICT 134 136 SDD -> BBS (in Ref. 9).  
 SO SEQUENCE 217 AA; 25020 MW; 235B0DC7A713FA31 CRC64;  
 Query Match 83.3%; Score 872.5; DB 1; Length 217;  
 Best local Similarity, 79.3%; Pred. No. 5.2e-71;  
 Matches 172; Conservative 11; Mismatches 19; Indels 15; Gaps 1;

QY 1 MATGSRSTLLAFGLCTPMLQEGSAFPTIPLSRLEFDNASIRAHRLHQLADPTIOEF--- 57  
 Db 1 NAPSRTSLULAFALLCLPMLQEGAGVQTVPLSRLEFDNASIRAHRLHQLADPTIOEFEEET 60  
 QY 58 -----NPQTSICFSESIPTPSNREETQOKSNLELRISILLIISQWLEPVQFLR 105  
 Db 61 YIPKQKYSFLHDSQTSFCFSDSIPTPSNREETQOKSNLELRISILLIISQWLEPVQFLR 120  
 QY 106 SVFANSLVYGASDSNVYDLKDLREGIQTLMRLLEDGSPRTGQIFKQTSKFDTSNHDND 165  
 Db 121 SMFANNLVYDTSDDYHLLKDLREGIQTLMRLLEDGSRRTQILKQTSKFDTSNHDND 180  
 QY 166 ALLKNGYGLLYCFRKMDKVEFLRIYQGRSVGSGCGF 202  
 Db 181 ALLKNGYGLLYCFRKMDKVEFLRIYQGRSVGSGCGF 217

Search completed: February 6, 2005, 13:04:28  
 Job time : 176 secs



GenCore version 5.1.6  
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OM protein - nucleic search, using frame\_plus\_p2n model

Run on: February 7, 2005, 13:27:15 ; Search time 3171 Seconds

(without alignments)  
2424.782 Million cell updates/sec

Title: US-09-856-796b-2

Sequence: 1 MARGRSLIARGLCLPW.....KVFPIRVGCRVSGSGP 202

Scoring table:

BLOSUM62  
Xgapop 10.0 , Xgapext 0.5  
Ygapop 10.0 , Ygapext 0.5  
Fgapop 6.0 , Fgapext 7.0  
Delop 6.0 , Delext 7.0

Searched: 3423544 seqs, 19032134700 residues

Total number of hits satisfying chosen parameters: 68479088

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%  
Listing first 45 summaries

Command line parameters:  
-MODEL=frame+ p2n.model -DEV=xlh  
-Q/cgn2.1/USPTO.spool\_h/US09856796/runat.06022005.12442.2578/app.query.fasta.1.391  
-DB=EST -QFMT=fastcap -SUFFIX=1st -MINMATCH=0.1 -LOOCL=0 -LOOEXT=0  
-UNITS=bits -START=1 -END=-1 -MATRIX=biosum62 -TRANS=human40.cdi -LIST=45  
-DOCLIGN=200 -THR SCORE=pct -THR MAX=100 -THR MIN=0 -ALIGN=15 -MODE=LOCAL  
-OUTFMT=ptc -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=200000000  
-USRR=US09856796 @CGN 1.1 3437 @runat.06022005.12442.2578 -NCPU=6 -ICPU=3  
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-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database :

EST:\*  
1: gb\_est1:\*  
2: gb\_est2:\*  
3: gb\_hic:\*  
4: gb\_est3:\*  
5: gb\_est4:\*  
6: gb\_est5:\*  
7: gb\_est6:\*  
8: gb\_gsa1:\*  
9: gb\_gsa2:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1042	99.5	755	6	CD513951 AGENCOURT
2	1042	99.5	759	6	CD106929 AGENCOURT
3	1042	99.5	770	6	CD105630 AGENCOURT
4	1042	99.5	817	6	CD251386 AGENCOURT
5	1036	98.9	818	6	CD556434 AGENCOURT
6	1025	97.9	768	6	CD108395 AGENCOURT
7	1024.5	97.9	797	6	CD107947 AGENCOURT
8	1024.5	97.9	798	6	CD107985 AGENCOURT
9	1024.5	97.9	800	6	CD251158 AGENCOURT

10	1024.5	97.9	801	6	CD108743 AGENCOURT
11	1024.5	97.9	802	6	CD108698 AGENCOURT
12	1024.5	97.9	802	6	CD513888 AGENCOURT
13	1024.5	97.9	803	6	CD106442 AGENCOURT
14	1024.5	97.9	803	6	CD108431 AGENCOURT
15	1024.5	97.9	804	6	CD105346 AGENCOURT
16	1024.5	97.9	808	6	CD105855 AGENCOURT
17	1024.5	97.9	808	6	CD251173 AGENCOURT
18	1024.5	97.9	809	6	CD105448 AGENCOURT
19	1024.5	97.9	810	6	CD107812 AGENCOURT
20	1024.5	97.9	810	6	CD109024 AGENCOURT
21	1024.5	97.9	811	6	CD108773 AGENCOURT
22	1024.5	97.9	814	6	CD513613 AGENCOURT
23	1024.5	97.9	816	6	CD108302 AGENCOURT
24	1024.5	97.9	817	6	CD513464 AGENCOURT
25	1024.5	97.9	818	6	CD105554 AGENCOURT
26	1024.5	97.9	818	6	CD106266 AGENCOURT
27	1024.5	97.9	818	6	CD106416 AGENCOURT
28	1024.5	97.9	819	6	CD106646 AGENCOURT
29	1024.5	97.9	819	6	CD108015 AGENCOURT
30	1024.5	97.9	819	6	CD108038 AGENCOURT
31	1024.5	97.9	819	6	CD108957 AGENCOURT
32	1024.5	97.9	820	6	CD512822 AGENCOURT
33	1024.5	97.9	820	6	CD105685 AGENCOURT
34	1024.5	97.9	822	6	CD251169 AGENCOURT
35	1024.5	97.9	824	6	CD107683 AGENCOURT
36	1024.5	97.9	824	6	CD513753 AGENCOURT
37	1024.5	97.9	826	6	CD513803 AGENCOURT
38	1024.5	97.9	826	6	CD108434 AGENCOURT
39	1024.5	97.9	831	6	CD109178 AGENCOURT
40	1024.5	97.9	833	6	CD251579 AGENCOURT
41	1024.5	97.9	831	6	CD2512835 AGENCOURT
42	1024.5	97.9	851	6	CD106037 AGENCOURT
43	1024.5	97.9	856	6	CD513085 AGENCOURT
44	1024.5	97.9	861	6	CD513266 AGENCOURT
45	1024.5	97.9	864	6	CD513147 AGENCOURT

## ALIGNMENTS

RESULT 1  
CD513951  
LOCUS  
DEFINITION AGENCOURT 14375351 NIH MGC 179 Homo sapiens CDNA clone  
IMAGE:30353581 5', mRNA sequence.  
ACCESSION CD513951  
VERSION CD513951.1 GI:31445669  
KEYWORDS EST.  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens

REFERENCE 1 (bases 1 to 755)  
AUTHORS NIH-MGC http://mgi.nci.nih.gov/  
TITLES National Institutes of Health, Mammalian Gene Collection (MGC)  
JOURNAL Unpublished (1999)  
COMMENT Contract: Daniela S. Gerhard, Ph.D.  
Office of Cancer Genomics  
National Cancer Institute / NIH  
Bldg. 31 Rm10A07 Bethesda, MD 20892  
Email: cga@bbs-remail.nih.gov  
Tissue Procurement: Dr. Michael Brownstein  
CDNA Library Preparation: Invitrogen Corp  
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)  
DNA Sequencing by: Agencourt Bioscience Corporation  
Clone distribution: MGC clone distribution information can be  
found through the I.M.A.G.E. Consortium/LLNL at:  
http://image.llnl.gov  
Plate: NDAM470 row: 1 column: 06  
High quality sequence stop: 705.  
Location/Qualifiers  
1..755  
/organism="Homo sapiens"

FEATURES  
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/mol\_type="rRNA"  
/db\_xref="taxon:9606"  
/clone="IMAGE:30368973"  
/tissue\_type="Pituitary"  
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/note="Organ: brain; Vector: pCMV-Sport6.1; Site: 1: EcoRV (destroyed); Site 2: NotI; Library is oligo-dT primed and directionally cloned (EcoRV site is destroyed upon cloning). Average insert size 1.1 kb. Library was constructed by (Invitrogen). Note: this is a NIH\_MGC Library."

## ORIGIN

## Alignment Scores:

Score: No.: 1,95e-114 Length: 755  
1042.00 Matches: 201  
Percent Similarity: 99.50% Conservative: 0  
Best Local Similarity: 99.50% Mismatches: 1  
Query Match: 99.52% Indels: 0  
Gaps: 0

US-09-856-796B-2 (1-202) x CD513951 (1-755)

QY 1 MetAlaThrglySerArgThrSerleuLeuAlaPheGlyLeuLeuCyseuProTrp 20  
DB 41 ATGGCTACAGAGCTCCGAGACCTCCCTGCTGCTTGGCTTGCCTGCTGCTGCTG 100  
QY 21 LeuGlnGluGlySerAlaPheProThrIleProLeuSerArgLeuPheAspAsnLaser 40  
DB 101 CTTCAAGAGGCAAGTGCCTTCCACCACTCCCTATCCAGGCTTTTGACAAGCTTANG 160  
QY 41 LeuArgAlaHisArgLeuHisGlnLeuAlaPheAspThrTyrglnGluPheAsnProGln 60  
DB 161 CTCGGCGCCATGCTGTGACACAGCTGGCTTGACACCTACCAGAGATTAAACCCCGAG 220  
QY 61 ThrSerLeuCyseuSerGluSerIleProThrProSerAsnArgGluThrGlnGln 80  
DB 221 ACCTCCTCTGTTTCTCAGAGTCTATTCGACACCTCCACAGGAGGAGAACACACAG 280  
QY 81 LysSerAsnLeuGlnLeuLeuArgIleSerleuLeuLeuIleGlnSerTrpLeuGluPro 100  
DB 281 AAATCCAACTAGAGCTGCTCCGCACTCTCCCTGCTCTCACTCACTGCTGCTGAGGCC 340  
QY 101 ValGlnPheLeuArgSerValPheAlaAsnSerLeuValTyrglnAlaSerAspSerAsn 120  
DB 341 GTGCAGTTCCTCAGAGGTGCTTCCGCAACAGCTGTGTGACCGCGCTCTGACAGCAAC 400  
QY 121 ValTyrrAspLeuLeuLysAspLeuGluGluGlyIleGlnThrLeuMetGlyArgLeuGlu 140  
DB 401 GCTATGAGCTCTTAAAGACCTAGAGAGGATCCAAACGCTGATGGGAGGCTGAAA 460  
QY 141 AspGlySerProArgThrGlyGlnIlePheLeuGlnThrTyrrSerIlePheAspThrAsn 160  
DB 461 GATGGAGGCCCCGAGCTGGGAGATCTTCAAGCAGACCTTACAGAGTTTGACACCAAC 520  
QY 161 SerHisAsnAspAspAlaLeuLeuLysAsnTyrrGlyLeuLeuTyrrCyseuPheArgIleAsp 180  
DB 521 TCACACAAACATGACGCACTACTCAAGAACTACGAGCTGCTACTGCTTACGAGAGAC 580  
QY 181 MetAspLysValGluThrPheLeuArgIleValGlnCyseuSerValGlnGlySerCys 200  
DB 581 ATGACACAAAGTGCAGACATTCCTGCGATCTGTGAGTCCGCTCTGTGAGAGGAGCTGT 640  
QY 201 GlyPhe 202  
DB 641 GGCTTC 646

RESULT 2  
CD106929 759 bp mRNA linear EST 15-MAY-2003  
LOCUS CD106929  
DEFINITION AGENCOURT\_13979169 NIH\_MGC\_179 Homo sapiens cDNA clone  
IMAGE:30368973 5' mRNA sequence.

## ACCESSION

CD106929  
CD106929.1 GI:30760187

## VERSION

EST.

## KEYWORDS

Homo sapiens (human)

## SOURCE

Homo sapiens  
Eukaryote; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

## ORGANISM

NIH-MGC <http://mgs.nci.nih.gov/>.

## REFERENCE

1 (bases 1 to 759)  
NIH-MGC <http://mgs.nci.nih.gov/>.

## AUTHORS

National Institutes of Health, Mammalian Gene Collection (MGC)

## TITLE

Unpublished (1999)

## JOURNAL

Contact: Robert Strausberg, Ph.D.

## COMMENT

Email: [cgabs-remail.nih.gov](mailto:cgabs-remail.nih.gov)

Tissue Procurement: Dr. Michael Brownstein  
CDNA Library Preparation: The I.M.A.G.E. Consortium (LNL)  
CDNA Library Arrayed by: The I.M.A.G.E. Consortium  
DNA Sequencing by: Agencourt Bioscience Corporation  
Clone distribution: MGC clone distribution information can be  
found through the I.M.A.G.E. Consortium/LNL at:  
<http://image.llnl.gov>  
Place: NDM432 row: 5 column: 22  
High quality sequence stop: 730.

## FEATURES

source

1..759  
Location/Qualifiers

/organism="Homo sapiens"

/mol\_type="rRNA"

/db\_xref="taxon:9606"

/clone="IMAGE:30368973"

/tissue\_type="Pituitary"

/lab\_host="DH10B-Ton A" ( T1 and T5 phage resistances )"

/note="Organ: brain; Vector: pCMV-Sport6.1; Site: 1: EcoRV (destroyed); Site 2: NotI; Library is oligo-dT primed and directionally cloned (EcoRV site is destroyed upon cloning). Average insert size 1.1 kb. Library was constructed by (Invitrogen). Note: this is a NIH\_MGC Library."

Library."

## ORIGIN

## Alignment Scores:

Score: No.: 1,97e-114 Length: 759  
1042.00 Matches: 201  
Percent Similarity: 99.50% Conservative: 0  
Best Local Similarity: 99.50% Mismatches: 1  
Query Match: 99.52% Indels: 0  
Gaps: 0

US-09-856-796B-2 (1-202) x CD106929 (1-759)

QY 1 MetAlaThrglySerArgThrSerleuLeuAlaPheGlyLeuLeuCyseuProTrp 20  
DB 43 ATGGCTACAGAGCTCCGAGACCTCCCTGCTGCTTGGCTGCTGCTGCTGCTG 102  
QY 21 LeuGlnGluGlySerAlaPheProThrIleProLeuSerArgLeuPheAspAsnLaser 40  
DB 103 CTTCAAGAGGCAAGTGCCTTCCACCACTCCCTATCCAGGCTTTTGACAAGCTTANG 162  
QY 41 LeuArgAlaHisArgLeuHisGlnLeuAlaPheAspThrTyrglnGluPheAsnProGln 60  
DB 163 CTCGCCGCCATGCTGTGACCAAGCTGGCTTTGACACTACAGAGATTAAACCCGAG 222  
QY 61 ThrSerLeuCyseuSerGluSerIleProThrProSerAsnArgGluThrGlnGln 80  
DB 223 ACCTCCTCTGTTTCTCAGAGTCTATTCGACACCTCCACAGGAGGAGAACACACAG 282  
QY 81 LysSerAsnLeuGlnLeuLeuArgIleSerleuLeuLeuIleGlnSerTrpLeuGluPro 100  
DB 283 AAATCCAACTAGAGTGTCCGCACTCTCCCTGCTGCTATCCAGTGTGCTGAGGCC 342  
QY 101 ValGlnPheLeuArgSerValPheAlaAsnSerLeuValTyrglnAlaSerAspSerAsn 120  
DB 343 GTGCAGTTCCTCAGAGGTGCTTCCGCAACAGCTGTGTGACCGCTCTGACAGCAAC 402

RESULT 3	
CD105630	
LOCUS	
DEFINITION	CD105630 770 bp mRNA linear EST 15-MAY-2003
ACCESSION	ABENCCOURT_14014E54 NIH MGC 179 Homo sapiens cDNA clone
	IMAGE:30568235 5', mRNA sequence.
	CD105630

VERSION	KEYWORDS	SOURCE	ORGANISM
CD105630.1	EST.	Homo sapiens (human)	Homo sapiens

REFERENCE  
AUTHORS  
TITLE  
JOURNAL  
COMMENT

1 (phases 1 to 770)  
NIH-MGC <http://mgc.nhl.nih.gov/>  
National Institutes of Health, Mammalian Gene Collection (MGC)  
Unpublished (1999)  
Contact: Robert Strausberg Ph.D.

Contact: Robert Strausberg, Ph.D.  
Email: cgsab8-r@mail.nih.gov  
Tissue Procurement: Dr. Michael Brownstein  
cDNA Library Preparation: Invitrogen Corp  
DNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)  
Clone Sequencing by: Agencourt Bioscience Corporation  
Clone distribution: MGC clone distribution information can be  
found through the I.M.A.G.E. Consortium/LLNL at:  
<http://image.llnl.gov>

FEATURES	high quality sequence stop: 585.
source	Location/Qualifiers
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/lab_host="DH10B-Ton A (T1 and T5 phage resistances)"
/clone_id="NH_MGC_179"
/notes="Organ brain; Vector: pCMV-Sport6.1; Site 1: EcoRV (destroyed); Site 2: NotI; library is oligo-dT primed and directionally cloned (EcoRV site is destroyed upon cloning). Average insert size 1.1 kb. library was constructed by (in vitro) transposition. Note: this is a NH_MGC library."

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ORIGIN  
Alignment Scores:  
Prod wa

File: NO:	2.01e-114	Length:	770
Score:	1042.00	Matches:	201
Percent Similarity:	99.50%	Conservative:	0
Beet Local Similarity:	99.50%	Mismatches:	1
Query Match:	99.52%	Indels:	0
DB:	6	Gaps:	0

03-09-856-796B-2 (1-202) x CDI05630 (1-770)

QY	1	MetAlaThrnglySerArgThrsSerLeuLeuLeuAlaPhegllyLeuLeuCybleuProTrp	20
Db	43	ATGGCTAAGAGCTCCCGAGACTCCCTGCTCTCGGCTTTGGCTGTGCTGTGCTCCCTGG	107
QY	21	LeuGlnGlnGlySerAlaPheProThrIleProLeuSerArgLeuPheAspAsnAlaSer	40
Db	103	CTTCAAGAGGGCAGATGGCTTCCCAACCATTCCTTATCCAGGGCTTTTGTGCAACGCTATG	163
QY	41	LeuArgAlaHisArgLeuHisGlnLeuAlaPheAspThrTyrglnGlnPheAsnProGln	60
Db	163	CTCCGGCCCCATCCTCTGCACACAGCTGGCTTTGACACCTACAGAGATTAAACCCCAAG	222
QY	61	ThrsLeuCyPheSerGlnSerIleIleProThrProSerAsnArgGlnGlnThrGlnGln	80
Db	223	ACCTCCCTCTGTTTCTCAGAGTCTATTTCGACACCTTCCAAACAGGAGGAACACAAACAG	282
QY	81	LyseSerAsnLeuGlnLeuLeuArgIleSerLeuLeuLeuIleGlnSerTrpleuGlnPro	100
Db	283	AAATCCAACTAGAGCTGGCTCCGCACTCCTCTGCTATTCAGTCCGTGGGTGAGCC	342
QY	101	ValGlnPheLeuArgSerValPheAlaAsnSerLeuValTyrglyAlaSerAspSerAsn	120
Db	343	GTTCACTTCTCAGAGGTGTTCTTCGCCAAACAGCTGGGTACGGGCTCTTACAGCAAC	402
QY	121	ValTyrgAspLeuLeuLyAspLeuGlnGlnIlyleGlnThrLeuMetGlyArgLeuGln	140
Db	403	GTTCTATGACTCTCTTAAGACCTTAAGAGAAAGGACATCCAAAGCTGATGGGAGGCTGAA	462
QY	141	AspGlySerProArgThrglyGlnIlePheIysGlnThrTyrserIysPheAspThrAsn	160
Db	463	GATGGCAACCCCCGGAGCTGGCGAGATCTTCAAGCAGACTTACAGCAAGTGTGACAAACAAC	522
QY	161	SerHisAsnAspAspAlaLeuLeuIlyAsnTyrglyLeuLeuTyrglyPheArgLyAsp	180
Db	523	TCACGACACGATGAGGACATCTAATAAACAACAGGGCTGTCTACTGCTTACAGAAAGAC	582
QY	181	MetAspIysValGlnThrPheLeuArgIleValGlnIysArgSerValGlnGlySerCys	200
Db	583	ATGCAACAAGTCGAGACATTCCTGCGCATGTGCAAGTGGCGCTCTGTGGAAGCAGACTGT	642
QY	201	GlyPhe	202
Db	643	GGCTTC	648

RESULT 4	
CD251386	
LOCUS	
DEFINITION	CD251386 817 bp mRNA linear EST 22-MAY-2003
ACCESSION	AGNCNCOURT 14204245 NIH_MGC_119 Homo sapiens CDNA clone
VERSION	IMAGE:30383392.5', mRNA sequence.
KEYWORDS	CD251386.CD251386.1 GI:31011852
SOURCE	EST.
ORGANISM	Homo sapiens (human)
	Homo sapiens
	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
	Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE	NIH-MGC <a href="http://mgs.nci.nih.gov/">http://mgs.nci.nih.gov/</a> .
AUTHORS	National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL	Unpublished (1999)
COMMENT	Contact: Daniela S Gerhard PhD D

Office of Cancer Genomics, Fm.D.  
National Cancer Institute / NIH  
Bldg. 31 Rm10A07 Bethesda, MD 20892  
Email: c9agbbs-r@mail.nih.gov  
Tissue Procurement: Dr. Michael Brownstein  
cDNA Library Preparation: Invitrogen Corp  
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)  
DNA Sequencing by: Agencourt Bioscience Corporation  
Clone distribution: MGC clone distribution information can be  
found through the I.M.A.G.E. Consortium/LNL at:  
<http://image.lnl.gov>

Plate: NDAM48 row: 1 column: 17  
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 High quality sequence stop: 636.  
 Location/Qualifiers

1. .817

/organism="Homo sapiens"  
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 /clone\_1b="NIH MGC 179"  
 /note="Organ: brain; Vector: PCMV-SPORT6.1; Site\_1: EcoRV (destroyed); Site\_2: NotI; Library is oligo-dT primed and directionally cloned (EcoRV site is destroyed upon cloning). Average insert size 1.1 kb. Library was constructed by (Invitrogen). Note: this is a NIH\_MGC library."

## ORIGIN

## Alignment Scores:

Pred. No.: 2,19e-114 Length: 817  
 Score: 1042.00 Matches: 201  
 Percent Similarity: 99.50% Conservative: 0  
 Best Local Similarity: 99.50% Mismatches: 1  
 Query Match: 99.52% Indels: 0  
 DB: 6 Gaps: 0

US-09-856-796B-2 (1-202) x CD251386 (1-817)

QY 1 MetAlaThrGlySerArgThrSerLeuLeuAlaPheGlyLeuLeuCysLeuProTrrp 20  
 DB 86 ATGGCTACAGAGCTCCGACGCTCCCTGCTCTGCTTTGGCTCTGCTGCTGCTG 145  
 QY 21 LeuGlnGluGlySerAlaPheProThrIleProLeuSerArgLeuPheAspAsnAlaSer 40  
 DB 146 CTTCACAGGGCACTGCTCCCAACATTCCTTATCCAGGCTTTTACAAACGCTATG 205  
 QY 41 LeuArgAlaHisArgLeuHisGlnLeuAlaPheAspThrTyrGlnGluPheAsnProGln 60  
 DB 206 CTCGGCGCCATCGTCTGCACCAAGCTGGCTTGAACACTACAGAGATTAAACCCCG 265  
 QY 61 ThrSerLeuCysPheSerGluSerIleProThrProSerAsnArgGluGlnThrGlnGln 80  
 DB 266 ACCTCCCTGTTTCTCAGAGTCTATTCGACACCTCCCAACGAGGAGGAACACACAG 325  
 QY 81 LysSerAsnLeuGluLeuLeuArgIleSerLeuLeuIleGlnSerTyrLeuGluPro 100  
 DB 326 AATCCAACTAGAGCTGCTCCGCACTCCCTGCTCTATCCAGTCTGCTGAGAGCC 385  
 QY 101 ValGlnPheLeuArgSerValPheAlaAsnSerLeuValTyrGlyAlaSerAspSerAsn 120  
 DB 386 GTGCAGTTCCTCAGGAGTGTCTTCGCCAACAAGCTGTTGACGCGCTCTGACAGCAAC 445  
 QY 121 ValTyrAspLeuLeuLysAspLeuGluGluGlyIleGlnThrLeuMetGlyArgLeuGlu 140  
 DB 446 GTCTAGACCTCTTAAGACCTTAGAGGAGGATCCAAAGCTGATGCGGAGGCTGAAA 505  
 QY 141 AspGlySerProArgThrGlyGlnIlePheLeuGlnThrTyrSerIysPheAspThrAsn 160  
 DB 506 GATGGACGCCCCCGAGATGGGCAATCTTCAAGCAGACCTACAGCAAGATTGACACAAAC 565  
 QY 161 SerHisAsnAspAspAlaLeuLeuLysAsnTyrGlyLeuLeuTyrCysPheArgLysAsp 180  
 DB 566 TCACACAAACATGACGACACTACAGAACTACGCGGCTCTTACTGCTTCAGGAAGAC 625  
 QY 181 MetAspLysValGluThrPheLeuArgIleValGlnCysArgSerValGluGlySerCys 200  
 DB 626 ATGGACAGAGTCGAGACATCTCTGCGCACTGTCAGTCCGCTCTGTGAGGAGGAGCTGT 685  
 QY 201 GlyPhe 202  
 DB 686 GGCTTC 691

RESULT 5  
 CD556434 818 bp mRNA linear EST 11-JUN-2003  
 LOCUS  
 DEFINITION  
 IMAGE:30383992 5', mRNA sequence.

ACCESSION  
 CD556434  
 VERSION  
 CD556434.1 GI:31582502  
 KEYWORDS  
 EST.  
 SOURCE  
 Homo sapiens (human)  
 ORGANISM  
 Homo sapiens

REFERENCE  
 AUTHORS  
 TITLE  
 JOURNAL  
 COMMENT  
 NIH-MGC http://mgs.nci.nih.gov/  
 National Institutes of Health, Mammalian Gene Collection (MGC)  
 Unpublished (1999)  
 Contact: Daniela S. Gerhard, Ph.D.  
 Office of Cancer Genomics / NIH  
 National Cancer Institute / NIH  
 Bldg. 31 Rm10A07 Bethesda, MD 20892  
 Email: dsgerha@mail.nih.gov

Tissue Procurement: Dr. Michael Brownstein  
 CDNA Library Preparation: Invitrogen Corp  
 CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)  
 DNA Sequencing by: Agencourt Bioscience Corporation  
 Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LNL at:  
 http://image.llnl.gov  
 Plate: NDAM469 row: d column: 24  
 High quality sequence start: 27  
 High quality sequence stop: 612.  
 Location/Qualifiers

## FEATURES

## source

1. .818  
 /organism="Homo sapiens"  
 /mol\_type="mRNA"  
 /db\_xref="taxon:9606"  
 /clone="IMAGE:30383992"  
 /tissue\_type="Pituitary"  
 /lab\_host="DH10B-Ton A ( T1 and T5 phage resistances)"  
 /clone\_1b="NIH MGC 179"  
 /note="Organ: brain; Vector: PCMV-SPORT6.1; Site\_1: EcoRV (destroyed); Site\_2: NotI; Library is oligo-dT primed and directionally cloned (EcoRV site is destroyed upon cloning). Average insert size 1.1 kb. Library was constructed by (Invitrogen). Note: this is a NIH\_MGC library."

## ORIGIN

## Alignment Scores:

Pred. No.: 1,16e-113 Length: 818  
 Score: 1036.00 Matches: 200  
 Percent Similarity: 99.01% Conservative: 0  
 Best Local Similarity: 99.01% Mismatches: 2  
 Query Match: 98.95% Indels: 0  
 DB: 6 Gaps: 0

US-09-856-796B-2 (1-202) x CD556434 (1-818)

QY 1 MetAlaThrGlySerArgThrSerLeuLeuAlaPheGlyLeuLeuCysLeuProTrrp 20  
 DB 68 ATGGCTACAGAGCTCCGACGCTCCCTGCTCTGCTTTGGCTGCTGCTGCTG 127  
 QY 21 LeuGlnGluGlySerAlaPheProThrIleProLeuSerArgLeuPheAspAsnAlaSer 40  
 DB 128 CTTCACAGGGCACTGCTCCCAACATTCCTTATCCAGGCTTTTGAACAGCTATG 187  
 QY 41 LeuArgAlaHisArgLeuHisGlnLeuAlaPheAspThrTyrGlnGluPheAsnProGln 60  
 DB 188 CTCGGCGCCATCGTCTGCACCAAGCTGGCTTGAACACTACAGAGATTAAACCCCG 247  
 QY 61 ThrSerLeuCysPheSerGluSerIleProThrProSerAsnArgGluGlnThrGlnGln 80

Db 248 ACCTCCCTCTGTTTCTCAGAGTCTAGTCCGACACCCCTCCACAGGAGGAAACACAGACAG 307

Qy 81 LysSerAsnLeuGluLeuLeuArg11SerLeuLeuLeu11GlnSerThrPheGluPro 100

Db 308 AAATCCAACTTAGACCTGCTCCGACATCTCCCTGCTGCTCATCTCATCTGCTGAGCC 367

Qy 101 ValGlnPheLeuArgSerValPheAlaAsnSerLeuVal1YrGlyAlaSerAspSer 120

Db 368 GTGACGTTCTCAGAGAGTCTTCCGCCACAGCCTGCTGTAACGGGGCTCTGACAGCAAC 427

Qy 121 Val1YrAspLeuLeuLeuAspLeuGluGlu1Yr11GlnThrLeuMetG1YrGluGlu 140

Db 428 GTCTATGACCTCTTAAGAGCACTAGAGAGAGCACTCAAGCTGATGGAGGCTGAA 487

Qy 141 AspGlySerProArgThrGlyGln11PheLeuGlnThr1YrSerLeuPheAspThrAsn 160

Db 488 GATGGCAGCCCTCCGACGCTGGCAGATCTTCAAGCAGCACTCAAGCAAGTTGACACAAAC 547

Qy 161 SerHisAsnAspAlaLeuLeuLeuLeuAsn1YrGlyLeuLeu1YrGlyPheArgLysAsp 180

Db 548 TCACACAACTAGACGCTAGCTACTCAAGAACTACGAGCTGCTCTACTGCTTCAAGAGGAC 607

Qy 181 MetAspLysValGluThrPheLeuArg11ValGlnCysArgSerValGluGlySerCys 200

Db 608 ATGGACAAAGTCCAGACATCTCTGCGCATGTCAGTGCCTCTGTGAGAGGCGAGCTGT 667

Qy 201 GlyPhe 202

Db 668 GGCTTC 673

RESULT 6

LOCUS CD108395 768 bp mRNA linear EST 15-MAY-2003

DEFINITION AGENCOURT 1401672 NIH MGC 179 Homo sapiens CDNA clone

ACCESSION IMAGE:30364686 5', mRNA sequence.

VERSION CD108395.1 GI:30761569

KEYWORDS EST.

SOURCE Homo sapiens (human)

ORGANISM Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

REFERENCE 1 (bases 1 to 768)

AUTHORS NIH-MGC <http://mgi.nci.nih.gov/>.

TITLE National Institutes of Health, Mammalian Gene Collection (MGC)

JOURNAL Unpublished (1999)

COMMENT Contact: Robert Strausberg, Ph.D.  
Email: [cgabbs-remail.nih.gov](mailto:cgabbs-remail.nih.gov)  
Tissue Procurement: Dr. Michael Brownstein  
CDNA Library Preparation: Invitrogen Corp  
DNA Sequencing by: The I.M.A.G.E. Consortium (LNL)  
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LNL at: <http://image.llnl.gov>  
Plate: NDAM421 row: h column: 07  
High quality sequence stop: 583.  
Location/Qualifiers  
1. 768

FEATURES

Source

Alignment Scores:

Pred. No.:	Score:	Percent Similarity:	Best Local Similarity:	Query Match:	Length:	Matches:	Conservative:	Mismatches:	Indels:	Gaps:
2,226-112	1025.00	99.01%	98.52%	97.90%	768	200	1	1	1	0

US-09-856-796b-2 (1-202) x CD108395 (1-768)

Qy 1 MetAlaThrGlySerArgThrSerLeuLeuLeu11aPheGlyLeuLeuCysLeuProThr 20

Db 33 ATGGCTACAGGCTCCGGAGAGTCCCTCTCTGCTTTGGCTGCTGCTGCTCCCTGG 92

Qy 21 LeuGlnGluGlySerAlaPheProThr11aProLeuSerArgLeuPheAspAlaSer 40

Db 93 CTTCAGAGGAGGAGTGCCTTCCCAACCATTCCTTATCCAGGCTTTTGAACAGCTATG 152

Qy 41 LeuArgAlaHisArgLeuH1GlnLeuAlaPheAspThr1YrGlnGluPheAsnProGln 60

Db 153 CTCGGCGCCATGCTGTGACACAGCTGGCTTTGACACCTTACAGAGATTAAACCCAG 212

Qy 61 ThrSerLeuCysPheSerGlnSer11aProThrProSerAsnArgGluGluThrGln 80

Db 213 ACCTCCCTCTGTTTCTCAGAGTCTATTCGACACCTCCCAACAGGAGGAAACACACAG 272

Qy 81 LysSerAsnLeuGluLeuLeuLeuArg11SerLeuLeuLeu11GlnSerThrPheGluPro 100

Db 273 AAATCCAACTTAGACGCTGCTCCGACATCTCCCTGCTCATCTCAAGTGTGGCTGAGGCC 332

Qy 101 ValGlnPheLeuArgSerValPheAlaAsnSerLeuVal1YrGlyAlaSerAspSerAsn 120

Db 333 GTGCAATTCCTCAGAGTGTCTTCCGCAACAGCTGTGTACGGCCCTCTGACAGCAAC 392

Qy 121 Val1YrAspLeuLeuLeuAspLeuGluGlu1Yr11GlnThrLeuMetG1YrGluGlu 140

Db 393 GTCTATGACCTCTTAAGAGCACTAGAGAGGATCAACAGCTGATGGAGGAGCTGGAA 452

Qy 141 AspGlySerProArgThrGlyGln11PheLeuGlnThr1YrSerLeuPheAspThrAsn 160

Db 453 GATGGCAGCCCTCCGACGCTGGCAGATCTTCAAGCAACCTTCAAGCAAGTTGACACAAAC 512

Qy 161 SerHisAsnAspAlaLeuLeuLeuLeuAsn1YrGlyLeuLeu1YrGlyPheArgLysAsp 180

Db 513 TCACACAACTAGACGCTAGCTACTCAAGAACTACGAGCTGCTTCAAGAGGAGAC 572

Qy 181 MetAspLysValGluThrPheLeuArg11ValGlnCysArgSerValGluGlySerCys 200

Db 573 ATGGACAAAGTCCAGACATCTCTGCGCATGTCAGTGCCTCTGTGAGAGGAGCTGT 632

Qy 200 GlyPhe 202

Db 633 TGGCTTC 639

RESULT 7

LOCUS CD107947 797 bp mRNA linear EST 15-MAY-2003

DEFINITION AGENCOURT 14016184 NIH MGC 179 Homo sapiens CDNA clone

ACCESSION IMAGE:30365079 5', mRNA sequence.

VERSION CD107947

KEYWORDS EST.

SOURCE Homo sapiens (human)

ORGANISM Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

REFERENCE 1 (bases 1 to 797)

AUTHORS NIH-MGC <http://mgi.nci.nih.gov/>.

TITLE National Institutes of Health, Mammalian Gene Collection (MGC)

JOURNAL Unpublished (1999)

COMMENT Contact: Robert Strausberg, Ph.D.  
Email: [cgabbs-remail.nih.gov](mailto:cgabbs-remail.nih.gov)

Tissue Procurement: Dr. Michael Brownstein  
 cDNA Library Preparation: Invitrogen Corp  
 DNA Sequencing by: The I.M.A.G.E. Consortium (LNL)  
 Clone distribution: MGC clone distribution information can be  
 found through the I.M.A.G.E. Consortium/LNL at:  
<http://image.lnl.gov>  
 Plate: NDM422 row: h column: 16  
 High quality sequence stop: 624.

## FEATURES

source

1..797  
 /organism="Homo sapiens"  
 /mol\_type="mRNA"  
 /db\_xref="taxon:9606"  
 /clone="IMAGE:30365079"  
 /tissue\_type="Pituitary"  
 /lab\_host="DH10B-Ton A ( T1 and T5 phage resistances)"  
 /clone\_1ib="NIH\_MGC\_179"  
 /note="Organ: Brain; Vector: pCMV-SPORT6.1; Site\_1: EcoRV  
 (destroyed); Site\_2: NotI; Library is oligo-dT primed and  
 directionally cloned (EcoRV site is destroyed upon  
 cloning). Average insert size 1.1 kb. Library was  
 constructed by (Invitrogen). Note: this is a NIH\_MGC  
 library."

## ORIGIN

## Alignment Scores:

Pred. No.: 2,7e-112 Length: 797  
 Score: 1024.50 Matches: 201  
 Percent Similarity: 92.63% Conservative: 0  
 Best Local Similarity: 92.63% Mismatches: 1  
 Query Match: 97.85% Indels: 15  
 DB: 6 Gaps: 1

US-09-856-796B-2 (1-202) x CD107947 (1-797)

1 MetAlaThGlySerArgThrSerLeuLeuAlaPheGlyLeuLeuCysLeuProTrrp 20  
 31 ATGGCTACAGGCTCCCGAGAGTCCCTGCTGCTTTGGCTGCTGCTGCTGCTGCTG 90  
 21 LeuGlnGlnGlySerAlaPheProThrIleProLeuSerArgLeuPheAspAsnAlaSer 40  
 91 CTTCAAGAGGCGAGTGGCTTCCCAACCATTCCTTATCCAGCTTTTGGACCAACGCTATG 150  
 41 LeuArgAlaHisArgLeuHisGlnLeuAlaPheAspThrTyrGlnGluPhe----- 57  
 151 CTCGGGGCCCATGCTCGACACAGCTGGCTTTGACACTTACAGAGAGTTGAAGAAGCC 210  
 58 -----AspProGlnThrSerLeuCysPhe 65  
 211 TATATCCCAAGACAGAACTATTCCTCGCAAAACCCCAACCTCCCTGCTTTC 270  
 66 SerGluSerIleProThrProSerAsnArgGlnGlnGlnGlnGlnGlnGlnGln 85  
 271 TCGAGAGCTATTCGACACCTCCACAGGAGGAGAAACAGAAATCCAACTAGAG 330  
 86 LeuLeuArgIleSerLeuLeuLeuGlnSerTyrPleuGlnProValGlnPheLeuArg 105  
 331 CTGCTCGGCACTCCCTGCTGCTCATTCAGTGTGGTGGAGCCCGTGCAGTTCCTCAG 390  
 106 SerValPheAlaAsnSerLeuValTyrGlyAlaSerAspSerAsnValTyrAspLeu 125  
 391 AGTGTCTTCCGCAACAGCTGTGTACGGCGCTCGACAGCAACCTATAGACCTCTCA 450  
 126 LysAspLeuGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGln 145  
 451 AAGGACCTTAGGAGAGGATCCAAAGCTGATGGGAGGCTGGAGATGGCAGCCCGG 510  
 146 ThrGlnGlnIlePheLeuGlnThrTyrSerIysPheAspThrAsnSerHisAsnAsp 165  
 511 ACTGGGAGATCTTCAAGCAGACCTACAGCAAGTTGACACAACTCAGCAACGATGAC 570  
 166 AlaLeuLeuLysAsnTyrGlyLeuLeuTyrCysPheArgLysAspMetAspLysValGlu 185

571 GCACTACTCAAGACTACGGGCTGCTCTACTCTTACAGAGAGACATGACAGGTCGAG 630  
 186 ThrPheLeuArgIleValGlnCysArgSerValGlnGlySerCysGlyPhe 202  
 631 ACATTCTGCGCATTCGTCAGTCCCGCTGCTGTGAGGAGGAGCTGTGGCTTC 681

RESULT 8  
 CD107985 798 bp mRNA linear EST 15-MAY-2003  
 LOCUS CD107985  
 DEFINITION AENNCOURT 13980152 NIH MGC 179 Homo sapiens cDNA clone  
 IMAGE:30367958 5', mRNA sequence.

ACCESSION CD107985  
 VERSION CD107985.1 GI:30761159  
 KEYWORDS EST.  
 SOURCE Homo sapiens (human)

REFERENCE  
 AUTHORS NIH-MGC <http://mgs.nci.nih.gov/>.  
 TITLE National Institutes of Health, Mammalian Gene Collection (MGC)  
 JOURNAL Unpublished (1999)  
 COMMENT Contact: Robert Strausberg, Ph.D.  
 Email: [cgabbs-remail.nih.gov](mailto:cgabbs-remail.nih.gov)  
 Tissue Procurement: Dr. Michael Brownstein  
 cDNA Library Preparation: Invitrogen Corp  
 cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)  
 DNA Sequencing by: Agencourt Bioscience Corporation  
 Clone distribution: MGC clone distribution information can be  
 found through the I.M.A.G.E. Consortium/LNL at:  
<http://image.lnl.gov>  
 Plate: NDM429 row: p column: 15  
 High quality sequence stop: 765.

## FEATURES

source

1..798  
 /organism="Homo sapiens"  
 /mol\_type="mRNA"  
 /db\_xref="taxon:9606"  
 /clone="IMAGE:30367958"  
 /tissue\_type="Pituitary"  
 /lab\_host="DH10B-Ton A ( T1 and T5 phage resistances)"  
 /clone\_1ib="NIH\_MGC\_179"  
 /note="Organ: brain; Vector: pCMV-SPORT6.1; Site\_1: EcoRV  
 (destroyed); Site\_2: NotI; Library is oligo-dT primed and  
 directionally cloned (EcoRV site is destroyed upon  
 cloning). Average insert size 1.1 kb. Library was  
 constructed by (Invitrogen). Note: this is a NIH\_MGC  
 library."

## ORIGIN

## Alignment Scores:

Pred. No.: 2,7e-112 Length: 798  
 Score: 1024.50 Matches: 201  
 Percent Similarity: 92.63% Conservative: 0  
 Best Local Similarity: 92.63% Mismatches: 1  
 Query Match: 97.85% Indels: 15  
 DB: 6 Gaps: 1

US-09-856-796B-2 (1-202) x CD107985 (1-798)

1 MetAlaThGlySerArgThrSerLeuLeuAlaPheGlyLeuLeuCysLeuProTrrp 20  
 31 ATGGCTACAGGCTCCCGAGAGTCCCTGCTGCTTTGGCTGCTGCTGCTGCTGCTG 90  
 21 LeuGlnGlnGlySerAlaPheProThrIleProLeuSerArgLeuPheAspAsnAlaSer 40  
 91 CTTCAAGAGGCGAGTGGCTTCCCAACCATTCCTTATCCAGCTTTTGGACCAACGCTATG 150  
 41 LeuArgAlaHisArgLeuHisGlnLeuAlaPheAspThrTyrGlnGlnGluPhe----- 57  
 151 CTCGGGGCCCATGCTCGACACAGCTGGCTTTGACACTTACAGAGAGTTGAAGAAGCC 210

QY 58 -----AsnProGlnThrSerLeuCyse 65  
 Db 211 TATATCCCAAGAGACAGATTTCATTCCTGCGAGACCCCGACGCTCCCTGTTTC 270  
 QY 66 SerGluSerIleProThrProSerAsnArgGluGlnThrGlnGlnSerAsnLeu 85  
 Db 271 TCAGAGCTATATCCGACACCTCCCAACAGAGGAAACACAGAAATCCAACTCAGAG 330  
 QY 86 LeuLeuArgIleSerLeuLeuLeuIleGlnSerTrpLeuGluProValGlnPheLeuArg 105  
 Db 331 CTGCTCCGATCTCCCTGCTGCTCACTCAGTCTGCTGAGACCCGCTGACGTTCTCCAG 390  
 QY 106 SerValPheAlaAsnSerLeuValTyrglyAlaSerAspSerAsnValTyrglyLeuLeu 125  
 Db 391 AGTCTCTCCGACCAAGCCCTGGTGTACGGCCCTCTGACAGCAACGCTATACCTCTCA 450  
 QY 126 LysAspLeuGluGluGlyIleGlnThrLeuMetGlyArgLeuGluAspGlySerProArg 145  
 Db 451 AAGGACCTAGAGAGAGGATCCAAACGCTGATGGGAGGCTGGAAGATGGCAGCCCGG 510  
 QY 146 ThrGlyGlnIlePheLeuGlnThrTyrglySerIlePheAspThrAsnSerHisAsnAsp 165  
 Db 511 ACTGGGCGATCTTCAACAGACAGCCTACAGCAAGTTCCAGCAACTCAACAAGATGAC 570  
 QY 166 AlaLeuLeuLysAsnTyrglyLeuLeuTyrglyPheArgLysAspMetAspLysValGlu 185  
 Db 571 GCATCTCTCAAGAACTACGGGCTGCTCTACTGCTTCAAGAGGACATGAGAGGTCGAG 630  
 QY 186 ThrPheLeuArgIleValGlnCysArgSerValGluGlySerGlyPhe 202  
 Db 631 ACATTCCTGGCATCTGCGAGTGCCTGCTGTGAGAGGCGACGTCGCTTC 681

RESULT 9 CD251158 800 bp mRNA linear EST 22-MAY-2003  
 LOCUS CD251158 IMAGE:30383909 5', mRNA sequence.  
 DEFINITION CD251158.1 GI:31011624  
 VERSION EST.  
 KEYWORDS Homo sapiens (human)  
 SOURCE Homo sapiens  
 ORGANISM Homo sapiens (human)  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
 NIH-MGC http://mgi.nci.nih.gov/  
 1 (bases 1 to 800)  
 National Institutes of Health, Mammalian Gene Collection (MGC)  
 Unpublished (1999)  
 Contact: Daniela S. Gerhard, Ph.D.  
 Office of Cancer Genomics  
 National Cancer Institute / NIH  
 Bldg. 31 Rm10A07 Bethesda, MD 20892  
 Email: c9abds-remail.nih.gov  
 Tissue Procurement: Dr. Michael Brownstein  
 cDNA Library Preparation: Invitrogen Corp  
 DNA Sequencing by: The I.M.A.G.E. Consortium (LLNL)  
 Clone distribution: MGC clone distribution information can be  
 found through the I.M.A.G.E. Consortium/LLNL at:  
 http://image.llnl.gov  
 Plate: NDMA48 row: 1 column: 06  
 High quality sequence stop: 634.  
 Location/Qualifiers  
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 /mol\_type="mRNA"  
 /db\_xref="taxon:9606"  
 /clone="IMAGE:30383909"  
 /tissue\_type="Pituitary"  
 /lab\_host="DH10B-Ton A ( T1 and T5 phage resistances)"  
 /clone\_id="NIH MGC 179"  
 /note="Organ: brain; Vector: pCMV-SPORT6.1; Site 1: EcoRV  
 (destroyed); Site 2: NotI; Library is oligo-dT primed and

directionally cloned (EcoRV site is destroyed upon  
 cloning). Average insert size 1.1 kb. Library was  
 constructed by (Invitrogen). Note: this is a NIH\_MGC  
 Library."

ORIGIN  
 Alignment Scores:  
 Pred. No.: 2,716-112 Length: 800  
 Score: 1024.50 Matches: 201  
 Percent Similarity: 92.63% Conservative: 0  
 Best Local Similarity: 92.63% Mismatches: 1  
 Query Match: 97.85% Indels: 15  
 DB: 6 Gaps: 1

US-09-856-796B-2 (1-202) x CD251158 (1-800)

QY 1 MetaLThrGlySerArgThrSerLeuLeuAlaPheGlyLeuLeuCyseLeuProTrp 20  
 Db 40 ATGGCTACAGGCTCCCGAGCGTCCCTGCTGCTTTGGCTGCTGCTGCTGCTGCTGCTG 99  
 QY 21 LeuGlnGluGlySerAlaPheProThrIleProLeuSerArgLeuPheAspAsnLaser 40  
 Db 100 CTTCAAGAGGCGACATGCTTCCCAACATTCCTTATCCAGGCTTTTGACAAACGCTATG 159  
 QY 41 LeuArgAlaHisArgLeuHisGlnLeuAlaPheAspThrTyrglyGlnPhe----- 57  
 Db 160 CTCCGCCCCATCGTTCGACACAGCTGCGCTTTACACCTACAGGAGATTGAAGAACCC 219  
 QY 58 -----AsnProGlnThrSerLeuCyse 65  
 Db 220 TATATCCCAAGAGACAGATTTCATTCCTGCGAGACCCCGACGCTCCCTGTTTC 279  
 QY 66 SerGluSerIleProThrProSerAsnArgGluGlnThrGlnGlnSerAsnLeu 85  
 Db 280 TCAGAGCTATATCCGACACCTCCCAACAGAGGAAACACAGAAATCCAACTCAGAG 339  
 QY 86 LeuLeuArgIleSerLeuLeuLeuIleGlnSerTrpLeuGluProValGlnPheLeuArg 105  
 Db 340 CTGCTCCGATCTCCCTGCTGCTCACTCAGTCTGCTGAGGCTGCGAGTTCCTCAGG 399  
 QY 106 SerValPheAlaAsnSerLeuValTyrglyAlaSerAspSerAsnValTyrglyLeuLeu 125  
 Db 400 AGTGTCTTCCGCAACAGCCTGGTGTACGGGCTCTGACAGCAACGCTATGACCTCTTA 459  
 QY 126 LysAspLeuGluGluGlyIleGlnThrLeuMetGlyArgLeuGluAspGlySerProArg 145  
 Db 460 AAGGACCTAGAGAGAGGATCCAAACGCTGATGGGAGGCTGGAAGATGGCAGCCCGG 519  
 QY 146 ThrGlyGlnIlePheLeuGlnThrTyrglySerIlePheAspThrAsnSerHisAsnAsp 165  
 Db 520 ACTGGGCGATCTTCAACAGACAGCCTACAGCAAGTTCCAGCAAACTCAACAACGATGAC 579  
 QY 166 AlaLeuLeuLysAsnTyrglyLeuLeuTyrglyPheArgLysAspMetAspLysValGlu 185  
 Db 580 GCATCTCTCAAGAACTACGGGCTGCTCTACTCTTCAAGAGGACATGAGAGGTCGAG 639  
 QY 186 ThrPheLeuArgIleValGlnCysArgSerValGluGlySerGlyPhe 202  
 Db 640 ACATTCCTGGCATCTGCGAGTGCCTGCTGTGAGAGGCGACGTCGTGCTTC 690

RESULT 10 CD108743 801 bp mRNA linear EST 15-MAY-2003  
 LOCUS CD108743 IMAGE:30368844 5', mRNA sequence.  
 DEFINITION CD108743  
 ACCESSION CD108743  
 VERSION EST.  
 KEYWORDS Homo sapiens (human)  
 SOURCE Homo sapiens  
 ORGANISM Homo sapiens (human)  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
 1 (bases 1 to 801)





QY	41	LeuArgAlaHisArgLeuHisGlnLeuAlaPheAspThrTyrGlnGluPhe-----	57
Db	162	CTCCGGCGCCATCGTGGTCGACCAAGCTGGCTTTTAACTTACCAAGAGGTTGAAGAAGCC	222
QY	58	-----AsnProGlnThrSerLeuCysPhe	65
Db	222	TATATCCCAAGAAGAACAGATATTCAATTCCTCGAAGAACCCCAAGACCTCCCTCGTTTC	283
QY	66	SerGluSerIleProThrProSerAsnArgGlnGluThrGlnGlnIlySerAsnLeuGlu	85
Db	282	TCGAGAGCTATTCGGAACCCCTCCAAAGGAGGAACACAAAGAAATCCAACTTAGAG	341
QY	86	LeuLeuArgIleSerLeuLeuLeuIleGlnSerTyrLeuGluProValGlnPheLeuArg	105
Db	342	CTCTCTCGGACATCTCCCTGCTGCTCATCACTCGTGAGGCCGCGAGCAATTCTCAGG	401
QY	106	SerValPheAlaAsnSerLeuValTyrGlyAlaSerAspSerAsnValTyrAspLeuLeu	125
Db	402	AGTGCTTTCGCCAACACAGCCTTGAGTGAACGGGCTTCGACAGCAACGCTTATGACTTCCTTA	461
QY	126	LysAspLeuGlnGlnGlyIleGlnThrLeuMetGlyArgLeuGlnLysAspGlySerProArg	145
Db	462	AAGAACTTAGAGGAAGGATCCAAAGCGTATGGGAGGCTGGAAGAATGGACCCCCGG	521
QY	146	ThrGlyGlnIlePheIlyGlnThrTyrSerLysPheAspThrAsnSerHisAsnAspAsp	165
Db	522	ACTGGGCGAGATCTTCAAGCAGACCTTACACCAAGTTGACACAAACTCAGCAACGATGAC	581
QY	166	AlaLeuLeuLysAsnTyrGlyLeuLeuTyrCysPheArgLysAspMetAspLysValGlu	185
Db	582	GGACTACTCAAGAACTACGGGGCTGGCTTACTCTTCAGAAAGGACATGACAAAGGCGAG	641
QY	186	ThrPheLeuArgIleValGlnCysArgSerValGlnGlySerCysGlyPhe	202
Db	642	ACATTCCTGGCGCATGTCGAGTGGCCGCTTGTGGAAGGCGAGCTGTGGGCTTC	692

RESULT	12
CD513888	
LOCUS	
DEFINITION	CD513888
ACCESSION	AGNCNCURR_14365159 NIH MGC 179 Homo sapiens cDNA clone IMAGE:30394616 5', mRNA sequence.
VERSION	CD513888
KEYWORDS	CD513888.1 GI:31445606
SOURCE	EST.
ORGANISM	Homo sapiens (human)
	Homo sapiens
	Homo sapiens

REFERENCE	AUTHORS	TITLE	JOURNAL	COMMENT
Eukaryota; Metazoa; Chordata; Craniata; Vertebrate; Euteleostomi; Mammalia; Eutheria; Primates; Carnathia; Homnidae; Homo.	1 (bases 1 to 802)	NIH-MGC <a href="http://mgc.nci.nih.gov/">http://mgc.nci.nih.gov/</a> .	National Institutes of Health, Mammalian Gene Collection (MGC)	Unpublished (1999)
Contact: Daniela S. Gerhard	ph n			

Office of Cancer Genomics  
National Cancer Institute / NIH  
Bldg. 31 Rm10A07 Bethesda, MD 20892  
Email: [cgaps-r@mail.nih.gov](mailto:cgaps-r@mail.nih.gov)  
Tissue Procurement: Dr. Michael Brownstein  
cDNA Library Preparation: Invitrogen Corp  
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LINTL)  
DNA Sequencing by: Agencourt Bioscience Corporation  
Clone distribution: MGC clone distribution information can be  
found through the I.M.A.G.E. Consortium/LINTL at:  
<http://image.llnl.gov>  
Plate: NDMA473 row: g column: 09  
High quality sequence stop: 701.

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location/Qualifiers
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/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clome="IMAGE:30394616"

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/tissue_type="Pituitary"
/lab_host="DH10B-Ton A ( T1 and T5 phage resistances )"
/clone_id="NIH_MGC_179"
/note="Organ: brain; Vector: pCMV-SPORT6.1; Site_1: EcoRV
(destroyed); Site_2: NotI; Library is oligo-dT primed and
directionally cloned (EcoRV site is destroyed upon
cloning). Average insert size 1.1 kb. Library was
constructed by (Invitrogen). Note: this is a NIH_MGC
Library."

```

Alignment Scores:

File: NO:	2_72e-112	Length:	802
Score:	1024.50	Matches:	0
Percent Similarity:	92.63%	Conservative:	0
Best Local Similarity:	92.63%	Mismatches:	1
Query Match:	97.85%	Indels:	15
DB:	6	Gaps:	1

US-09-856-796B-2 (1-202) x CD513888 (1-802)

Qy	1	MetIaThrGlySerArgThrSerLeuLeuAlaIheGlyLeuLeuCySLeuProTrp	20
Db	23	ATGGCTACAGGCTCCCGGACGCTCCGCTCCTGGCTTTTGGCCCTGCTCGCTCCCTGG	82
Qy	21	LeuGlnGluGlySerAlaPheProThrIleProLeuSerArgLeuPheAspAlaSer	40
Db	83	CTTCAGAGGGCAGTGGCTTCCCAACCATTCCTTATCCAGGGCTTTTGTGCAACGGCTATG	142
Qy	41	LeuArgIaHisArgLeuHisGlnLeuAlaPheAspThrTyrGlnGluPhe-----	57
Db	143	CTCCGGGCCATGCTGTGACCAAGCTGGCTTTGACACCTTACAGGAGTGTGGAAGAGCC	202
Qy	58	-----AsnProGlnThrSerLeuCyS	Phe 65
Db	203	TATATCCCAAGGACAGAAAGTATTTCATTTCCTGACAAACCCCAAGCTCTCTGTTTC	262
Qy	66	SerGluSerIleProThrProSerAsnArgGluGluThrGlnGlnIlySerAsnLeuGlu	85
Db	263	TGAGACTTATTCGACACCTTCCAACGAGGAGAAACACACAGAAATTCACACTTAGAG	322
Qy	86	LeuLeuArgIleSerLeuLeuLeuIleGlnSerTrpLeuGluProValGlnPheLeuArg	105
Db	323	CTGCTCCGGATCTCCCTGCTGCTCATCCAGTGGTGGCTGAGCCCGTGAAGTTCTCAGG	382
Qy	106	SerValIlePheAlaAsnSerLeuValTyrGlyAlaSerAspSerAsnValTyrAspLeuLeu	125
Db	383	ATGTCCTTCGCCAAGCCATCGGTGTACCGCGCTCTGACAGCAACGTCTATACCTCCTAA	442
Qy	126	LysAspLeuGluGluGlyIleGlnThrLeuMetGlyArgLeuGluAspGlySerProArg	145
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Qy	146	ThrGlyGlnIlePheIyegIlnThrTyrSerIyPheAspTrpAsnSerHisAsnAspAsp	165
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Db	563	GCACCTACTCAAGAACTACGGGCTGCTCTACTGCTTCCAGAAAGACATGACAAAGTTCGAG	622
Qy	186	ThrPheLeuArgIleValGlnCyArgSerValGluGlySerCySGlyPhe	202
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DEFINITION	CD106442	803 bp mRNA linear EST 15-MAY-2003	
ACCESSION	CD106442	AGENCOURT 14018626 NIH MGC 179 Homo sapiens cDNA clone	
VERSION	CD106442.1	IMAGE:30367261 5', mRNA sequence.	
FEATURES			

SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
REFERENCE Mammalia; Chordata; Craniata; Vertebrata; Euteleostomi;  
AUTHORS Eukaryota; Metazoa; Primates; Carnivora; Hominoidea; Homo.  
TITLE 1. (bases 1 to 803)  
JOURNAL NIH-MGC http://mgs.nci.nih.gov/  
COMMENT National Institutes of Health, Mammalian Gene Collection (MGC)  
Unpublished (1999)  
Contact: Robert Strausberg, Ph.D.  
Email: cgabs-remail.nih.gov  
Tissue Procurement: Dr. Michael Brownstein  
CDNA Library Preparation: Invitrogen Corp  
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)  
DNA Sequencing by: Agencourt Bioscience Corporation  
Clone distribution: MGC clone distribution information can be  
found through the I.M.A.G.E. Consortium/LNL at:  
http://image.lnl.gov  
Plate: NDMA428 row: c column: 14  
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/lab\_host="DH10B-Ton A ( T1 and T5 phage resistances)"  
/note="Organ: brain; Vector: PCMV-SPORE.1; Site: 1: EcoRV  
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directionally cloned (EcoRV site is destroyed upon  
cloning). Average insert size 1.1 kb. Library was  
constructed by (Invitrogen). Note: this is a NIH-MGC  
library."  
ORIGIN  
Alignment Scores:  
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Best Local Similarity: 92.63% Mismatches: 1  
Query Match: 97.85% Indels: 15  
Gaps: 1  
US-09-856-796b-2 (1-202) x CD106442 (1-803)  
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Db 104 CTTCAAGAGGAGGAGTGGCTTCCCAACCATTCCTTATCCAGGCTTTTGACACAGCTATG 163  
QY 41 LeuArgAlaHisArgLeuHisGlnLeuAlaPheAspThrTyrGlnGluPhe----- 57  
Db 164 CTCGGGCGCCATCTGTCACACAGCTGGCTTTGACACTACCAAGAGTTTGAAGAGCC 223  
QY 58 -----AanProGlnThrSerLeuCysPhe 65  
Db 224 TATATCCCAAGAAAGACAGATATTATTCTCTGCAAGACCCCAAGACCTCCCTGTTTC 283  
QY 66 SerGlnSerIleProThrProSerAsnArgGluThrGlnGlnIleSerLeuGln 85  
Db 284 TCAGAGCTATTCCGACACCTCCCAAGAGGAGAAACCAACAGAAATCCAACTCAG 343  
QY 86 LeuLeuArgIleSerLeuLeuLeuIleGlnSerTyrPheGlnProValGlnPheLeuArg 105  
Db 344 CTGCTCCGCAATCTCCCTGCTCATCCAGTGTGCTGAGAGCCGCTGAGATTCTCAGG 403  
QY 106 SerValPheAlaAsnSerLeuValTyrGlnAlaSerAspSerAsnValTyrAspLeuLeu 125  
Db 404 AGTGTCTTGGCCAAAGCCTGTGTGAGGCGGCTTGACAGCAACGCTTATGACCTCTCA 463

QY 126 LysAspLeuGluGlnGlyIleGlnThrLeuMetGlyArgLeuGlnAspGlySerProArg 145  
Db 464 AAGGACCTTAGAGAGGAGGATCCAAACGCTGATGGGAGGCTGGAAGATGGAGCCCGG 523  
QY 146 ThrGlnGlnIlePheLeuGlnThrTyrSerIlePheAspThrAsnSerHisAsnAsp 165  
Db 524 ACTGGGAGATTTTCAAGACAGCACTACAGCAAGTTGACACAACTCACAACAGATGAC 583  
QY 166 AlaLeuLeuLysAsnTyrGlyLeuLeuTyrCysPheArgIleAspMetAspLysValGlu 185  
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QY 186 ThrPheLeuArgIleValGlnCysArgSerValGlnGlySerCysGlyPhe 202  
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LOCUS  
DEFINITION AGENCOURT 14016902 NIH-MGC\_179 Homo sapiens CDNA clone  
IMAGE:30365268 5', mRNA sequence.  
ACCESSION CD108431  
VERSION  
KEYWORDS  
SOURCE  
ORGANISM Homo sapiens (human)  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Carnivora; Hominoidea; Homo.  
REFERENCE 1 (bases 1 to 803)  
AUTHORS NIH-MGC http://mgs.nci.nih.gov/  
TITLES National Institutes of Health, Mammalian Gene Collection (MGC)  
JOURNAL Unpublished (1999)  
COMMENT Contact: Robert Strausberg, Ph.D.  
Email: cgabs-remail.nih.gov  
Tissue Procurement: Dr. Michael Brownstein  
CDNA Library Preparation: Invitrogen Corp  
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)  
DNA Sequencing by: Agencourt Bioscience Corporation  
Clone distribution: MGC clone distribution information can be  
found through the I.M.A.G.E. Consortium/LNL at:  
http://image.lnl.gov  
Plate: NDMA422 row: p column: 13  
High quality sequence stop: 635.  
Location/Qualifiers  
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/lab\_host="DH10B-Ton A ( T1 and T5 phage resistances)"  
/note="Organ: brain; Vector: PCMV-SPORE.1; Site: 1: EcoRV  
(destroyed); Site 2: NotI; Library is destroyed upon  
directionally cloned (EcoRV site is destroyed upon  
cloning). Average insert size 1.1 kb. Library was  
constructed by (Invitrogen). Note: this is a NIH-MGC  
library."  
ORIGIN  
Alignment Scores:  
Pred. No.: 2,73e-112 Length: 803  
Score: 1024.50 Matches: 201  
Percent Similarity: 92.63% Conservative: 0  
Best Local Similarity: 92.63% Mismatches: 1  
Query Match: 97.85% Indels: 15  
Gaps: 1  
US-09-856-796b-2 (1-202) x CD108431 (1-803)  
QY 1 MetAlaThrGlySerArgThrSerLeuLeuAlaPheGlyLeuLeuCysLeuProTyr 20

[illegible]

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/clone="IMAGE:30367288"
/tissue_type="Pituitary"
/lab_host="DH10B-Ton A ( T1 and T5 phage resistances )"
/clone_1lb="NIH_MGC_179"
/note="Organ: brain; Vector: pCMV-SPORE6.1; Site_1: EcoRV
(destroyed) ; Site_2: NotI; library is oligo-dT primed and
directionally cloned (EcoRV site is destroyed upon
cloning). Average insert size 1.1 kb. library was
constructed by (Invitrogen). Note: this is a NIH_MGC
library."

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Best Local Similarity:	92.63%	Conservative:	0
Query Match:	92.63%	Mismatches:	1
DB:	97.85%	Indels:	15
		Gaps:	1

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QY      21 LeuGInGluGlySerAlaPheProThrIleProLeuSerArgLeuPheAspAlaSer 40
Db      104 CTTCAAGAGGGCAGTGCCTTCCCAACCATTCCTTATTCAGGCTTTTGGACACGCTATG 16:
QY      41 LeuArgAlaHisArgLeuHisGlnLeuAlaPheAspThrTyrGlnGluPhe----- 57
Db      164 CTCGGCGCCCATGCTCTGACACAGCTGGCTTGGACACCTACAGGAGGTGGAAAGAGCC 22:
QY      58 -----AsnProGlnThrSerLeuCyPhe 65
Db      224 TATATCCCAAGAACAGAGTATTCATTCCTCTGACAGACCCCAAGACCTCCCTGTTTC 283
QY      66 SerGluSerIleProThrProSerAsnArgGluGluThrGlnGlnIlySerAsnLeuGlu 85
Db      284 TCGAGCTCTATTCGACACCCCTCCACAGGAGGAAACACACAGAAATCCACTTAGAG 343
QY      86 LeuLeuArgIleSerLeuLeuLeuIleGlnSerTrpLeuGluProValGlnPheLeuArg 105
Db      344 CTGCTCCGCACTCTCCCTGCTGCTCATCCAGTCAGTGGCTGAGCCCGTGCAAGTTCTCAAG 403
QY      106 SerValPheAlaAsnSerLeuValTyrGlyAlaSerAspSerAsnValTyrAsnLeuLeu 125
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Db      464 AAGGACTTAGAGAGAGGAGCATCCAAACGCTGATGGGAGGCTGGAAAGATGGAGCCCGG 523
QY      146 ThrGlyGlnIlePheLeuGlnThrTyrSerIysPheAspThrAsnSerHisAsnAspAsp 165
Db      524 ACTGGGCGAGATCTTCACAGCAGACCTACAGCAAGTTCCACACAACTCACACAAAGATGAC 583
QY      166 AlaLeuLeuLysAsnTyrGlyLeuLeuTyrCyPheArgLysAspMetAspLysValGlu 185
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QY      186 ThrPheLeuArgIleValGlnCysArgSerValGluGlySerCysGlyPhe 202
Db      644 ACATTCCTGGCGCATCTGCAAGTGCCTGCTGTGAGAGGCGAGCTGTGCTTC 694

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GenCore version 5.1.6  
Copyright (c) 1993 - 2005 CompuGen Ltd.

OM protein - protein search, using SW model

Run on: February 6, 2005, 12:55:23 ; Search time 40 Seconds

(without alignments)  
485,895 Million cell updates/sec

Title: US-09-856-796B-2

Perfect score: 1047

Sequence: 1 MATGSRSTLLAFLGLCLPW.....KYETFLRIYVCRSVSGSGF 202

Scoring table:

BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 283416 segs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0  
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%  
Maximum Match 100%

Listing first 45 summaries

Database :

PIR.79:\*  
1: pir1.\*  
2: pir2.\*  
3: pir3.\*  
4: pir4.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1024.5	97.9	217	1	STHU
2	981.5	93.7	217	1	STHU
3	939.5	89.7	217	1	STHUV
4	873.5	83.4	217	1	E32435
5	872.5	83.3	217	1	LCIHC
6	866.5	82.8	217	2	I67409
7	850.5	81.2	217	2	I53267
8	843.5	80.6	217	2	I67411
9	842.5	80.5	215	2	A26449
10	831.5	79.4	212	2	I67408
11	779.5	74.5	199	2	B32435
12	698	66.3	216	2	I46145
13	687	65.1	216	1	STPG
14	682	65.1	216	2	JC4632
15	682	65.1	216	2	S49483
16	679	64.9	216	2	B49159
17	679	64.9	216	1	STMS
18	677	64.7	217	1	STBO
19	672	64.2	216	2	A37782
20	666	63.6	217	1	STGT
21	666	63.6	217	1	STSH
22	666	63.6	217	1	S32682
23	661	63.1	216	1	STRT
24	614	58.6	256	1	STHUV2
25	603	57.6	190	2	JK0219
26	602	57.5	190	2	PN0140
27	601	57.4	190	1	A61584
28	598	57.1	190	2	US0429
29	596	56.9	190	1	STHO

30	551	52.6	216	2	S04929	somatotropin precu
31	550	52.5	216	2	A60509	somatotropin precu
32	542	51.8	216	2	UC1514	somatotropin precu
33	536	51.2	191	2	A60625	somatotropin - gre
34	480	45.8	190	2	S21750	somatotropin - Rus
35	471.5	45.0	215	2	JS0037	somatotropin - bul
36	467.5	44.7	215	2	IS1188	somatotropin - bul
37	465	44.4	195	2	IS1250	somatotropin - bul
38	449	42.9	190	2	A56816	somatotropin - bul
39	421.5	40.3	133	2	UN0387	somatotropin - bul
40	394.5	37.7	163	2	S04353	somatotropin - sel
41	386.5	36.9	209	2	UT0483	somatotropin I pre
42	374.5	35.8	183	2	A60623	somatotropin - blu
43	279.5	26.7	210	2	IS0763	somatotropin - nob
44	279.5	26.7	210	2	S21915	somatotropin - nob
45	278.5	26.6	210	2	S69262	somatotropin - nob

#### ALIGNMENTS

##### RESULT 1

STHU

somatotropin 1 precursor [validated] - human

N/Alternate names: growth hormone 1; hGH-N; pituitary somatotropin

N/Contains: growth hormone 5K peptide; somatotropin 1, long form; somatotropin 1, short

C/Species: Homo sapiens (man)

C/Date: 24-Apr-1984 #sequence\_revision 10-Feb-1995 #text\_change 09-Jul-2004

R/Accession: A93731; A32435; A93694; A94247; A90051; A93397; A93778; A91764; A90217; A9

R/Idenoto, F.M.; Moore, D.D.; Goodman, H.M.

Nucleic Acids Res. 9, 3719-3730, 1981

A/Title: Human growth hormone DNA sequence and mRNA structure: possible alternative spl

A/Reference number: A93731; MUID:6201939; PMID:6269091

A/Accession: A93731

A/Molecule type: DNA

A/Residues: 1-217 <CHES>

A/Cross-references: UNIPROT:P01241; GB:V00520

R/Roskam, W.; Rougeon, F.

Nucleic Acids Res. 7, 305-320, 1979

A/Title: Molecular cloning and nucleotide sequence of the human growth hormone structural

A/Reference number: A93694; MUID:80034477; PMID:386281

A/Accession: A93694

A/Molecule type: mRNA

A/Residues: 1-217 <ROS>

A/Cross-references: GB:V00519

R/Martini, J.A.; Halliwell, R.A.; Baxter, J.D.; Goodman, H.M.

Science 205, 602-607, 1979

A/Title: Human growth hormone: complementary DNA cloning and expression in bacteria.

A/Reference number: A94247; MUID:79203293; PMID:377496

A/Accession: A94247

A/Molecule type: mRNA

A/Residues: 1-217 <MAR>

R/Li, C.H.; Dixon, J.S.; Liu, W.K.

Arch. Biochem. Biophys. 133, 70-91, 1969

A/Title: Human pituitary growth hormone. XIX. The primary structure of the hormone.

A/Contents: annotation

R/Li, C.H.; Dixon, J.S.

Arch. Biochem. Biophys. 146, 233-236, 1971

A/Title: Human pituitary growth hormone. XXXII. The primary structure of the hormone: rev

A/Reference number: A90051; MUID:72143935; PMID:5144027

A/Accession: A90051

A/Molecule type: protein

C/Comment: The gene for this hormone is transcribed only in somatotrophic cells of the rat.

C/Comment: About 90% of somatotropin is the 22k long form.

C/Genetics:

A:Gene: GDB:GHI

A:Cross-references: GDB:119982; OMIM:139250

A:Map position: 17q23.1-17q23.3

A:introns: 4/1; 57/3; 97/3; 152/3

C:Superfamily: prolactin

C:Keywords: alternative splicing; hormone; pituitary

F:1-26/Domain: signal sequence #status predicted <SIG>

F:27-217/Product: somatotropin 1, long form #status experimental <SOL>

F:27-69/Product: growth hormone 5k peptide #status experimental <SKP>

F:27-57,73-217/Product: somatotropin 1, short form #status experimental <SOS>

F:79-191,208-215/Disulfide bonds: #status experimental

Query Match

Best Local Similarity 97.9%; Score 1024.5; DB 1; Length 217;

Matches 201; Conservative 92.6%; Pred. No. 5,9e-86; Indels 15; Gaps 1;

Matches 201; Conservative 0; Mismatches 1;

QY 1 MATGRTSLILAFGLICLPWLOEGSAFPTIPISRLFDNMLSRARHQAFTDYQEEF--- 57

1 MATGRTSLILAFGLICLPWLOEGSAFPTIPISRLFDNMLSRARHQAFTDYQEEEA 60

DB 61 YIPKEQYAFLOPPQTSCLGSSBIPSPNSREETQOKSNLELARSILLIQSWLEPVQFLR 120

QY 58 -----NPQTSCLGSSBIPSPNSREETQOKSNLELARSILLIQSWLEPVQFLR 105

106 SVFANSLVYGASDSNYVDLLKDLKEGIQTLMGRLDEGSPRTGQIPKQYTSKFTDTSNDD 165

121 SVFANSLVYGASDSNYVDLLKDLKEGIQTLMGRLDEGSPRTGQIPKQYTSKFTDTSNDD 180

QY 166 ALKNYGLLYCFPRKMDKVFPLRIVQCRSVEGSCGF 202

181 ALKNYGLLYCFPRKMDKVFPLRIVQCRSVEGSCGF 217

DB

RESULT 2

167410

Somatotropin - rhesus macaque

N:Alternate names: growth hormone

C:Species: Macaca mulatta (rhesus macaque)

C>Date: 31-May-1996 #sequence\_revision 31-May-1996 #text\_change 09-Jul-2004

C:Accession: 167410; A05094

R:Gelos, T.G.; Durning, M.; Fisher, J.M.; Fowler, P.D.

Endocrinology 133, 1744-1752, 1993

A>Title: Cloning of four growth hormone/chorionic somatomammotropin-related complementary

A:Reference number: I53267; MUID:94008724; PMID:8404617

A:Accession: 167410

A:Status: translated from GB/EMBL/DBJ

A:Statistic type: mRNA

A:Residue type: 1-217 <RES>

A:Cross-references: UNIPROT:P33093; GB:LI6556; NID:9293114; PIDN:AAA18842.1; PID:9293115

R:Li, C.H.; Chung, D.; Lahm, H.W.; Stein, S.

Arch. Biochem. Biophys. 245, 287-291, 1986

A>Title: The primary structure of monkey pituitary growth hormone.

A:Reference number: A05094; MUID:86129460; PMID:3080959

A:Accession: A05094

A:Molecule type: protein

A:Residues: 27-99, 'Q', 101-178, 'D', 180-217 <LIC>

A>Note: The monkey species is not identified in the reference

R:Raben, M.S.

Science 125, 883-884, 1957

A>Title: Preparation of growth hormone from pituitaries of man and monkey.

A:Reference number: A44774

A:Contents: annotation; identification of source organism

C:Superfamily: Prolactin

Query Match

93.7%; Score 981.5; DB 2; Length 217;

Best Local Similarity 88.9%; Pred. No. 4,9e-82;

Matches 193; Conservative 3; Mismatches 6; Indels 15; Gaps 1;

1 MATGRTSLILAFGLICLPWLOEGSAFPTIPISRLFDNMLSRARHQAFTDYQEEF--- 57

Db 1 MAAGSRTSLILAFALCLPWLQEGSAFPTTPIPLSRLEFDNAMLRAHRLHQAADTYQEEFA 60  
 QY 58 -----NPQTSICFSESIPTPSNREETOQKSNLELRISLLIQSWLEPVQFLR 105  
 Db 61 YIPKQKYSFLOQVQTSICFSESIPTPSNREETOQKSNLELRISLLIQSWLEPVQFLR 120  
 QY 106 SVFANSILVYGASDSNVYDLKDLKEGIGTLMGRLEDSGSPRTQGFQKQTSKPDTSNHNDD 165  
 Db 121 SVFANSILVYGTSVSDYVDLKDLEEGIGTLMGRLEDSGSPRTQGFQKQTSKPDTSNHNDD 180  
 QY 166 ALKKNYGLLYCFRKMDKVEFTFLRIYVQCRSVGSGCF 202  
 Db 181 ALKKNYGLLYCFRKMDKVEFTFLRIYVQCRSVGSGCF 217

## RESULT 3

## STHUV

somatotropin 2 precursor - human  
 N:Alternate names: growth hormone 2; growth hormone variant; hGH-V; placental somatotropin  
 N:Contains: somatotropin 2, long splice form; somatotropin 2, short splice form  
 C:Species: Homo sapiens (man)  
 C>Date: 17-Dec-1982 #sequence\_revision 10-Feb-1995 #text\_change 09-Jul-2004  
 C:Accession: D32435; B28072; A01511; I52104; A60711  
 R:Chen, E.Y.; Liao, Y.C.; Smith, D.H.; Barrera-Saldana, H.A.; Gelinas, R.E.; Seeburg, P.  
 Genomics 4, 479-497, 1989  
 A>Title: The human growth hormone locus: nucleotide sequence, biology, and evolution.  
 A:Reference number: A32435; MUID:89307277; PMID:2744760  
 A:Accession: D32435  
 A:Molecule type: DNA  
 A:Residues: 1-217 <CHE>  
 A:Cross-references: UNIPROT:P01242; GB:J03071; NID:G183148; PIDN:AAA52552.1; PID:G183152  
 R:Cooke, N.E.; Ray, J.; Emery, J.G.; Liebhauer, S.A.  
 J. Biol. Chem. 263, 9001-9006, 1988  
 A>Title: Two distinct species of human growth hormone-variant mRNA in the human placenta  
 A:Reference number: A92725; MUID:88243769; PMID:3379057  
 A:Accession: B28072  
 A:Molecule type: mRNA  
 A:Residues: 1-217 <COO>  
 R:Seeburg, P.H.  
 DNA 1, 239-249, 1982  
 A>Title: The human growth hormone gene family: nucleotide sequences show recent divergent  
 A:Reference number: A01511; MUID:83182010; PMID:7169009  
 A:Accession: A01511  
 A:Molecule type: DNA  
 A:Residues: 1-34, 'P', 36-217 <SEE>  
 R:Igout, A.; Scippo, M.L.; Frankeme, F.; Hennen, G.  
 Arch. Int. Physiol. Biochim. 96, 63-67, 1988  
 A>Title: Cloning and nucleotide sequence of placental hGH-V cDNA.  
 A:Reference number: I52104; MUID:89024984; PMID:2460050  
 A:Accession: I52104  
 A:Status: preliminary; translated from GB/EMBL/DBJ  
 A:Molecule type: mRNA  
 A:Residues: 1-217 <IGO>  
 A:Cross-references: GB:M38451; NID:G183179; PIDN:AAA35891.1; PID:G183180  
 R:Frankeme, F.; Scippo, M.L.; Van Beunen, J.; Igout, A.; Hennen, G.  
 J. Clin. Endocrinol. Metab. 71, 15-18, 1990  
 A>Title: Identification of placental human growth hormone as the growth hormone-V gene  
 A:Reference number: A60711; MUID:90317018; PMID:2196278  
 A:Accession: A60711  
 A:Molecule type: protein  
 A:Residues: 27-44/46-57 <FRA>  
 A:Experimental source: tissue placenta  
 A>Note: partial glycosylation was demonstrated by lectin binding  
 C:Comment: This gene is expressed by the placenta.  
 C:Genetics:  
 A:Gene: GDB:GH2  
 A:Cross-references: GDB:119983; OMIM:139240  
 A:Map position: 17q22-17q24  
 A:Introns: 4/1, 57/3, 97/3, 152/3  
 C:Superfamily: prolactin  
 C:Keywords: alternative splicing; glycoprotein; hormone; placenta  
 F:1-26/Domin: signal sequence #status predicted <StG>  
 F:27-217/Product: somatotropin 2, long splice form #status predicted <SOL>

F:27-57, 73-217/Product: somatotropin 2, short splice form #status predicted <SOS>  
 F:79-191, 208-215/Dissulfide bonds: #status predicted  
 F:166/Binding site: carbohydrate (Asn) (covalent) #status predicted

## Query Match

Best Local Similarity 89.7%; Score 939.5; DB 1; Length 217;  
 Matches 187; Conservative 4; Mismatches 11; Indels 15; Gaps 1;

QY 1 MATGSRSTSLILAFALCLPWLQEGSAFPTTPIPLSRLEFDNAMLRAHRLHQAADTYQEEF--- 57  
 Db 1 MAAGSRTSLILAFALCLPWLQEGSAFPTTPIPLSRLEFDNAMLRAHRLHQAADTYQEEFA 60  
 QY 58 -----NPQTSICFSESIPTPSNREETOQKSNLELRISLLIQSWLEPVQFLR 105  
 Db 61 YIPKQKYSFLOQVQTSICFSESIPTPSNREETOQKSNLELRISLLIQSWLEPVQFLR 120  
 QY 106 SVFANSILVYGASDSNVYDLKDLKEGIGTLMGRLEDSGSPRTQGFQKQTSKPDTSNHNDD 165  
 Db 121 SVFANSILVYGASDSNVYRLKDLKEGIGTLMGRLEDSGSPRTQGFQKQTSKPDTSNHNDD 180  
 QY 166 ALKKNYGLLYCFRKMDKVEFTFLRIYVQCRSVGSGCF 202  
 Db 181 ALKKNYGLLYCFRKMDKVEFTFLRIYVQCRSVGSGCF 217

## RESULT 4

## B32435

## choriomamotropin B precursor - human

N:Alternate names: chorionic somatomamotropin 2  
 C:Species: Homo sapiens (man)  
 C>Date: 29-Dec-1989 #sequence\_revision 29-Dec-1989 #text\_change 09-Jul-2004  
 C:Accession: B32435  
 R:Chen, E.Y.; Liao, Y.C.; Smith, D.H.; Barrera-Saldana, H.A.; Gelinas, R.E.; Seeburg, P.  
 Genomics 4, 479-497, 1989  
 A>Title: The human growth hormone locus: nucleotide sequence, biology, and evolution.  
 A:Reference number: A32435; MUID:89307277; PMID:2744760  
 A:Accession: B32435  
 A:Molecule type: DNA  
 A:Residues: 1-217 <CHE>  
 A:Cross-references: UNIPROT:Q14407; GB:J03071; NID:G183148; PIDN:AAA52553.1; PID:G18315  
 A:Status: preliminary  
 A:Gene: GDB:CSH2  
 A:Cross-references: GDB:119813; OMIM:118820  
 A:Map position: 17q22-17q24  
 C:Superfamily: prolactin

Query Match 83.4%; Score 873.5; DB 2; Length 217;  
 Best Local Similarity 79.3%; Pred. No. 3,4e-72;  
 Matches 172; Conservative 11; Mismatches 19; Indels 15; Gaps 1;

QY 1 MATGSRSTSLILAFALCLPWLQEGSAFPTTPIPLSRLEFDNAMLRAHRLHQAADTYQEEF--- 57  
 Db 1 MAAGSRTSLILAFALCLPWLQEGSAFPTTPIPLSRLEFDNAMLRAHRLHQAADTYQEEFA 60  
 QY 58 -----NPQTSICFSESIPTPSNREETOQKSNLELRISLLIQSWLEPVQFLR 105  
 Db 61 YIPKQKYSFLOQVQTSICFSESIPTPSNREETOQKSNLELRISLLIQSWLEPVQFLR 120  
 QY 106 SVFANSILVYGASDSNVYDLKDLKEGIGTLMGRLEDSGSPRTQGFQKQTSKPDTSNHNDD 165  
 Db 121 SVFANSILVYDSDYDLKDLKEGIGTLMGRLEDSGSPRTQGFQKQTSKPDTSNHNDD 180  
 QY 166 ALKKNYGLLYCFRKMDKVEFTFLRIYVQCRSVGSGCF 202  
 Db 181 ALKKNYGLLYCFRKMDKVEFTFLRIYVQCRSVGSGCF 217

## RESULT 5

## LCHUC

choriomamotropin A precursor [validated] - human  
 N:Alternate names: chorionic somatomamotropin 1; placental lactogen  
 C:Species: Homo sapiens (man)

C>Date: 23-Oct-1981 #sequence, revision 23-Oct-1981 #text, change 09-Jul-2004  
 C/Accession: G32435; A94422; I52342; A93833; A93192; A90054; A94427; A61283; I55229; I59  
 R/Chen, E.Y.; Liao, Y.C.; Smith, D.H.; Barrera-Saldana, H.A.; Gelinas, R.E.; Seeburg, P.  
 Genomics 4, 479-497, 1989  
 A/Title: The human growth hormone locus: nucleotide sequence, biology, and evolution.  
 A/Reference number: A32435; MUID:89307277; PMID:2744760  
 A/Accession: G32435  
 A/Molecule type: DNA  
 A/Residues: 1-217 <CHE>  
 A/Cross-references: UNIPROT:P01243; GB:J03071; NID:G183148; PIDN:AAA52551.1; PID:G183151  
 R/Goodman, H.M.; Denoto, F.; Fiddes, J.C.; Hallowell, R.A.; Page, G.S.; Smith, S.; Tisch  
 R/Goodman, H.M.; Denoto, F.; Fiddes, J.C.; Hallowell, R.A.; Page, G.S.; Smith, S.; Tisch  
 in Mobilization and Reassembly of Genetic Information, Scott, W.A., Werner, R., Joseph,  
 A/Reference number: A94422  
 A/Accession: A94422  
 A/Molecule type: mRNA  
 A/Residues: 1-217 <COO>  
 R/Tanaka, M.; Masuda, N.; Watahiki, M.; Yamakawa, M.; Shimizu, K.; Nagai, J.; Nakashima,  
 Biochem. Int. 16, 287-292, 1988  
 A/Title: cDNA cloning of human chorionic somatomammotropin-1 mRNA whose transcription wa  
 A/Reference number: I52342; MUID:88209096; PMID:2833050  
 A/Accession: I52342  
 A/Status: translated from GB/EMBL/DBJ  
 A/Molecule type: mRNA  
 A/Residues: 1-3 <TRAN>  
 A/Cross-references: GB:M35419; NID:G506822  
 R/Seeburg, L.M.; Birstein, Y.; Schechter, I.  
 Proc. Natl. Acad. Sci. U.S.A. 76, 3819-3823, 1979  
 A/Title: Primary structure of the NH-2-terminal extra piece of the precursor to human pl  
 A/Reference number: A93833; MUID:80034970; PMID:291043  
 A/Accession: A93833  
 A/Molecule type: protein  
 A/Residues: 1,3-26 <SHE>  
 A/Experimental source: placenta  
 R/Shine, J.; Seeburg, P.H.; Martial, J.A.; Baxter, J.D.; Goodman, H.M.  
 Nature 270, 494-499, 1977  
 A/Title: Construction and analysis of recombinant DNA for human chorionic somatomammotr  
 A/Reference number: A93192; MUID:78071761; PMID:593368  
 A/Accession: A93192  
 A/Molecule type: DNA  
 A/Residues: 50-217 <SHI>  
 A/Experimental source: placenta  
 R/Li, C.H.; Dixon, J.S.; Chung, D.  
 Arch. Biochem. Biophys. 155, 95-110, 1973  
 A/Title: Amino acid sequence of human chorionic somatomammotropin.  
 A/Reference number: A90054; MUID:73201971; PMID:4712450  
 A/Accession: A90054  
 A/Molecule type: protein  
 A/Residues: 27-217 <LIC>  
 A/Experimental source: placenta  
 R/Niell, H.D.  
 in Prolactin and Carcinogenesis, Proc. Fourth Tenovus Workshop Prolactin, Griffiths, K.,  
 A/Title: The chemistry of the human lactogenic hormones.  
 A/Reference number: A94427  
 A/Accession: A94427  
 A/Molecule type: protein  
 A/Residues: 27-217 <NIA>  
 A/Experimental source: placenta  
 R/Nic A Bhaid, N.; Tipton, K.R.  
 Biochem. Soc. Trans. 19, 205, 1991  
 A/Title: Catechol-O-methyltransferase from human placenta: purification and some propert  
 A/Reference number: A61283; MUID:91244006; PMID:2037148  
 A/Accession: A61283  
 A/Molecule type: protein  
 A/Residues: 27-46 <NTC>  
 A/Note: Chorionmammotropin apparently copurified with placental catechol-O-methyltransfer  
 R/Seeburg, L.M.; Handwerker, S.; McLaurin, W.D.; Lanner, M.  
 Nature New Biol. 233, 59-61, 1971  
 A/Title: Amino-acid sequence of human placental lactogen.  
 A/Reference number: A93401; MUID:72016313; PMID:5286363  
 A/Contents: annotation  
 R/Seeburg, L.M.; Handwerker, S.; McLaurin, W.D.; Lanner, M.  
 Nature New Biol. 235, 64, 1972  
 A/Reference number: A93405

A/Contents: annotation  
 R/Schneider, A.B.; Kowalski, K.; Russell, J.; Sherwood, L.M.  
 J. Biol. Chem. 254, 3782-3787, 1979  
 A/Title: Identification of the interchain disulfide bonds of dimeric human placental lact  
 A/Reference number: A92251; MUID:79173081; PMID:438159  
 A/Contents: annotation; dimeric disulfide bonds  
 R/Selby, M.J.; Barta, A.; Baxter, J.D.; Bell, G.I.; Eberhardt, N.L.  
 J. Biol. Chem. 259, 13131-13138, 1984  
 A/Title: Analysis of a major human chorionic somatomammotropin gene. Evidence for two fu  
 A/Reference number: I55229; MUID:85030426; PMID:6208192  
 A/Accession: I55229  
 A/Status: translated from GB/EMBL/DBJ  
 A/Molecule type: DNA  
 A/Residues: 1-217 <RES>  
 A/Cross-references: GB:K02401; NID:G181120; PIDN:AAA52115.1; PID:G181121  
 R/Seeburg, P.H.; Shine, J.; Martial, J.A.; Ullrich, A.; Goodman, H.  
 Trans. Assoc. Am. Physicians 90, 109-116, 1977  
 A/Title: Nucleotide sequence of a human gene coding for a polypeptide hormone.  
 A/Reference number: I59658; MUID:78160787; PMID:611657  
 A/Accession: I59658  
 A/Status: translated from GB/EMBL/DBJ  
 A/Molecule type: mRNA  
 A/Residues: 160-217 <RES>  
 A/Cross-references: GB:M25118; NID:G181124; PIDN:AAA5721.1; PID:G181125  
 C/Genetics:  
 A/Gene: GDB:CSH1  
 A/Cross-references: GDB:119084; OMIM:150200  
 A/Map position: 17q22-17q24  
 A/Intons: 4/1; 57/3; 97/3; 152/3  
 C/Superfamily: prolactin  
 C/Keywords: hormone; placenta  
 F/1-26/Domain: signal sequence #status experimental <SIG>  
 F/27-217/Product: chorionmammotropin A #status experimental <MAT>  
 F/79-191/Disulfide bonds: #status experimental  
 F/208-215/Disulfide bonds: (in monomeric form) #status experimental  
 F/208/Disulfide bonds: interchain (to 215 in dimeric form) #status experimental  
 F/215/Disulfide bonds: interchain (to 208 in dimeric form) #status experimental

Query Match 83.3%; Score 872.5; DB 1; Length 217;  
 Best Local Similarity 79.3%; Pred. No. 4.2e-72;  
 Matches 172; Conservative 11; Mismatches 19; Indels 15; Gaps 1;

QY	1	MATGSRISLLAFGLLCLPMTQEGSAFFPIPLSRFPNASTRAHRLQLAFDYQEF--	57
DB	1	MAPSRISLLAFGLLCLPMTQEGSAFFPIPLSRFPNASTRAHRLQLAFDYQEF--	60
QY	58	-----NPQSLCFSESIPTPSNREETQKSNLELRISLLISQSWLEPVQFLR	105
DB	61	YIPDQKYSFLHDSQTSFCFSDSIPTPEMETQKSNLELRISLLISQSWLEPVQFLR	120
QY	106	SVPANSLVYGASDSNVYDLKDLLEGITLMGRLEDSPRTGQIFKQYKSEPDNNSHND	165
DB	121	SWFANMLVYDSDSDYHLKDLLEGITLMGRLEDSPRTGQILKQYKSEPDNNSHND	180
QY	166	ALLKNYGLLYCPRKMDKYEFTLRIVQCRSVGSGCF	202
DB	181	ALLKNYGLLYCPRKMDKYEFTLRIVQCRSVGSGCF	217

RESULT 6  
 167409  
 chorionic somatomammotropin-3 - rhesus macaque  
 C/Species: Macaca mulatta (rhesus macaque)  
 C/Date: 31-May-1996 #sequence, revision 31-May-1996 #text, change 09-Jul-2004  
 C/Accession: I67409  
 R/Coloe, T.G.; Durning, M.; Fisher, J.M.; Fowler, P.D.  
 Endocrinology 133, 1744-1752, 1993  
 A/Title: Cloning of four growth hormone/chorionic somatomammotropin-related complementary  
 A/Reference number: I53267; MUID:94008724; PMID:8404617  
 A/Accession: I67409  
 A/Status: preliminary; translated from GB/EMBL/DBJ  
 A/Molecule type: mRNA  
 A/Residues: 1-217 <RES>



A:Cross-references: UNIPROT:Q07369; GB:LI6554; NID:g293112; PIDN:AAA18841.1; PID:g293113  
C:Superfamily: prolactin

## Query Match

Best Local Similarity 82.8%; Score 866.5; DB 2; Length 217;  
Matches 168; Conservative 14; Mismatches 20; Indels 15; Gaps 1;

QY 1 MATGSRSTLLAFGLCLPWLQEGSAPPTPLSLRFLDNASLRARHLQALAFDTYQEF--- 57  
DB 1 MAAGSRSTLLVFLVLLCLPWLQEGSAPPTPLSLRFLDNASLRARHLQALAFDTYQEF--- 57  
QY 58 -----NPQSLCFSESIPPTSNREETOQKSNLELRISLLLIQSWLEPVQFLR 105  
DB 61 YIPKEKHSIMGNPQASFCFSSESIPPTSNREETOQKSNLELRISLLLIQSWLEPVQFLR 120  
QY 106 SVFANSLVYGASDSNVYDLKDLREGIQTLMGRLEDSPRTGOIFKQYTSKPDTSNND 165  
DB 121 SVFANNLVYGTSSDAVDLKNLEBGIQTLMRKQDSSPRTGOIFKQYTSKPDTSNND 180  
QY 166 ALLKXVGLLYCFRKMDKVEFLRIYVQCRSVGSGCF 202  
DB 181 SLKKNYELHCFRKMDKVEFLRIYVQCRSVGSGCF 217

## RESULT 7

153267

chorionic somatomammotropin-1 - rhesus macaque  
C:Species: Macaca mulatta (rhesus macaque)

C:Date: 31-May-1996 #sequence\_revision 31-May-1996 #text\_change 09-Jul-2004

C:Accession: I53267

R:Golios, T.G.; Dunning, M.; Fisher, J.M.; Fowler, P.D.

Endocrinology 133, 1744-1752, 1993

A:Title: Cloning of four growth hormone/chorionic somatomammotropin-related complementat

A:Reference number: I53267; MUID:94008724; PMID:8404617

A:Accession: I53267

A:Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: mRNA

A:Residues: 1-217 <RES>

A:Cross-references: UNIPROT:Q07367; GB:LI6552; NID:g293108; PIDN:AAA18839.1; PID:g293109

C:Superfamily: prolactin

## Query Match

Best Local Similarity 81.2%; Score 850.5; DB 2; Length 217;  
Matches 164; Conservative 18; Mismatches 20; Indels 15; Gaps 1;

QY 1 MATGSRSTLLAFGLCLPWLQEGSAPPTPLSLRFLDNASLRARHLQALAFDTYQEF--- 57  
DB 1 MAAGSRSTLLVFLVLLCLPWLQEGSAPPTPLSLRFLDNASLRARHLQALAFDTYQEF--- 57  
QY 58 -----NPQSLCFSESIPPTSNREETOQKSNLELRISLLLIQSWLEPVQFLR 105  
DB 61 YIPKEKHSIMGNPQASFCFSSESIPPTSNREETOQKSNLELRISLLLIQSWLEPVQFLR 120  
QY 106 SVFANSLVYGASDSNVYDLKDLREGIQTLMGRLEDSPRTGOIFKQYTSKPDTSNND 165  
DB 121 SVFANNLVYGTSSDAVDLKNLEBGIQTLMRKQDSSPRTGOIFKQYTSKPDTSNND 180  
QY 166 ALLKXVGLLYCFRKMDKVEFLRIYVQCRSVGSGCF 202  
DB 181 SLKKNYELHCFRKMDKVEFLRIYVQCRSVGSGCF 217

## RESULT 8

167411

somatotropin - rhesus macaque  
N:Alternate names: growth hormone

C:Species: Macaca mulatta (rhesus macaque)

C:Date: 31-May-1996 #sequence\_revision 31-May-1996 #text\_change 09-Jul-2004

R:Golios, T.G.; Dunning, M.; Fisher, J.M.; Fowler, P.D.

Endocrinology 133, 1744-1752, 1993

A:Title: Cloning of four growth hormone/chorionic somatomammotropin-related complementat

A:Reference number: I53267; MUID:94008724; PMID:8404617

C:Accession: I53267

C:Superfamily: prolactin

A:Accession: I67411

A:Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: mRNA

A:Residues: 1-217 <RES>

A:Cross-references: UNIPROT:Q07370; GB:LI6555; NID:g293116; PIDN:AAA20180.1; PID:g293117

C:Superfamily: prolactin

## Query Match

Best Local Similarity 80.6%; Score 843.5; DB 2; Length 217;  
Matches 166; Conservative 14; Mismatches 22; Indels 15; Gaps 1;

QY 1 MATGSRSTLLAFGLCLPWLQEGSAPPTPLSLRFLDNASLRARHLQALAFDTYQEF--- 57  
DB 1 MAAGSRSTLLVFLVLLCLPWLQEGSAPPTPLSLRFLDNASLRARHLQALAFDTYQEF--- 57  
QY 58 -----NPQSLCFSESIPPTSNREETOQKSNLELRISLLLIQSWLEPVQFLR 105  
DB 61 YIPKEKHSIMGNPQASFCFSSESIPPTSNREETOQKSNLELRISLLLIQSWLEPVQFLR 120  
QY 106 SVFANSLVYGASDSNVYDLKDLREGIQTLMGRLEDSPRTGOIFKQYTSKPDTSNND 165  
DB 121 SVFANNLVYGTSSDAVDLKNLEBGIQTLMRKQDSSPRTGOIFKQYTSKPDTSNND 180  
QY 166 ALLKXVGLLYCFRKMDKVEFLRIYVQCRSVGSGCF 202  
DB 181 SLKKNYELHCFRKMDKVEFLRIYVQCRSVGSGCF 217

## RESULT 9

A26449

choriomammotropin precursor (allele hCS-3) - human  
C:Species: Homo sapiens (man)

C:Date: 30-Jun-1988 #sequence\_revision 30-Jun-1988 #text\_change 09-Jul-2004

C:Accession: A26449

R:Hirt, H.; Kimmelman, J.; Birnbaum, M.J.; Chen, E.Y.; Seeburg, P.H.; Eberhardt, N.L.; B

DNA 6, 59-70, 1987

A:Title: The human growth hormone gene locus: structure, evolution, and allelic variati

A:Reference number: A26449; MUID:87161235; PMID:3030680

A:Accession: A26449

A:Molecule type: DNA

A:Residues: 1-215 <HIR>

A:Cross-references: UNIPROT:P01243

C:Superfamily: prolactin

F:1-26/Domain: signal sequence #status predicted <SIG>

F:27-215/Product: choriomammotropin, hCS-3 allele #status predicted <MAN>

Query Match

Best Local Similarity 80.5%; Score 842.5; DB 2; Length 215;  
Matches 169; Conservative 12; Mismatches 19; Indels 17; Gaps 3;

QY 1 MATGSRSTLLAFGLCLPWLQEGSAPPTPLSLRFLDNASLRARHLQALAFDTYQEF--- 57  
DB 1 MAAGSRSTLLVFLVLLCLPWLQEGSAPPTPLSLRFLDNASLRARHLQALAFDTYQEF--- 57  
QY 58 -----NPQSLCFSESIPPTSNREETOQKSNLELRISLLLIQSWLEPVQFLR 105  
DB 61 YIPKEKHSIMGNPQASFCFSSESIPPTSNREETOQKSNLELRISLLLIQSWLEPVQFLR 120  
QY 106 SVFANSLVYGASDSNVYDLKDLREGIQTLMGRLEDSPRTGOIFKQYTSKPDTSNND 165  
DB 121 SVFANNLVYGTSSDAVDLKNLEBGIQTLMRKQDSSPRTGOIFKQYTSKPDTSNND 180  
QY 166 ALLKXVGLLYCFRKMDKVEFLRIYVQCRSVGSGCF 202  
DB 179 SLKKNYELHCFRKMDKVEFLRIYVQCRSVGSGCF 215

## RESULT 10

167408

chorionic somatomammotropin-2 - rhesus macaque (fragment)  
C:Species: Macaca mulatta (rhesus macaque)

C:Date: 31-May-1996 #sequence\_revision 31-May-1996 #text\_change 09-Jul-2004

C:Accession: I67408



R.Su. T.  
 Gene 69, 81-89, 1988  
 A:Title: A multistate-directed mutagenesis using T7 DNA polymerase: application for reor  
 A:Reference number: 146585; MUID:89137997; PMID:3224824  
 A:Accession: 146585  
 A:Status: preliminary; translated from GB/EMBL/DBJ  
 A:Molecule type: mRNA  
 A:Residues: 1-8, 'V', 10-21, 'Q', 23-42 <STX>  
 A:Cross-references: GB:M22761; NID:9164479; PIDN:AAA31046.1; PID:9164480  
 R.Yang, Q.; Zhu, B.L.; Zhou, S.W.; Qi, S.Z.  
 Chinese J. Biotechnol. 8, 318-323, 1992  
 A:Title: Cloning and partly sequencing of the porcine growth hormone (pGH) gene from pit  
 A:Reference number: PC1063  
 A:Accession: PC1063  
 A:Molecule type: mRNA  
 A:Residues: 97-108, 'E', 110-158 <YAN>  
 A:Experimental source: pituitary  
 R.Mills, J.B.; Howard, S.C.; Scapa, S.; Wilhelm, A.E.  
 J. Biol. Chem. 245, 3407-3415, 1970  
 A:Title: Cyanogen bromide cleavage and partial amino acid sequence of porcine growth hor  
 A:Reference number: A01516; MUID:7023161; PMID:4918150  
 A:Accession: A01516  
 A:Molecule type: protein  
 A:Residues: 27-30; 149-194, 'N', 196-216 <MTL>  
 R.Mills, J.B.  
 submitted to the Atlas, May 1971  
 A:Reference number: A94594  
 A:Accession: A94594  
 A:Molecule type: protein  
 A:Residues: 140-148 <MT2>  
 C:Genetics:  
 A:Gene: gh  
 A:Introns: 4/1; 57/3; 96/3; 150/3  
 C:Superfamily: prolactin  
 C:Keywords: anterior pituitary; growth factor; hormone  
 F:1-26/Domain: signal sequence #status predicted <SIG>  
 F:27-216/Product: somatotropin #status predicted <MAT>  
 F:206-214/Disulfide bonds: #status predicted  
 F:206-214/Disulfide bonds: #status experimental

Query Match 66.3%; Score 694; DB 1; Length 216;  
 Best Local Similarity 64.1%; Pred. No. 7.8e-56;  
 Matches 139; Conservative 20; Mismatches 42; Indels 16; Gaps 3;

QY 1 MATSRTSLIAFGILCLPWLQGSAPFTTILSRFDNASTLRARHLHQLAFDTYQEF--- 57  
 Db 1 MAAGPRTSALIAFALLCLPWTREVGAFAFAMPLSLFANAVLRAGHLHQLAADTYKEFERA 60  
 QY 58 -----NPQSLCFSESIPTPSNRETOOKSNLELRISLLILQSWLEPVQFLRS 106  
 Db 61 YIPBGQRYSIQNAQAACFCSETTIPAPTGKDEAQORSDEVLIRFSLILIQSWLGPVQFLSR 120  
 QY 107 VFANSLVYGASDSNVYDLKDLKEGIQTLMGRLLEDSPRTGQIFKQTYSKPTNSHND 166  
 Db 121 VFTNSLVFGTSD-RVYEKLDLEBGIQALMRELEDSPPRGQILKQTYDKFTNLRSDDA 179  
 QY 167 LKKNYGLLYCFKMDKVTETFLRIYQCRS-VEGSGCF 202  
 Db 180 LKKNYGLILSCFKDLHKAETYLIRVMKCRFPVSSCAF 216

RESULT 14  
 UC4632  
 somatotropin precursor - cat  
 N:Alternate names: growth hormone  
 C:Species: Felis silvestris catus (domestic cat)  
 C:Date: 10-Apr-1996 #sequence\_revision 24-May-1996 #text\_change 09-Jul-2004  
 C:Accession: UC4632  
 R.Warren, W.C.; Bentley, K.A.; Bogosian, G.  
 Gene 168, 247-249, 1996  
 A:Title: Cloning of the cDNA coding for cat growth hormone and prolactin.  
 A:Reference number: UC4631; MUID:96194906; PMID:8654953  
 A:Accession: UC4632

A:Molecule type: mRNA  
 A:Residues: 1-216 <WAR>  
 A:Cross-references: UNIPROT:P46404; GB:U25973; NID:9825768; PIDN:AAA67294.1; PID:98257  
 A:Experimental source: pituitary  
 C:Genetics:  
 A:Gene: gh  
 C:Superfamily: prolactin  
 C:Keywords: pituitary  
 F:1-26/Domain: signal sequence #status predicted <SIG>  
 F:27-216/Product: somatotropin #status predicted <MAT>

Query Match 65.6%; Score 687; DB 2; Length 216;  
 Best Local Similarity 63.6%; Pred. No. 3.4e-55;  
 Matches 138; Conservative 20; Mismatches 43; Indels 16; Gaps 3;

QY 1 MATSRTSLIAFGILCLPWLQGSAPFTTILSRFDNASTLRARHLHQLAFDTYQEF--- 57  
 Db 1 MAAGPRTSALIAFALLCLPWTREVGAFAFAMPLSLFANAVLRAGHLHQLAADTYKEFERA 60  
 QY 58 -----NPQSLCFSESIPTPSNRETOOKSNLELRISLLILQSWLEPVQFLRS 106  
 Db 61 YIPBGQRYSIQNAQAACFCSETTIPAPTGKDEAQORSDEVLIRFSLILIQSWLGPVQFLSR 120  
 QY 107 VFANSLVYGASDSNVYDLKDLKEGIQTLMGRLLEDSPRTGQIFKQTYSKPTNSHND 166  
 Db 121 VFTNSLVFGTSD-RVYEKLDLEBGIQALMRELEDSPPRGQILKQTYDKFTNLRSDDA 179  
 QY 167 LKKNYGLLYCFKMDKVTETFLRIYQCRS-VEGSGCF 202  
 Db 180 LKKNYGLILSCFKDLHKAETYLIRVMKCRFPVSSCAF 216

RESULT 15  
 S49483  
 somatotropin precursor - rabbit  
 N:Alternate names: growth hormone  
 C:Species: Oryctolagus cuniculus (domestic rabbit)  
 C:Date: 20-Feb-1995 #sequence\_revision 20-Feb-1995 #text\_change 09-Jul-2004  
 C:Accession: S49483  
 R.Wallis, O.C.; Wallis, M.  
 submitted to the EMBL Data Library, October 1994  
 A:Description: Cloning and sequencing of the gene for rabbit growth hormone.  
 A:Reference number: S49483  
 A:Accession: S49483  
 A:Status: preliminary  
 A:Molecule type: DNA  
 A:Residues: 1-216 <MAL>  
 A:Cross-references: UNIPROT:P46407; EMBL:Z38127; NID:9558682; PIDN:CAA86287.1; PID:9558  
 C:Superfamily: prolactin  
 A:Introns: 4/1; 57/3; 96/3; 150/3

Query Match 65.1%; Score 682; DB 2; Length 216;  
 Best Local Similarity 63.1%; Pred. No. 9.7e-55;  
 Matches 137; Conservative 21; Mismatches 43; Indels 16; Gaps 3;

QY 1 MATSRTSLIAFGILCLPWLQGSAPFTTILSRFDNASTLRARHLHQLAFDTYQEF--- 57  
 Db 1 MAAGPRTSALIAFALLCLPWTREVGAFAFAMPLSLFANAVLRAGHLHQLAADTYKEFERA 60  
 QY 58 -----NPQSLCFSESIPTPSNRETOOKSNLELRISLLILQSWLEPVQFLRS 106  
 Db 61 YIPBGQRYSIQNAQAACFCSETTIPAPTGKDEAQORSDEVLIRFSLILIQSWLGPVQFLSR 120  
 QY 107 VFANSLVYGASDSNVYDLKDLKEGIQTLMGRLLEDSPRTGQIFKQTYSKPTNSHND 166  
 Db 121 VFTNSLVFGTSD-RVYEKLDLEBGIQALMRELEDSPPRGQILKQTYDKFTNLRSDDA 179  
 QY 167 LKKNYGLLYCFKMDKVTETFLRIYQCRS-VEGSGCF 202  
 Db 180 LKKNYGLILSCFKDLHKAETYLIRVMKCRFPVSSCAF 216

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GenCore version 5.1.6  
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OM protein - nucleic search, using frame\_plus\_p2n model

Run on: February 7, 2005, 14:57:22 ; Search time 533 Seconds

(without alignments)

2181.351 Million cell updates/sec

Title:

Perfect score: US-09-856-796B-2

Sequence: 1 MATGSRSLIARGLCLPW.....KVEPLIRVQCRVSGSCGF 202

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Ygapop 10.0 , Ygapext 0.5  
Delop 6.0 , Delext 7.0

Searched: 4313806 segs, 287871033 residues

Total number of hits satisfying chosen parameters: 8627612

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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-FGAPOP=6 -FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

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7: /cg2\_6/ptodata/1/pubna/US08\_NEW\_PUB.seq.\*  
8: /cg2\_6/ptodata/1/pubna/US08\_PUBCOMB.seq.\*  
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23: /cg2\_6/ptodata/1/pubna/US60\_PUBCOMB.seq.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

Result No.	Score	Query Match	Length	ID	Description
1	1029.5	98.3	654	US-09-853-688-1	Sequence 1, Appli
2	1029.5	98.3	654	US-09-853-688-3	Sequence 3, Appli
3	1029.5	98.3	654	US-10-788-318-1	Sequence 1, Appli
4	1029.5	98.3	654	US-10-788-318-3	Sequence 3, Appli
5	1017.5	97.2	799	US-09-804-409A-17	Sequence 17, Appli
6	1017.5	97.2	799	US-10-411-037-47	Sequence 47, Appli
7	1017.5	97.2	799	US-10-411-037-47	Sequence 47, Appli
8	1017.5	97.2	799	US-10-411-037-47	Sequence 47, Appli
9	1017.5	97.2	799	US-10-411-037-47	Sequence 47, Appli
10	1017.5	97.2	799	US-10-411-037-47	Sequence 47, Appli
11	1017.5	97.2	799	US-10-411-037-47	Sequence 47, Appli
12	1017.5	97.2	799	US-10-411-037-47	Sequence 47, Appli
13	1017.5	97.2	799	US-10-411-037-47	Sequence 47, Appli
14	1017.5	97.2	799	US-10-411-037-47	Sequence 47, Appli
15	1016.5	97.1	651	US-10-410-913-47	Sequence 47, Appli
16	1010.5	96.5	821	US-10-477-651-1	Sequence 1, Appli
17	976.5	93.3	821	US-09-969-746C-3	Sequence 3, Appli
18	902	86.2	603	US-10-289-845-1	Sequence 1, Appli
19	902	86.2	606	US-10-621-693-46	Sequence 46, Appli
20	902	86.2	606	US-10-621-693-44	Sequence 44, Appli
21	898.5	85.8	1185	US-10-621-693-48	Sequence 48, Appli
22	898.5	85.8	1185	US-10-621-693-50	Sequence 50, Appli
23	898.5	85.8	1179	US-10-621-693-52	Sequence 52, Appli
24	898.5	85.8	1179	US-10-621-693-54	Sequence 54, Appli
25	898.5	85.8	2445	US-10-621-693-75	Sequence 75, Appli
26	895.5	85.5	587	US-10-621-693-81	Sequence 81, Appli
27	895.5	85.5	592	US-10-621-693-81	Sequence 81, Appli
28	895.5	85.5	645	US-10-153-207-5	Sequence 5, Appli
29	895.5	85.5	1158	US-10-621-693-36	Sequence 36, Appli
30	895.5	85.5	1158	US-10-621-693-36	Sequence 36, Appli
31	895.5	85.5	1737	US-10-621-693-83	Sequence 83, Appli
32	895.5	85.5	1743	US-10-621-693-31	Sequence 31, Appli
33	895.5	85.5	2307	US-10-621-693-85	Sequence 85, Appli
34	895.5	85.5	4867	US-10-153-207-7	Sequence 7, Appli
35	892.5	85.2	600	US-10-621-693-67	Sequence 67, Appli
36	892.5	85.2	602	US-10-621-693-65	Sequence 65, Appli
37	892.5	85.2	639	US-10-621-693-65	Sequence 65, Appli
38	892.5	85.2	740	US-10-621-693-69	Sequence 69, Appli
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40	891.5	85.1	573	US-10-311-473-8	Sequence 8, Appli
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43	891.5	85.1	579	US-09-819-094-19	Sequence 19, Appli
44	891.5	85.1	582	US-10-714-067-19	Sequence 19, Appli
45	891.5	85.1	588	US-10-332-733-29	Sequence 29, Appli
			17	US-10-621-693-7	Sequence 7, Appli

#### ALIGNMENTS

RESULT 1  
US-09-853-688-1, Application US/09853688  
Patent No. US20020081605A1  
GENERAL INFORMATION:  
APPLICANT: COOPER, DAVID N.  
APPLICANT: PROCTER, ANNIE M.  
APPLICANT: GREGORY, JOHN  
APPLICANT: MILLAR, DAVID S.  
TITLE OF INVENTION: METHOD FOR DETECTING GROWTH HORMONE VARIATIONS IN  
TITLE OF INVENTION: HUMANS, THE VARIATIONS AND THEIR USES  
FILE REFERENCE: WCM/8  
CURRENT APPLICATION NUMBER: US/09/853, 688  
CURRENT FILING DATE: 2001-05-14  
NUMBER OF SEQ ID NOS: 66  
SOFTWARE: PatentIn Ver. 2.1  
SEQ ID NO 1  
LENGTH: 654  
TYPE: DNA  
ORGANISM: Homo sapiens

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; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1) .. (651)
US-09-853-688-1

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Alignment Scores:

Pred. No.:	1029.50	Matches:	202
Score:			

Score:	93.09%	Conservative:	0
Percent Similarity:	93.09%	Mismatches:	0

Best Local Similarity:	95.02%	Indels:	15
Best Match:	98.33%	Indels:	1

DB: 9

US-09-856-796B-2 (1-202) x US-09-853-688-1 (1-654)

1 MetAlaThrGlySerArgThrSerLeuLeuAlaPheGly

Db  
1 ATGCTACAGGCTCCCGGACGTCCCTGCTTGGCC

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; APPLICANT: MILLAR, DAVID S.
; TITLE OF INVENTION: METHOD FOR DETECTING GROWTH HORMONE VARIATIONS IN
; FILE REFERENCE: WCM/8
; CURRENT APPLICATION NUMBER: US/10/788,318
; NUMBER OF FILING DATE: 2004-03-01
; NUMBER OF SEQ ID NOS: 66
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1
; LENGTH: 654
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)..(651)
; US-10-788-318-1

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Alignment Scores:
Pred. No.: 1.87e-129 Length: 654
Score: 1029.50 Matches: 202
Percent Similarity: 93.09% Conservative: 0
Best Local Similarity: 93.09% Mismatches: 0
Query Match: 98.33% Indels: 15
DB: 18 Gaps: 1

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US-09-856-796b-2 (1-202) x US-10-788-318-1 (1-654)

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QY 21 LeuGlnGluGlySerAlaPheProThrIleProLeuSerArgLeuPheAspAlaSer 40
Db 61 CTTCAGAGAGGCGAGCTGCTTCCCAACCATTCCTTACAGGCTTTTGACAAAGCTAGT 120
QY 41 LeuArgAlaHisArgLeuHisGlnLeuAlaPheAspThrTyrGlnGluPhe----- 57
Db 121 CTCGGCGCCCATGCTGACACAGCTGCTTGACACCTACAGAGGTTTGAAAGAACCC 180
QY 58 -----AsnProGlnThrSerLeuCysPhe 65
Db 181 TATATCCCAAGAGACAGAAATTCATTCCTGACAGACCCCAAGACCTCCCTGTTTC 240
QY 66 SerGlnSerIleProThrProSerAsnArgGluGlnThrGlnIleGlySerAsnLeuGlu 85
Db 241 TCAAGATCTATTCGACACCTCCCAACAGGAGGAAACACACAGAAATCCAACTAGAG 300
QY 86 LeuLeuArgIleSerLeuLeuLeuIleGlnSerTyrPheGlnProValGlnPheLeuArg 105
Db 301 CTGCTCCGATCTCCCTGCTGCTCATCTGCTGAGTCCGCTGAGCCCGTGCAGTTCC 360
QY 106 SerValPheAlaAsnSerLeuValTyrGlnAlaSerAspSerAsnValTyrAspLeuLeu 125
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QY 126 LysAspLeuGluGluGlyIleGlnThrLeuMetGlyArgLeuGluAspGlySerProArg 145
Db 421 AAGGACCTTAGAGAGAGGAGCATCCAAACGCTGATGGGAGGCTGGAAGATGGACGCC 480
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QY 166 AlaLeuLeuLysAsnTyrGlyLeuLeuTyrCysPheArgLysAspMetAspLysValGlu 185
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RESULT 4  
US-10-788-318-3

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; Sequence 3, Application US/10788318
; Publication No. US20040137510A1
; GENERAL INFORMATION:
; APPLICANT: COOPER, DAVID N.
; APPLICANT: PROCTER, ANNIE M.
; APPLICANT: GREGORY, JOHN
; APPLICANT: MILLAR, DAVID S.
; TITLE OF INVENTION: METHOD FOR DETECTING GROWTH HORMONE VARIATIONS IN
; FILE REFERENCE: WCM/8
; CURRENT APPLICATION NUMBER: US/10/788,318
; NUMBER OF FILING DATE: 2004-03-01
; NUMBER OF SEQ ID NOS: 66
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 3
; LENGTH: 654
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)..(651)
; US-10-788-318-3

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Alignment Scores:
Pred. No.: 1.87e-129 Length: 654
Score: 1029.50 Matches: 202
Percent Similarity: 93.09% Conservative: 0
Best Local Similarity: 93.09% Mismatches: 0
Query Match: 98.33% Indels: 15
DB: 18 Gaps: 1

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US-09-856-796b-2 (1-202) x US-10-788-318-3 (1-654)

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Db 1 ATGGCTACAGGCTCCGAGAGCTCCCTGCTGCTTTGGCTGCTGCTGCTGCTGCTGCTG 60
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Db 61 CTTCAGAGAGGCGAGCTGCTTCCCAACCATTCCTTACAGGCTTTTGACAAAGCTAGT 120
QY 41 LeuArgAlaHisArgLeuHisGlnLeuAlaPheAspThrTyrGlnGluPhe----- 57
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QY 58 -----AsnProGlnThrSerLeuCysPhe 65
Db 181 TATATCCCAAGAGACAGAAATTCATTCCTGACAGACCCCAAGACCTCCCTGTTTC 240
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QY 126 LysAspLeuGluGluGlyIleGlnThrLeuMetGlyArgLeuGluAspGlySerProArg 145
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QY 146 ThrGlyGlnIlePhePheGlnThrTyrSerIlePheAspThrAsnSerHisAsnAspAsp 165
Db 481 ACTGGGAGATCTTCAAGAGACCTTACAGCAAGTTCCACAAACTCCACACACATGAC 540
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QY 186 ThrPheLeuArgIleValGlnCysArgSerValGlnGlySerCysGlyPhe 202  
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RESULT 5  
US-09-804-409A-17  
Sequence 17, Application US/09804409A  
Patent No. US20020155100A1  
GENERAL INFORMATION:  
APPLICANT: KIEFFER, TIMOTHY J.  
APPLICANT: CHEUNG, ANTHONY T.  
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR REGULATED PROTEIN  
TITLE OF INVENTION: EXPRESSION IN GUT  
FILE REFERENCE: 02996/027 8721  
CURRENT APPLICATION NUMBER: US/09/804,409A  
CURRENT FILING DATE: 2001-03-12  
NUMBER OF SEQ ID NOS: 18  
SOFTWARE: PatentIn Ver. 2.1  
SEQ ID NO 17  
LENGTH: 799  
TYPE: DNA  
ORGANISM: Homo sapiens  
US-09-804-409A-17

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Pred. No.: 1,1e-127 Length: 799  
Score: 1017.50 Matches: 200  
Percent Similarity: 92.17% Conservative: 0  
Best Local Similarity: 92.17% Mismatches: 2  
Query Match: 97.18% Indels: 15  
DB: 9 Gaps: 1

US-09-856-796B-2 (1-202) x US-09-804-409A-17 (1-799)

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QY 21 LeuGlnGlnGlySerAlaPheProThrIleProLeuSerArgLeuPheAspAlaSer 40  
DB 101 CTTCAAGAGGGCGAGTCCCTCCCAACCACTTATCCAGGCCCTTTGACAGCGCTATG 160  
QY 41 LeuArgAlaHisArgLeuHisGlnLeuAlaPheAspThrTyrgInGluPhe----- 57  
DB 161 CTCGGGCGCCATGCTGTGCACACGCTGCTTGAACCTACAGAGATTGAAGAGCC 220  
QY 58 -----AspProGlnThrSerLeuCysPhe 65  
DB 221 TATATCCCAAGAGACAGAGATTATTCCTGCGAAGACCCCGACCTCCTCTGTTTC 280  
QY 66 SerGluSerIleProThrProSerAsnArgGlnGluThrGlnGlnLeuSerAsnLeuGlu 85  
DB 281 TCAGAGCTATTCCTCGACACCTCCCAACAGGAGAAACAAACAAATCCAACTAGAG 340  
QY 86 LeuLeuArgIleSerLeuLeuLeuIleGlnSerTrpLeuGlnProValGlnPheLeuArg 105  
DB 341 CTGCTCGGCACTCCCTGCTGCTCATCAAGTCGTGAGAGCCCTGTGAGATTCTCAGG 400  
QY 106 SerValPheAlaAsnSerLeuValTyrgIlaSerAspSerAsnValTyrgAspLeuLeu 125  
DB 401 AGGTCTCTCCCAACAGCTGTGTATCGGCGCTCTGACAGCAAGCTTATACCTCTCA 460  
QY 126 LysAspLeuGlnGlnGlyIleGlnThrLeuMetGlyArgLeuGlnAspGlySerProArg 145  
DB 461 AAGGAGCTAGAGGAGAGGATCCAAACGCTGATGGGAGGCTGGAGATGGAGCCCGCG 520  
QY 146 ThrIlyGlnIlePheLeuGlnThrTyrgSerLysPheAspThrAsnSerHisAsnAsp 165  
DB 521 ACTGGGCGATCTTCACAGCAAGCTTACAGCAAGATTGACAAACCAACAGATGAG 580  
QY 166 AlaLeuLeuLysAsnTyrgIlyLeuLeuTyrgPheArgLysAspPheLysValGlu 185  
DB 581 GCACCTACTCAAGAACTAGGGGCTGTCTACTGCTTACAGAGAGCAATGACAAAGTCTGAG 640

QY 186 ThrPheLeuArgIleValGlnCysArgSerValGlnGlySerCysGlyPhe 202  
DB 641 ACAATCTCGGCGATCGTGCATGCGCTCTGTGGAGGGAGCTGTGGCTTC 691

RESULT 6  
US-10-411-037-47  
Sequence 47, Application US/10411037  
Publication No. US20040043446A1  
GENERAL INFORMATION:  
APPLICANT: Neose Technologies, Inc.  
APPLICANT: DeFrees, Shawn  
APPLICANT: Zopf, David  
APPLICANT: Bayer, Robert  
APPLICANT: Hakes, David  
APPLICANT: Chen, Xi  
APPLICANT: Bove, Carym  
TITLE OF INVENTION: ALPHA GALACTOSIDASE A: REMODELING AND GLYCOCONJUGATION OF ALPHA  
TITLE OF INVENTION: GALACTOSIDASE A  
FILE REFERENCE: 040853-01-5082  
CURRENT APPLICATION NUMBER: US/10/411,037  
CURRENT FILING DATE: 2003-04-09  
PRIOR APPLICATION NUMBER: US 60/328,523  
PRIOR FILING DATE: 2001-10-10  
PRIOR APPLICATION NUMBER: US 60/344,692  
PRIOR FILING DATE: 2001-10-19  
PRIOR APPLICATION NUMBER: US 60/387,292  
PRIOR FILING DATE: 2002-06-07  
PRIOR APPLICATION NUMBER: US 60/391,777  
PRIOR FILING DATE: 2002-06-25  
PRIOR APPLICATION NUMBER: US 60/396,594  
PRIOR FILING DATE: 2002-07-17  
PRIOR APPLICATION NUMBER: US 60/404,249  
PRIOR FILING DATE: 2002-08-16  
PRIOR APPLICATION NUMBER: US 60/407,527  
PRIOR FILING DATE: 2002-08-28  
NUMBER OF SEQ ID NOS: 75  
SOFTWARE: PatentIn version 3.2  
SEQ ID NO 47  
LENGTH: 799  
TYPE: DNA  
ORGANISM: Homo sapiens  
US-10-411-037-47

Alignment Scores:  
Pred. No.: 1,1e-127 Length: 799  
Score: 1017.50 Matches: 200  
Percent Similarity: 92.17% Conservative: 0  
Best Local Similarity: 92.17% Mismatches: 2  
Query Match: 97.18% Indels: 15  
DB: 17 Gaps: 1

US-09-856-796B-2 (1-202) x US-10-411-037-47 (1-799)

QY 1 MetAlaThrGlySerArgThrSerLeuLeuAlaPheGlyLeuLeuCysLeuProTrp 20  
DB 41 ATGGCTACAGGCTCCCGGAGTCCCTGCTCTGCTTTGGCTGCTGCTGCTGCTGCTG 100  
QY 21 LeuGlnGlnGlySerAlaPheProThrIleProLeuSerArgLeuPheAspAlaSer 40  
DB 101 CTTCAAGAGGGCGAGTCCCTCCCAACCACTTATCCAGGCCCTTTGACAGCGCTATG 160  
QY 41 LeuArgAlaHisArgLeuHisGlnLeuAlaPheAspThrTyrgInGluPhe----- 57  
DB 161 CTCGGGCGCCATGCTGTGCACACGCTGCTTGAACCTACAGAGATTGAAGAGCC 220  
QY 58 -----AspProGlnThrSerLeuCysPhe 65  
DB 221 TATATCCCAAGAGACAGAGATTATTCCTGCGAAGACCCCGACCTCCTGTTTC 280  
QY 66 SerGluSerIleProThrProSerAsnArgGlnGluThrGlnGlnLeuSerAsnLeuGlu 85  
DB 281 TCAGAGCTATTCCTCGACACCTCCCAACAGGAGAAACAAACAAATCCAACTAGAG 340



QY 86 LeuLeuArgIleSerLeuLeuIleGlnSerTrpLeuGluProValGlnPheLeuArg 105  
Db 341 CTCTCCGCAATCTCCCTGCTGCTATCATCTCGTGGTGAAGCCGCGAGTCTTCAAG 400  
QY 106 SerValPheAlaIleSerLeuValTyrGlyAlaSerAspSerValTyrAspLeuLeu 125  
Db 401 AGTGCTTCGCAAGAGCCGCTGTGTAGCGGCGCTCTGACAGCAACGCTATGACTCTTA 460  
QY 126 LysAspLeuGluGluGlyIleGlnThrLeuMetGlyAArgLeuGluAspGlySerProArg 145  
Db 461 AAGCACTTGAAGAGAGCAAGCACTCAAGCAAGTTGACACAACTCACACAGATGAC 520  
QY 146 ThrGlyGlnIlePheLeuGlnThrTyrSerLysPheAspThrAsnSerHisAsnAsp 165  
Db 521 ACTGGGCAATCTTCAAGCAAGCACTCAAGCAAGTTGACACAACTCACACAGATGAC 580  
QY 166 AlaLeuLeuLysAsnTyrGlyLeuLeuTyrCysPheArgLysAspMetAspLysValGlu 185  
Db 581 GCACCTACTCAAGACTAGCGGCTGCTCTTCTGAGAGAGCAATGACAGAGTCTGAG 640  
QY 186 ThrPheLeuArgIleValGlnCysArgSerValGluGlySerCysGlyPhe 202  
Db 641 ACATTCTGCGCATCTGCGATGCGCGCTCTGTGAGAGGCACTGTGCTTC 691

## RESULT 7

US-10-411-026-47  
Sequence 47, Application US/10411026  
Publication No. US20040063911A1  
GENERAL INFORMATION:  
APPLICANT: Neose Technologies, Inc.  
APPLICANT: Defrees, Shawn  
APPLICANT: Zopf, David  
APPLICANT: Bayer, Robert  
APPLICANT: Hakes, David  
APPLICANT: Chen, Xi  
TITLE OF INVENTION: PROTEIN REMODELING METHODS AND PEPTIDES PRODUCED BY THE  
FILE REFERENCE: 040853-01-5053  
CURRENT APPLICATION NUMBER: US/10/411,026  
PRIOR FILING DATE: 2003-04-09  
PRIOR APPLICATION NUMBER: US 60/328,523  
PRIOR FILING DATE: 2001-10-10  
PRIOR APPLICATION NUMBER: US 60/344,692  
PRIOR FILING DATE: 2001-10-19  
PRIOR APPLICATION NUMBER: US 60/387,292  
PRIOR FILING DATE: 2002-06-07  
PRIOR APPLICATION NUMBER: US 60/391,777  
PRIOR FILING DATE: 2002-06-25  
PRIOR APPLICATION NUMBER: US 60/396,594  
PRIOR FILING DATE: 2002-07-17  
PRIOR APPLICATION NUMBER: US 60/404,249  
PRIOR FILING DATE: 2002-08-16  
PRIOR APPLICATION NUMBER: US 60/407,527  
PRIOR FILING DATE: 2002-08-28  
NUMBER OF SEQ ID NOS: 75  
SOFTWARE: PatentIn version 3.2  
SEQ ID NO 47  
LENGTH: 799  
TYPE: DNA  
ORGANISM: Homo sapiens  
US-10-411-026-47

## Alignment Scores:

Pred. No.: 1,1e-127 Length: 799  
Score: 1017.50 Matches: 200  
Percent Similarity: 92.17% Conservative: 0  
Best Local Similarity: 92.17% Mismatches: 2  
Query Match: 97.18% Indels: 15  
DB: 17 Gaps: 1

US-09-856-796b-2 (1-202) x US-10-411-026-47 (1-799)

QY 1 MetaLThrGlySerArgTrpSerLeuLeuAlaPheGlyLeuLeuCysLeuProTyr 20  
Db 41 ATGGCTTCAAGAGCTCCCGAGAGCTCTGCTCTTCTGCTTCTGCTCTGCTCTGCTG 100  
QY 21 LeuGlnGluGlySerAlaPheProThrIleProLeuSerArgLeuPheAsnAlaSer 40  
Db 101 CTTCAGAGAGGAGCTGCTCTTCCCAACATTCCTTATCCAGGCTTTTGAACAGCTATG 160  
QY 41 LeuArgAlaHisArgLeuHisGlnLeuAlaPheAspThrTyrGlnGluPhe----- 57  
Db 161 CTTCGGGCCATCTGTGACCAAGCTGCGCTTGAACCTACAGAGATTGAAGAAGCC 220  
QY 58 -----AspProGlnThrSerLeuCysPhe 65  
Db 221 TATATCCAAAGAGACAGAAATTCATTCCTGCAAGACCCCAAGACTCTCTGTTTC 280  
QY 66 SerGluSerIleProThrProSerAsnArgGluGluThrGlnGlnLysSerLeuGlu 85  
Db 281 TCAGAGTCAATTCACAGACCTTCCAAAGAGAGAGAAACACAGAAATCCAACTTAG 340  
QY 86 LeuLeuArgIleSerLeuLeuIleGlnSerTrpLeuGluProValGlnPheLeuArg 105  
Db 341 CTGCTCCGCAATCTCCCTGCTCATCAAGTGTGCTGAGACCCGCTGCAAGTCTCTCAG 400  
QY 106 SerValPheAlaIleSerLeuValTyrGlyAlaSerAspSerAsnValTyrAspLeuLeu 125  
Db 401 AGTGCTTCGCAAGAGCCGCTGTGTAGCGGCTCTGACAGCAAGCTATGACTCTTA 460  
QY 126 LysAspLeuGluGluGlyIleGlnThrLeuMetGlyAArgLeuGluAspGlySerProArg 145  
Db 461 AAGCACTTGAAGAGAGCAAGCACTCAAGCAAGTTGACACAACTCACACAGATGAC 520  
QY 146 ThrGlyGlnIlePheLeuGlnThrTyrSerLysPheAspThrAsnSerHisAsnAsp 165  
Db 521 ACTGGGCAATCTTCAAGCAAGCACTCAAGCAAGTTGACACAACTCACACAGATGAC 580  
QY 166 AlaLeuLeuLysAsnTyrGlyLeuLeuTyrCysPheArgLysAspMetAspLysValGlu 185  
Db 581 GCACCTACTCAAGACTAGCGGCTGCTCTTCTGAGAGAGCAATGACAGAGTCTGAG 640  
QY 186 ThrPheLeuArgIleValGlnCysArgSerValGluGlySerCysGlyPhe 202  
Db 641 ACATTCTGCGCATCTGCGATGCGCGCTCTGTGAGAGGCACTGTGCTTC 691

## RESULT 8

US-10-410-962-47  
Sequence 47, Application US/10410962  
Publication No. US20040077836A1  
GENERAL INFORMATION:  
APPLICANT: Neose Technologies, Inc.  
APPLICANT: Defrees, Shawn  
APPLICANT: Zopf, David  
APPLICANT: Bayer, Robert  
APPLICANT: Hakes, David  
APPLICANT: Chen, Xi  
TITLE OF INVENTION: GRANULOCYTE COLONY STIMULATING FACTOR: REMODELING AND  
FILE REFERENCE: 040853-01-5054  
CURRENT APPLICATION NUMBER: US/10/410,962  
PRIOR FILING DATE: 2003-04-09  
PRIOR APPLICATION NUMBER: US 60/328,523  
PRIOR FILING DATE: 2001-10-10  
PRIOR APPLICATION NUMBER: US 60/344,692  
PRIOR FILING DATE: 2001-10-19  
PRIOR APPLICATION NUMBER: US 60/387,292  
PRIOR FILING DATE: 2002-06-07  
PRIOR APPLICATION NUMBER: US 60/391,777  
PRIOR FILING DATE: 2002-06-25  
PRIOR APPLICATION NUMBER: US 60/396,594  
PRIOR FILING DATE: 2002-07-17  
PRIOR APPLICATION NUMBER: US 60/404,249  
PRIOR FILING DATE: 2002-08-16

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? PRIOR APPLICATION NUMBER: US 60/407,527
? PRIOR FILING DATE: 2002-08-28
? NUMBER OF SEQ ID NOS: 75
? SOFTWARE: PatentIn version 3.2
? SEQ ID NO: 47
? LENGTH: 789
? TYPE: DNA
? ORGANISM: Homo sapiens
? US-10-410-962-47

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Alignment Scores:	
Pred. No.:	1.1e-127
Score:	1017.50
Percent Similarity:	92.17%
Best Local Similarity:	92.17%
Query Match:	97.18%
DB:	17
Length:	796
Matches:	0
Conservative:	20
Mismatches:	2
Indels:	15
Gaps:	1

QY	1	MetAlaThrIleGlySerAlaGlnThrSerLeuLeuLeuAlaPheGlyLeuLeuGlyCysLeuProThr	20
Db	41	ATGGCTACAGAGGCTCCCGAGAGCTCCGCTCTGCTGCTTGGCTTGGCTCTGCTGCTGCTGCTG	100
QY	21	LeuGlnGlnGlySerAlaPheProThrIleProLeuSerArgLeuPheAspAlaSer	40
Db	101	CTTCAGAGGAGGAGTGGCTTCCACCACTTCCCTTATCCAGGCGCTTTTGACACGCTATG	160
QY	41	LeuArgAlaHisArgLeuHisGlnLeuAlaPheAspThrTyrGlnGluPhe-----	57
Db	161	CTCCGCGCCCATCGCTCTGACACAGCTGGCTTTGACACCTACAGGAGGTGTGAAGAGGCC	220
QY	58	-----AsnProGlnThrSerLeuGlyPhe	65
Db	221	TATATCCCAAGAAACAGAGTATTCTCTCTGACGAACCCCGACCTCCCTCTGTTTC	280
QY	66	SerGlnSerIleProThrProSerAsnArgGlnGlnThrGlnGlnGlySerAsnLeuGln	85
Db	281	TCAAGAGCTATTCCGACACCTCCCAACGGGAGGAAACACACAGAAATCCAACTTAGAG	340
QY	86	LeuLeuArgIleSerLeuLeuLeuIleGlnSerTyrLeuGlnProValGlnPheLeuArg	105
Db	341	CTGCTCGGCATCTCCCTGCTGCTCATCCAGTGTGGCTGGAGCCGTCAGTACTCTCAGG	400
QY	106	SerValPheAlaAsnSerLeuValTyrGlnAlaSerAspSerAsnValTyrAspLeuLeu	125
Db	401	AGTGTCTTCGCCAAGAGCTGGTGTGACGGCGCTCTGACAGCAAGCTTATGACTCTCTTA	460
QY	126	LysAspLeuGlnGlnGlyTyrIleGlnThrLeuMetGlyArgLeuGlnAspGlySerProArg	145
Db	461	AAGGACCTAAGAGGAGGATCCAAACGCTGATGGGAGGAGCTGGAGAGTGGAGGCCCGGG	520
QY	146	ThrGlyGlnIlePheLeuGlnThrTyrSerLysPheAspThrAsnSerHisAsnAspAsp	165
Db	521	ACTGGCGAGATCTTCAAGCAGACTTACACCAAGTTGACACAAATCTCACACACAGATGAC	580
QY	166	AlaLeuLeuLysAsnTyrGlyLeuLeuTyrCysPheArgLysAspMetAspLysValGln	185
Db	581	GGACTACTAAGAGACTAAGGGCTGCTCTACTGCTTACAGGAAGACATGTGACAAGGTGAG	640
QY	186	ThrPheLeuArgIleValGlnCysArgSerValGlnGlySerCysGlyPhe	202
Db	641	ACATTCTCTGCGATCGTGGACGTGCGCTGTGTGAGGAGGACGCTGTGTGCTTC	691

RESULT 9  
US-10-411-049-47  
; Sequence 47, Application US/10411049  
; Publication No. US2004008206A1  
GENERAL INFORMATION:  
APPLICANT: Neose Technology, Inc.  
APPLICANT: DeFeets, Shawn  
APPLICANT: Zopf, David  
APPLICANT: Bayer, Robert

```

? APPLICANT: Takes, David
?
? APPLICANT: Chen, Xi
?
? APPLICANT: Bowe, Caryn
?
? TITLE OF INVENTION: INTERFERON ALPHA: REMODELLING AND GLYCOCONJUGATION OF INTERFERON
?
? TITLE OF INVENTION: ALPHA
?
? FILE REFERENCE: 040853-01-5055
?
? CURRENT APPLICATION NUMBER: US/10/411,049
?
? CURRENT FILING DATE: 2003-04-09
?
? PRIOR APPLICATION NUMBER: US 60/328,523
?
? PRIOR FILING DATE: 2001-10-10
?
? PRIOR APPLICATION NUMBER: US 60/344,692
?
? PRIOR FILING DATE: 2001-10-19
?
? PRIOR APPLICATION NUMBER: US 60/387,292
?
? PRIOR FILING DATE: 2002-06-07
?
? PRIOR APPLICATION NUMBER: US 60/391,777
?
? PRIOR FILING DATE: 2002-06-25
?
? PRIOR APPLICATION NUMBER: US 60/396,594
?
? PRIOR FILING DATE: 2002-07-17
?
? PRIOR APPLICATION NUMBER: US 60/404,249
?
? PRIOR FILING DATE: 2002-08-16
?
? PRIOR APPLICATION NUMBER: US 60/407,527
?
? PRIOR FILING DATE: 2002-08-28
?
? NUMBER OF SEQ ID NOS: 75
?
? SOFTWARE: PatentIn version 3.2
?
? SEQ ID NO 47
?
? LENGTH: 799
?
? TYPE: DNA
?
? ORGANISM: Homo sapiens
?
? US-10-411-049-47

```

Alignment Scores:		
Pred. No.:	1.1e-127	length: 799
Score:	1017.50	Matches: 200
Percent Similarity:	92.17%	Conservative: 0
Best Local Similarity:	92.17%	Mismatches: 2
Query Match:	97.18%	Indels: 15
DB:	17	Gaps: 1

Qy	1	MetalarngIySerArgThrserleuleuualaphedgIyleuCybleuProTyr	20
Db	41	ATGGGTACAGGCTCCCGGACGTCTCGTCTCGGTGGCTTTGGCTGCTCTGCTGCTCGG	100
Qy	21	LeuGInGluGlySerIalapherProthrIleProleuSerArgLeuPheAspAsnAlaser	40
Db	101	CTTCAGAGAGGAGAGTGCTTCCCAACCAATCCCTTATCCAGGCTTTTGACAAGGCTATG	160
Qy	41	LeuArgAlaHisArgLeuHisGlnleuAlaphesPrThrTyGInGluPhe-----	57
Db	161	CTCCGGCCCATCGTCTGTGACACAGCTGGCTTTGACACCTACAGAGATTGAGAGAGCC	220
Qy	58	-----AsnProGlnThrSerleuCybPhe	65
Db	221	TATATCCCAAGGACAGAGATTATCATCTCGACAGACCCCAACCTCTCTGTGTTTC	280
Qy	66	SerGlnSerIleProThrProserAnaArgGluGlnThrgInGluLysSerAsnleuGlu	85
Db	281	TCAGAGCTATTCGACACCTCTCCACAGGAGGAAACACAGAAATCCAACCTAGAG	340
Qy	86	LeuLeuArgIleSerleuLeuLeuIleGlnSerTyrLeuGluProValGlnPheleuArg	105
Db	341	CTGGTCGGCACTCTCCGTGCTCAATCCAGTCGTGGCTGAGGCCGTGACGATGTCCTCAGG	400
Qy	106	SerValPheAlaAsnSerLeuValTyrgIyAlaSerAspSerAsnAlaTyrspleuLeu	125
Db	401	AGTGTCTTCCGCCAACACCTGCTGTAGAGGGGCTCTGACAGCAACCTTATAGACCTCTTA	460
Qy	126	LysAspLeuGluGluGlyIleGlnThrLeuMetGlyArgLeuGluAspGlySerProArg	145
Db	461	AAGAGCCTAGAGGAAAGCATCCAAACCTGATGGGGAGGTGGAAATGGACACCCCGG	520
Qy	146	ThrGlyGlnIleleuPyrGlnThrTySerLysPheAspThrAsnSerHisAsnAspAsp	165

Db 521 ACTGGGAGATCTTCAAGAGAGCTTACAGAGTTGACACAACTCAACAGATGAC 580  
 Qy 166 AAlauleuLysAsnTyrGlyLeuTyrCyspheArgLysAspMetAspLysValGlu 185  
 Db 581 GCACCTACTCAAGAACTACCGGCTGCTCTACTCTTACAGAGAGCAATGACAAAGTCCAG 640  
 Qy 186 ThrPheLeuArgIleValGlnCysArgSerValGluGlySerCysGlyPhe 202  
 Db 641 ACATTCTGGCATCTGTGAGTGCCTCTGTGAGAGGAGGAGCTGTGCTTC 691

## RESULT 10

US-10-410-930-47  
 ; Sequence 47, Application US/10410930  
 ; Publication No. US20040115168A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Neose Technologies, Inc.  
 ; APPLICANT: Defrees, Shawn  
 ; APPLICANT: Zopf, David  
 ; APPLICANT: Bayer, Robert  
 ; APPLICANT: Hakes, David  
 ; APPLICANT: Chen, Xi  
 ; APPLICANT: Bove, Caryn  
 ; TITLE OF INVENTION: INTERFERON BETA: REMODELING AND GLYCOCONJUGATION OF INTERFERON  
 ; FILE REFERENCE: 040853-01-5056  
 ; CURRENT APPLICATION NUMBER: US/10/410, 930  
 ; PRIOR FILING DATE: 2003-04-09  
 ; PRIOR APPLICATION NUMBER: US 60/328,523  
 ; PRIOR FILING DATE: 2001-10-10  
 ; PRIOR APPLICATION NUMBER: US 60/344,692  
 ; PRIOR FILING DATE: 2001-10-19  
 ; PRIOR APPLICATION NUMBER: US 60/387,292  
 ; PRIOR FILING DATE: 2002-06-07  
 ; PRIOR APPLICATION NUMBER: US 60/391,777  
 ; PRIOR FILING DATE: 2002-06-25  
 ; PRIOR APPLICATION NUMBER: US 60/396,594  
 ; PRIOR FILING DATE: 2002-07-17  
 ; PRIOR APPLICATION NUMBER: US 60/404,249  
 ; PRIOR FILING DATE: 2002-08-16  
 ; PRIOR APPLICATION NUMBER: US 60/407,527  
 ; PRIOR FILING DATE: 2002-08-28  
 ; NUMBER OF SEQ ID NOS: 75  
 ; SOFTWARE: PatentIn version 3.2  
 ; SEQ ID NO 47  
 ; LENGTH: 799  
 ; TYPE: DNA  
 ; ORGANISM: Homo sapiens  
 US-10-410-930-47

## Alignment Scores:

Pred. No.: 1,1e-127 Length: 799  
 Score: 1017.50 Matches: 200  
 Percent Similarity: 92.17% Conservative: 0  
 Best Local Similarity: 92.17% Mismatches: 2  
 Query Match: 97.18% Indels: 15  
 DB: 18 Gaps: 1

US-09-856-796b-2 (1-202) x US-10-410-930-47 (1-799)

Qy 1 MetaLathRGLysArgThrSerLeuLeuLeuAlaPheGlyLeuLeuCysLeuProTyr 20  
 Db 41 ATGGCTAACAGGCTCCCGAGAGCTCCCTGCTCTGCTTGGCTTGGCTGCTGCTGCTG 100  
 Qy 21 LeuGlnGluGlySerAlaPheProThrIleProLysSerArgLeuPheAspAsnAlaSer 40  
 Db 101 CTTCAAGAGGAGGAGGAGCTTCCCAACCAATTCCTTATCCAGGCTTTTGACAAACCTATG 160  
 Qy 41 LeuArgAlaIleArgLeuHisGlnLeuAlaPheAspThrTyrGlnGluPhe----- 57  
 Db 161 CTCGGCGCCCATCGTCTGACACAGCTGGCTTTGACACCTTACAGAGATTGAAGAACCC 220  
 Qy 58 -----AasnProGlnThrSerLeuCysPhe 65

Db 221 TATATCCAAAGAAAGAGATTATTCCTCCGAAAGACCCCAAGCTCTCTGTTTC 280  
 Qy 66 SerGluSerIleProThrProSerAsnArgGluGlnGlnGlnIleSerAsnLeuGlu 85  
 Db 281 TCAGAGTCTATTCCAGACCCCTCCAAACAGGAGGAAACACAGAAATCCAACTTAGAG 340  
 Qy 86 LeuLeuArgIleSerLeuLeuLeuIleGlnSerTyrPheGluProValGlnPheLeuArg 105  
 Db 341 CTGCTCCGATCTCTCTGCTCTGCTATCCAGTGTGAGTGTGAGCCCGTGCAGTTCCTCAGG 400  
 Qy 106 SerValPheAlaAsnSerLeuValTyrGlyValAspSerAsnValTyrAspLeuLeu 125  
 Db 401 AGTCTTCCGCAACAGCTCTGTGTACGGCCCTCTTGACACCAAGCTATGACCTCTTA 460  
 Qy 126 LysAspLeuGlnGluGlyIleGlnThrLeuMetGlyArgLeuGluAspGlySerProArg 145  
 Db 461 AAGGACCTAGAGAGAGGATCCAAACGCTGATGGGAGGCTGGAGAGATGGAGCCCTCCG 520  
 Qy 146 ThrGlyGlnIlePheLeuGlnThrTyrSerLysPheAspThrAsnSerHisAsnAspAsp 165  
 Db 521 ACTGGGAGATCTTCAAGAGAGAGCTTACAGAGTTGACACCAACTACACAGATGAC 580  
 Qy 166 AAlauleuLysAsnTyrGlyLeuTyrCyspheArgLysAspMetAspLysValGlu 185  
 Db 581 GCACCTACTCAAGAACTACCGGCTGCTCTACTGCTTACAGAGAGCAATGACAAAGTCCAG 640  
 Qy 186 ThrPheLeuArgIleValGlnCysArgSerValGluGlySerCysGlyPhe 202  
 Db 641 ACATTCTGGCATCTGTGAGTGCCTCTGTGAGAGGAGGAGCTGTGCTTC 691

## RESULT 11

US-10-410-997-47  
 ; Sequence 47, Application US/10410997  
 ; Publication No. US20040126838A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Neose Technologies, Inc.  
 ; APPLICANT: Defrees, Shawn  
 ; APPLICANT: Zopf, David  
 ; APPLICANT: Bayer, Robert  
 ; APPLICANT: Hakes, David  
 ; APPLICANT: Chen, Xi  
 ; APPLICANT: Bove, Caryn  
 ; TITLE OF INVENTION: FOLLICLE STIMULATING HORMONE: REMODELING AND GLYCOCONJUGATION OF  
 ; FILE REFERENCE: 040853-01-5059  
 ; CURRENT APPLICATION NUMBER: US/10/410, 997  
 ; PRIOR FILING DATE: 2003-04-09  
 ; PRIOR APPLICATION NUMBER: US 60/328,523  
 ; PRIOR FILING DATE: 2001-10-10  
 ; PRIOR APPLICATION NUMBER: US 60/344,692  
 ; PRIOR FILING DATE: 2001-10-19  
 ; PRIOR APPLICATION NUMBER: US 60/387,292  
 ; PRIOR FILING DATE: 2002-06-07  
 ; PRIOR APPLICATION NUMBER: US 60/391,777  
 ; PRIOR FILING DATE: 2002-06-25  
 ; PRIOR APPLICATION NUMBER: US 60/396,594  
 ; PRIOR FILING DATE: 2002-07-17  
 ; PRIOR APPLICATION NUMBER: US 60/404,249  
 ; PRIOR FILING DATE: 2002-08-16  
 ; PRIOR APPLICATION NUMBER: US 60/407,527  
 ; PRIOR FILING DATE: 2002-08-28  
 ; NUMBER OF SEQ ID NOS: 75  
 ; SOFTWARE: PatentIn version 3.2  
 ; SEQ ID NO 47  
 ; LENGTH: 799  
 ; TYPE: DNA  
 ; ORGANISM: Homo sapiens  
 US-10-410-997-47

## Alignment Scores:

Pred. No.: 1,1e-127 Length: 799  
 Score: 1017.50 Matches: 200



Sequence 47, Application US/10287994  
Publication No. US20040137557A1  
GENERAL INFORMATION:  
APPLICANT: Neose Technologies, Inc.  
APPLICANT: Defrees, Shawn  
APPLICANT: Zopf, David  
APPLICANT: Bayer, Robert  
APPLICANT: Bower, Caryn  
APPLICANT: Hakes, David  
APPLICANT: Chen, Xi  
TITLE OF INVENTION: REMODELING AND GLYCOCONJUGATION OF PEPTIDES  
FILE REFERENCE: 040853-01-5052-00  
CURRENT APPLICATION NUMBER: US/10/287,994  
PRIOR FILING DATE: 2002-11-05  
PRIOR APPLICATION NUMBER: US 60/328,523  
PRIOR FILING DATE: 2001-10-10  
PRIOR APPLICATION NUMBER: US 60/344,692  
PRIOR FILING DATE: 2001-10-19  
PRIOR APPLICATION NUMBER: US 60/387,292  
PRIOR FILING DATE: 2002-06-07  
PRIOR APPLICATION NUMBER: US 60/391,777  
PRIOR FILING DATE: 2002-06-25  
PRIOR APPLICATION NUMBER: US 60/396,594  
PRIOR FILING DATE: 2002-07-17  
PRIOR APPLICATION NUMBER: US 60/404,249  
PRIOR FILING DATE: 2002-08-16  
PRIOR APPLICATION NUMBER: US 60/407,527  
NUMBER OF SEQ ID NOS: 62  
SOFTWARE: PatentIn version 3.1  
SEQ ID NO 47  
LENGTH: 799  
TYPE: DNA  
ORGANISM: Homo sapiens  
US-10-287-994-47

Alignment Scores:  
Pred. No.: 1,1e-127 Length: 799  
Score: 1017.50 Matches: 200  
Percent Similarity: 92.17% Conservative: 0  
Best Local Similarity: 92.17% Mismatches: 2  
Query Match: 97.18% Indels: 15  
Gaps: 1

US-09-856-796B-2 (1-202) x US-10-287-994-47 (1-799)

QY 1 MetAlaThrGlySerArgThrSerLeuLeuAlaPheGlyLeuLeuCysLeuProTyr 20  
DB 41 ATGGCTACAGGCTCCCGACGCTCTGCTGCTTTGGCTTGTCTGCTCTGCTCTGCTG 100  
QY 21 LeuGlnGluGlySerAlaPheProThrIleProLeuSerArgLeuPheAspAlaSer 40  
DB 101 CTTCAAGAGGCGAGTGGCTTCCCAACATTCCTTATCCAGGCTTTTGACAAAGCTATG 160  
QY 41 LeuArgAlaHisArgLeuHisGlnLeuAlaPheAspThrTyrGlnGluPhe----- 57  
DB 161 CTCGGGCGCCATGCTGTGACACGCTGGCTTGACACCTACAGAGGTTGAAGAACCC 220  
QY 58 -----AsnProGlnThrSerLeuCysPhe 65  
DB 221 TATATCCCAAGAAAGAAATTCATTCCTCCAGAACCCCGACGCTCCCTGTTTC 280  
QY 66 SerGlnSerIleProThrProSerAsnArgGlnGluThrGlnGlnGlySerAsnLeuGln 85  
DB 281 TCAGAGTCTATTCCGACACCTCCCAAGAGAGAAACACAAAGAAATCAACTAGAG 340  
QY 86 LeuLeuArgIleSerLeuLeuLeuIleGlnSerTyrIleGlnProValGlnPheLeuArg 105  
DB 341 CTGGCTCCGATCTCCCTGCTGCTCATCCAGTGTGCTGAGGCGGTGAGTTCCTCAG 400  
QY 106 SerValPheAlaAsnSerLeuValTyrGlyAlaSerAspSerAsnValTyrAspLeuLeu 125  
DB 401 AGTGTCTTGCCAAAGCCTGTGTATGAGGCGCTTGACAGCAAGCTATATACCTCTCA 460

QY 126 LysAspLeuGlnGluGlyIleGlnThrLeuMetGlyValGlnLeuAspGlySerProArg 145  
DB 461 AAGACCTTAGAGAAAGGACATCCAAAGCTGAGGGAGGAGCTGGAAGATGAGCCCGG 520  
QY 146 ThrGlyGlnIlePheLeuGlnThrTyrSerIlePheAspThrAsnSerHisAsnAsp 165  
DB 521 ACTGGCAGATCTTCAACACACCTACAGCAAGTTGACACAACTCACAAACGATGAC 580  
QY 166 AlaLeuLeuAsnTyrGlyLeuLeuTyrCysPheArgIleAspMetAspIleValGlu 185  
DB 581 GCATCTACAGAACTACAGGAGCTGCTGCTGCTTACAGAGGACATGACAGAGTTCAG 640  
QY 186 ThrPheLeuArgIleValGlnGlyArgSerValGlnGlySerCysGlyPhe 202  
DB 641 ACATTCCTGCGCATCTGTCAGTGGCTGCTGCTGAGAGGAGGAGCTGCTGCTTC 691

RESULT 14  
US-10-410-913-47  
Sequence 47, Application US/10410913  
Publication No. US20040142856A1  
GENERAL INFORMATION:  
APPLICANT: Neose Technologies, Inc.  
APPLICANT: Defrees, Shawn  
APPLICANT: Zopf, David  
APPLICANT: Bayer, Robert  
APPLICANT: Hakes, David  
APPLICANT: Chen, Xi  
TITLE OF INVENTION: GLYCOCONJUGATION METHODS AND PROTEINS/PEPTIDES PRODUCED BY THE  
FILE REFERENCE: 040853-01-5081  
CURRENT APPLICATION NUMBER: US/10/410,913  
PRIOR FILING DATE: 2003-04-09  
PRIOR APPLICATION NUMBER: US 60/328,523  
PRIOR FILING DATE: 2001-10-10  
PRIOR APPLICATION NUMBER: US 60/344,692  
PRIOR FILING DATE: 2001-10-19  
PRIOR APPLICATION NUMBER: US 60/387,292  
PRIOR FILING DATE: 2002-06-07  
PRIOR APPLICATION NUMBER: US 60/391,777  
PRIOR FILING DATE: 2002-06-25  
PRIOR APPLICATION NUMBER: US 60/396,594  
PRIOR FILING DATE: 2002-07-17  
PRIOR APPLICATION NUMBER: US 60/404,249  
PRIOR FILING DATE: 2002-08-16  
PRIOR APPLICATION NUMBER: US 60/407,527  
NUMBER OF SEQ ID NOS: 75  
SOFTWARE: PatentIn version 3.2  
SEQ ID NO 47  
LENGTH: 799  
TYPE: DNA  
ORGANISM: Homo sapiens  
US-10-410-913-47

Alignment Scores:  
Pred. No.: 1,1e-127 Length: 799  
Score: 1017.50 Matches: 200  
Percent Similarity: 92.17% Conservative: 0  
Best Local Similarity: 92.17% Mismatches: 2  
Query Match: 97.18% Indels: 15  
Gaps: 1

US-09-856-796B-2 (1-202) x US-10-410-913-47 (1-799)

QY 1 MetAlaThrGlySerArgThrSerLeuLeuAlaPheGlyLeuLeuCysLeuProTyr 20  
DB 41 ATGGCTACAGGCTCCCGACGCTCTGCTGCTTTGGCTTGTCTGCTCTGCTGCTG 100  
QY 21 LeuGlnGluGlySerAlaPheProThrIleProLeuSerArgLeuPheAspAlaSer 40  
DB 101 CTTCAAGAGGCGAGTGGCTTCCCAACATTCCTTATCCAGGCTTTTGACAAAGCTATG 160

Tue Feb 8 14:23:54 2005

QY 41 LeuArgLahIaSaRgLeuHlEgInLeuAlaPheAspThrTyrgInGluPhe----- 57  
 DB 161 CTCGGCGCCATCGTCTGACCAAGCTGGCTTGAACCTACAGAGATTGAAAGACC 220  
 QY 58 -----AsnProGlnInhrSerLeuCySphe 65  
 DB 221 TATATCCCAAGAACAGAAATTATTCATCTCTGACAAACCCCAAGACTCTCTGTTTC 280  
 QY 66 SerGluSerIleProThrProSerAsnArgGluInThrgInGlnInlySerAsnLeuGlu 85  
 DB 281 TCAGAGTATATCCCAACACCTTCCAAACAGGAGAAACACAAAGAAATCCAACTTAG 340  
 QY 86 LeuLeuArgIleSerLeuLeuLeuIleGlnSerTrpLeuGluProValGlnPheLeuArg 105  
 DB 341 CTGCTCCGCAATCTCCCTGCTGCTCATTCAGTCTGGGTGGAGCCCGGCAAGTCTCAGG 400  
 QY 106 SerValPheAlaAsnSerLeuValTyrgIylAlaSerAspSerAsnValTyrgAspLeuLeu 125  
 DB 401 AGTGCTTTCACCAACAGCTCGTGTAAGGGCCCTGTACAGCAACGTCATATGACCTCTTA 460  
 QY 126 LysAspLeuGluGluGlyIleGlnInhrLeuWeGlyArgLeuGluAspGlySerProArg 145  
 DB 461 AAGGACCTAGAGAGAGGACATCCAAACGCTGATGGGAGGCTGGAAGATGGAGCCCGCG 520  
 QY 146 ThrGlyGlnIlePheIleGlnInhrTyrgSerIlePheAspThrAsnSerIleAsnAspAsp 165  
 DB 521 ACTGGGCAAGTCTTCAAGACCACTTACAGCAAGTTCGACAAATCTCACACACATGAC 580  
 QY 166 AlaLeuLeuLysAsnTyrgIylLeuLeuTyrgCysPheArgLysAspMetAspLysValGlu 185  
 DB 581 GCACACTCAAGAACTACGAGGCTGCTCTACTGCTTACGGAAGACATGAGCAAGCTGAG 640  
 QY 186 ThrPheLeuArgIleValGlnCysArgSerValGluGlySerCysGlyPhe 202  
 DB 641 ACATTCCTGCCCATCTGTCAGTGCCTGTGAGAGGCGAGCTGTGCTTC 691

RESULT 15

US-10-477-651-1  
 ; Sequence 1, Application US/10477651  
 ; Publication No. US20040158046A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Loh, Yoke Peng  
 ; APPLICANT: Cawley, Niamh  
 ; APPLICANT: Baum, Bruce J  
 ; APPLICANT: Sneli, Christopher R  
 ; TITLE OF INVENTION: MODIFIED GROWTH HORMONE  
 ; FILE REFERENCE: 225223  
 ; CURRENT APPLICATION NUMBER: US/10/477,651  
 ; CURRENT FILING DATE: 2003-11-14  
 ; PRIOR APPLICATION NUMBER: PCT/US02/15172  
 ; PRIOR FILING DATE: 2002-05-14  
 ; PRIOR APPLICATION NUMBER: 60/290,836  
 ; NUMBER OF SEQ ID NOS: 3  
 ; SOFTWARE: PatentIn version 3.2  
 ; SEQ ID NO 1  
 ; LENGTH: 651  
 ; TYPE: DNA  
 ; ORGANISM: Homo sapiens  
 ; US-10-477-651-1

Alignment Scores:  
 Pred. No.: 1,08e-127 Length: 651  
 Score: 1016.50 Matches: 200  
 Percent Similarity: 92.17% Conservative: 0  
 Best Local Similarity: 92.17% Mismatches: 2  
 Query Match: 97.09% Indels: 15  
 DB: 18 Gaps: 1

US-09-856-796b-2 (1-202) x US-10-477-651-1 (1-651)

QY 1 MetAlaThrGlySerArgThrSerLeuLeuAlaPheGlyLeuLeuCysLeuProTrp 20

DB 1 ATGGCTACAGGCTCCCGGACGTCCCTGCTCTGCTTTGGCCTTGTCTGCTGCTGCTG 60  
 QY 21 LeuGlnGluGlySerAlaPheProThrIleProLeuSerArgLeuPheAsnAlaSer 40  
 DB 61 CTCAGAGGAGGAGTGCTTCCCAACCATTCCTTATCCAGGCTTTTGAACAACCTTAG 120  
 QY 41 LeuArgLahIaSaRgLeuHlEgInLeuAlaPheAspThrTyrgInGluPhe----- 57  
 DB 121 CTCGGCGCCATCGTCTGACCAAGCTGGCTTGAACCTTACAGAGATTGAAAGACC 180  
 QY 58 -----AsnProGlnInhrSerLeuCySphe 65  
 DB 181 TATATCCCAAGAACAGAAATTATTCATCTCTGACAAACCCCAAGACTCTCTGTTTC 240  
 QY 66 SerGluSerIleProThrProSerAsnArgGluInThrgInGlnInlySerAsnLeuGlu 85  
 DB 241 TCAGAGTATATCCCAACACCTTCCAAACAGGAGAAACAAAGAAATCCAACTTAGAG 300  
 QY 86 LeuLeuArgIleSerLeuLeuLeuIleGlnSerTrpLeuGluProValGlnPheLeuArg 105  
 DB 301 CTGCTCCGCAATCTCCCTGCTGCTCATTCAGTCTGGGTGGAGCCCGGCAAGTCTCAGG 360  
 QY 106 SerValPheAlaAsnSerLeuValTyrgIylAlaSerAspSerAsnValTyrgAspLeuLeu 125  
 DB 361 AGTGCTTTCACCAACAGCTCGTGTAAGGGCCCTGTACAGCAACGTCATATGACCTCTTA 420  
 QY 126 LysAspLeuGluGluGlyIleGlnInhrLeuWeGlyArgLeuGluAspGlySerProArg 145  
 DB 421 AAGGACCTAGAGAGAGGACATCCAAACGCTGATGGGAGGCTGGAAGATGGACGCCCGCG 480  
 QY 146 ThrGlyGlnIlePheIleGlnInhrTyrgSerIlePheAspThrAsnSerIleAsnAspAsp 165  
 DB 481 ACTGGGCAAGTCTTCAAGACCACTTACAGCAAGTTCGACAAATCTCACACACATGAC 540  
 QY 166 AlaLeuLeuLysAsnTyrgIylLeuLeuTyrgCysPheArgLysAspMetAspLysValGlu 185  
 DB 541 GCACACTCAAGAACTACGAGGCTGCTCTACTGCTTACGGAAGACATGAGCAAGCTGAG 600  
 QY 186 ThrPheLeuArgIleValGlnCysArgSerValGluGlySerCysGlyPhe 202  
 DB 601 ACATTCCTGCCCATCTGTCAGTGCCTGTGAGAGGCGAGCTGTGCTTC 651

Search completed: February 7, 2005, 17:06:43  
 Job time : 538 secs

GenCore version 5.1.6  
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OM protein - nucleic search, using frame\_plus\_p2n model

Run on: February 7, 2005, 13:31:05 ; Search time 180 Seconds

(without alignments)

1836.266 Million cell updates/sec

Title: US-09-856-796B-2  
Perfect score: 1047  
Sequence: 1 MATGSRSLIARGLCLPW.....KXETFLRIQVCRSEVSGSGP 202

Scoring table: BLOSUM62

Xgapop 10.0 , Xgapext 0.5  
Ygapop 10.0 , Ygapext 0.5  
Fgapop 6.0 , Fgapext 7.0  
Delop 6.0 , Delext 7.0

Searched: 1202784 seqs, 818138359 residues

Total number of hits satisfying chosen parameters: 2405568

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%  
Listing first 45 summaries

Command line parameters:  
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-Q=/cgn2\_1/USPTO.spool.h/US09856796/runat.06022005.124443.2590/app.query.fasta\_1.391  
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-LOOEXT=0 -UNITS=bits -START=1 -END=1 -MATRIX=Blosum62 -TRANS=human40.cdd  
-MODE=45 -DOCALLIGN=200 -THR SCORE=PCT -THR MAX=100 -THR MIN=0 -ALIGN=15  
-USBR=US09856796 -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=2000000000  
-NO MMAP -LARGEOUDRY -NEG\_SCORES=0 -WAIT -DSBLOCK=100 -LONGLOG  
-DEV TIMEOUT=120 -MARK TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6  
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database : Issued Patents NA.\*

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2: /cgn2\_6/ptodata/1/ina/5B COMB.seq.\*  
3: /cgn2\_6/ptodata/1/ina/6A COMB.seq.\*  
4: /cgn2\_6/ptodata/1/ina/6B COMB.seq.\*  
5: /cgn2\_6/ptodata/1/ina/PTUS COMB.seq.\*  
6: /cgn2\_6/ptodata/1/ina/backfile1.seq.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1024.5	97.9	663	US-09-284-878-2	Sequence 2, Appl
2	1024.5	97.9	5594	US-09-380-190A-29	Sequence 29, Appl
3	1024.5	97.9	7080	US-09-380-190A-21	Sequence 21, Appl
4	996	95.1	821	US-09-949-016-2779	Sequence 2779, Ap
5	996	95.1	821	US-09-949-016-2780	Sequence 2780, Ap
6	996	95.1	821	US-09-949-016-2781	Sequence 2781, Ap
7	996	95.1	821	US-09-949-016-2782	Sequence 2782, Ap
8	996	95.1	821	US-09-949-016-2783	Sequence 2783, Ap
9	959.5	91.6	1132	US-09-949-016-2789	Sequence 2789, Ap
10	959.5	91.6	1132	US-09-949-016-2790	Sequence 2790, Ap
11	959.5	91.6	1132	US-09-949-016-2791	Sequence 2791, Ap
12	959.5	91.6	1132	US-09-949-016-2792	Sequence 2792, Ap

13	959.5	91.6	1132	US-09-949-016-2793	Sequence 2793, Ap
14	927.5	88.6	654	US-08-187-756C-1	Sequence 1, Appl
15	927.5	88.6	654	US-08-710-324A-1	Sequence 1, Appl
16	927.5	88.6	654	US-09-411-657-1	Sequence 1, Appl
17	922.5	88.1	859	US-08-117-809A-1	Sequence 1, Appl
18	917.5	87.6	859	US-08-117-809A-2	Sequence 2, Appl
19	897	85.7	597	US-08-187-756C-2	Sequence 2, Appl
20	897	85.7	597	US-08-187-756C-1	Sequence 2, Appl
21	897	85.7	597	US-08-710-324A-2	Sequence 2, Appl
22	891.5	85.1	735	US-09-411-657-2	Sequence 2, Appl
23	891.5	85.1	1383	US-09-280-030-52	Sequence 52, Appl
24	891.5	85.1	1383	US-09-916-229A-1	Sequence 1, Appl
25	888.5	84.9	702	US-09-916-229A-3	Sequence 3, Appl
26	888.5	84.9	702	US-09-949-016-2784	Sequence 2784, Ap
27	888.5	84.9	702	US-09-949-016-2785	Sequence 2785, Ap
28	888.5	84.9	702	US-09-949-016-2786	Sequence 2786, Ap
29	888.5	84.9	702	US-09-949-016-2787	Sequence 2787, Ap
30	886.5	84.7	702	US-09-949-016-2788	Sequence 2788, Ap
31	885.5	84.6	596	US-08-093-383-2	Sequence 2, Appl
32	885.5	84.6	695	US-07-826-928A-29	Sequence 29, Appl
33	885.5	84.6	2086	US-09-554-451-2	Sequence 2, Appl
34	885.5	84.6	2086	US-08-589-028-9	Sequence 2, Appl
35	885.5	84.6	2086	US-08-784-582-9	Sequence 9, Appl
36	884.5	84.5	1275	US-09-420-819-35	Sequence 35, Appl
37	876.5	83.7	573	US-08-785-271-9	Sequence 15, Appl
38	867.5	82.9	573	US-08-800-215C-15	Sequence 15, Appl
39	867.5	82.9	573	US-08-800-215C-17	Sequence 17, Appl
40	864.5	82.6	2771	US-08-800-215C-19	Sequence 19, Appl
41	864.5	82.6	2771	US-08-273-411-5	Sequence 5, Appl
42	859.5	82.1	1822	US-08-321-686B-1	Sequence 8, Appl
43	854.5	81.6	1204	US-09-929-918-8	Sequence 1, Appl
44	835	79.8	5636	US-09-420-819-38	Sequence 38, Appl
45	835	79.8	5636	US-09-949-016-14526	Sequence 14526, A
				US-09-949-016-14527	Sequence 14527, A

#### ALIGNMENTS

RESULT 1  
US-09-284-878-2  
Sequence 2, Application US/09284878  
Patent No. 6342375  
GENERAL INFORMATION:  
APPLICANT: Olazaran, Martha Guerrero  
APPLICANT: Saldana, Hugo Barrera  
TITLE OF INVENTION: Genetically Modified Methylophilic P. pastoris Yeast for the  
FILE REFERENCE: 1829.0010000  
CURRENT APPLICATION NUMBER: US/09/284,878  
PRIOR FILING DATE: 1999-07-21  
PRIOR APPLICATION NUMBER: PCT/MX97/00033  
NUMBER OF SEQ ID NOS: 9  
SOFTWARE: Patentin Ver. 2.1  
SEQ ID NO 2  
LENGTH: 663  
TYPE: DNA  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: Description of Artificial Sequence: DNA encoding  
OTHER INFORMATION: the mature human growth hormone, containing an  
OTHER INFORMATION: artificial XbaI site introduced by modifying  
US-09-284-878-2  
Alignment Scores:  
Pred. No.: 4.33e-118  
Score: 1024.50  
Percent Similarity: 92.63%  
Best Local Similarity: 92.63%  
Query Match: 97.85%  
Matches: 663  
Conservative: 201  
Mismatch: 0  
Indel: 15  
Gaps: 1

US-09-856-796B-2 (1-202) x US-09-284-878-2 (1-663)

QY 1 MetAlaThrGlySerArgThrSerLeuLeuAlaPheGlyLeuLeuCysLeuProTIP 20  
 DB 1 ATGGCTACAGGCTCCCGACGCTCCGCTCTGCTTTGGCTGCTGCTGCTGCTGCTG 60

QY 21 LeuGlnGluGlySerAlaPheProThrIleProLeuSerArgLeuPheAspAlaSer 40  
 DB 61 CTCACAGGAGGAGTCTCCCAACCATCTCCCTTATCTAGACTTTTGGCAAGCTATG 120

QY 41 LeuArgAlaHisArgLeuHisGlnLeuAlaPheAspThrTyrglnGluPhe----- 57  
 DB 121 CTCGGGCGCCATCGTCTGACACGAGCTGGCTTGGACCTTACCGAGAGTTTGAAGAACCC 180

QY 58 -----AsnProGlnThrSerLeuCysPhe 65  
 DB 181 TATATCCCAAGAGACAGATATTCTCTCGACAAACCCCGACAGCTCCCTGCTTTC 240

QY 66 SerGlnSerIleProThrProSerAsnArgGlnGlnThrGlnGlnLeuSerAsnLeu 85  
 DB 241 TCAGAGCTATTCGACACCTCCACAGGAGGAAACAAAGAAATCCAACTTAGAG 300

QY 86 LeuLeuArgIleSerLeuLeuLeuIleGlnSerTyrLeuGlnProValGlnPheLeuArg 105  
 DB 301 CTGCTCCGATCTCTCGTCTCATCTCATCGTGTGAGCCCGCTGAGTTCTCTAGG 360

QY 106 SerValPheAlaAsnSerLeuValTyrglyAlaSerAspSerAsnValTyrAspLeuLeu 125  
 DB 361 AGTGCTTCGCGACAGCTGTGTACGCGCGCTCTGACAGACGCTTATGACCTCTTA 420

QY 126 LysAspLeuGlnGluGlyIleGlnThrLeuMetGlyArgLeuGlnAspGlySerProArg 145  
 DB 421 AAGGACCTAGAGGAGGATCCAAAGCTGATGGGAGGCTGGAAGATGGACGCCCGG 480

QY 146 ThrGlyGlnIlePheLeuGlnThrTyrglySerLysPheAspThrAsnSerHisAsnAspAsp 165  
 DB 481 ACTGGCGATCTTCAAGCAGACTTACAGAGAGTTGACACAACTCACACAGATGAC 540

QY 166 AlaLeuLeuLysAsnTyrglyLeuLeuTyrglyPheArgLysAspMetAspLysValGlu 185  
 DB 541 GCACACTCAGAGACTAGGGGCTCTACTGCTTCAGAGAGGACATGAGAGAGTGAG 600

QY 186 ThrPheLeuArgIleValGlnCysArgSerValGlnGlySerCysGlyPhe 202  
 DB 601 ACATTCCTGCGATCGTGCAGTGCCCTCTGTGAGAGGCGAGCTGTGGCTTC 651

RESULT 2  
 US-09-380-190A-29  
 Sequence 29, Application US/09380190A  
 Patent No. 6410220  
 GENERAL INFORMATION:  
 APPLICANT: NATURE TECHNOLOGY CORPORATION, ET AL.  
 TITLE OF INVENTION: SELF-ASSEMBLING GENES, VECTORS AND USES THEREOF  
 NUMBER OF SEQUENCES: 74  
 CORRESPONDENCE ADDRESS:  
 ADDRESSEE: MURTING, RAASCH & GEBHARDT, P.A.  
 STREET: 119 NORTH FOURTH STREET, SUITE 203  
 CITY: MINNEAPOLIS  
 STATE: MINNESOTA  
 COUNTRY: USA  
 ZIP: 55401  
 COMPUTER READABLE FORM:  
 MEDIUM TYPE: Floppy disk  
 COMPUTER: IBM PC compatible  
 OPERATING SYSTEM: PC-DOS/MS-DOS  
 SOFTWARE: Patentin Release #1.0, Version #1.30  
 CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/09/380,190A  
 FILING DATE: 26-Aug-1999  
 CLASSIFICATION: <Unknown>  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: PCT/US98/03918

FILING DATE: 28-FEB-98  
 ATTORNEY/AGENT INFORMATION:  
 NAME: MURTING, ANN M.  
 REGISTRATION NUMBER: 33,977  
 REFERENCE//DOCKET NUMBER: 228,00010201  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: 612-305-1217  
 TELEFAX: 612-305-1228  
 INFORMATION FOR SEQ ID NO: 29:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 5594 base pairs  
 TYPE: nucleic acid  
 STRANDEDNESS: single  
 TOPOLOGY: linear  
 MOLECULE TYPE: DNA (genomic)  
 SEQUENCE DESCRIPTION: SEQ ID NO: 29:  
 US-09-380-190A-29

Alignment Scores:  
 Pred. No.: 1,166-116 Length: 5594  
 Score: 1024.50 Matches: 201  
 Percent Similarity: 92.63% Conservative: 0  
 Best Local Similarity: 92.63% Mismatches: 1  
 Query Match: 97.85% Indels: 15  
 DB: 3 Gaps: 1

US-09-856-796B-2 (1-202) x US-09-380-190A-29 (1-5594)

QY 1 MetAlaThrGlySerArgThrSerLeuLeuAlaPheGlyLeuLeuCysLeuProTIP 20  
 DB 2270 ATGGCTACAGGCTCCCGACGCTCCGCTCTGCTTTGGCTGCTGCTGCTGCTGCTG 2329

QY 21 LeuGlnGluGlySerAlaPheProThrIleProLeuSerArgLeuPheAspAlaSer 40  
 DB 2330 CTCACAGGAGGAGTCTCCCAACCATCTCCCTTATCTAGACTTTTGGCAAGCTATG 2389

QY 41 LeuArgAlaHisArgLeuHisGlnLeuAlaPheAspThrTyrglnGluPhe----- 57  
 DB 2390 CTCGGCGCCATCGTCTGACACGCTGGCTTGGACACTTACCGAGAGGAGTTGAAGAACCC 2449

QY 58 -----AsnProGlnThrSerLeuCysPhe 65  
 DB 2450 TATATCCCAAGAGACAGATATTCTCTCGACAAACCCCGACAGCTCCCTGCTTTC 2509

QY 66 SerGlnSerIleProThrProSerAsnArgGlnGlnThrGlnGlnLeuSerAsnLeu 85  
 DB 2510 TCAGAGCTATTCGACACCTCCACAGGAGGAAACAAAGAAATCCAACTTAGAG 2569

QY 86 LeuLeuArgIleSerLeuLeuLeuIleGlnSerTyrLeuGlnProValGlnPheLeuArg 105  
 DB 2570 CTGCTCCGATCTCTCGTCTCATCTCATCGTGTGAGCCCGCTGACAGCTTCTCTCAGG 2629

QY 106 SerValPheAlaAsnSerLeuValTyrglyAlaSerAspSerAsnValTyrAspLeuLeu 125  
 DB 2630 AGTGCTTCGCGACAGCTGTGTACGCGCGCTCTGACAGACGCTTATGACCTCTTA 2689

QY 126 LysAspLeuGlnGluGlyIleGlnThrLeuMetGlyArgLeuGlnAspGlySerProArg 145  
 DB 2690 AAGGACCTAGAGGAGGATCCAAAGCTGATGGGAGGCTGGAAGATGGAGCCCGCG 2749

QY 146 ThrGlyGlnIlePheLeuGlnThrTyrglySerLysPheAspThrAsnSerHisAsnAspAsp 165  
 DB 2750 ACTGGCGATCTTCAAGCAGACTTACAGAGAGTTGACACAACTCACACAGATGAC 2809

QY 166 AlaLeuLeuLysAsnTyrglyLeuLeuTyrglyPheArgLysAspMetAspLysValGlu 185  
 DB 2810 GCACACTCAGAGACTAGGGGCTCTACTGCTTCAGAGAGGACATGACAGAGCTGAG 2869

QY 186 ThrPheLeuArgIleValGlnCysArgSerValGlnGlySerCysGlyPhe 202  
 DB 2870 ACATTCCTGCGATCGTGCAGTGCCCTCTGTGAGAGGCGAGCTGTGGCTTC 2920

RESULT 3



US-09-380-190A-21

Sequence 21, Application US/09380190A

Patent No. 6410220

GENERAL INFORMATION:

APPLICANT: NATURE TECHNOLOGY CORPORATION, ET AL.

TITLE OF INVENTION: SELF-ASSEMBLING GENES, VECTORS AND USES THEREOF

NUMBER OF SEQUENCES: 74

CORRESPONDENCE ADDRESS:

ADDRESSEE: MOETTING, RAASCH &amp; GEBHARDT, P.A.

STREET: 119 NORTH FOURTH STREET, SUITE 203

CITY: MINNEAPOLIS

STATE: MINNESOTA

COUNTRY: USA

ZIP: 55401

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.30

CURRENT APPLICATION NUMBER: US/09/380,190A

FILING DATE: 26-Aug-1999

CLASSIFICATION: &lt;Unknown&gt;

PRIOR APPLICATION DATA:

APPLICATION NUMBER: PCT/US98/03918

FILING DATE: 28-FEB-98

ATTORNEY/AGENT INFORMATION:

NAME: MOETTING, ANN M.

REGISTRATION NUMBER: 33,977

REFERENCE/DOCKET NUMBER: 228,00010201

TELECOMMUNICATION INFORMATION:

TELEPHONE: 612-305-1217

TELEFAX: 612-305-1228

INFORMATION FOR SEQ ID NO: 21:

SEQUENCE CHARACTERISTICS:

LENGTH: 7080 base pairs

TYPE: nucleic acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: DNA (genomic)

SEQUENCE DESCRIPTION: SEQ ID NO: 21:

US-09-380-190A-21

Alignment Scores:

Pred. No.:

Score:

Percent Similarity:

Best Local Similarity:

Query Match:

DB:

US-09-856-796B-2 (1-202) x US-09-380-190A-21 (1-7080)

QY

1

MetalAlThrGlySerArgThrSerLeuLeuAlaPheGlyLeuLeuCysLeuProTyr

Db

2848

ATGGCTACAGGCTCCGAGAGTCCCTGCTCTGCTTTGGCTTGGCTGCTGCTGCTG

QY

21

LeuGlnGluGlySerAlaPheProThrIleProLeuSerArgLeuPheAspAlaSer

Db

2908

CTTCAAGAGGCGAGTCTCTCCACCATTCCTTATCCAGGCTTTTGAACAACGCTAAG

QY

41

LeuAlaGlyAlaHisArgLeuHisGlnLeuAlaPheAspThrTyrGlnGluPhe

Db

2968

CTCCGCGCCCATCGTCTGACCACTGCGCTTTGACACCTACCAAGAGTTTGAAGAAGCC

QY

58

-----AsnProGlnThrSerLeuCysPhe

Db

3028

TATATCCCAAGAAAGAAATATTCTCTGACGAAGCCCAAGACCTCTCTGTTTC

QY

66

SerGlnSerIleProThrProSerAsnArgGlnGluThrGlnGlnIlePheSerAsnLeuGlu

Db

3088

TCAAGCTTATATCCGACACCTCCCAACAGGAGGAGAAACAAAGAAATCCAACTAAG

3147

QY

86

LeuLeuArgIleSerLeuLeuLeuIleGlnSerTyrLeuGluProValGlnPheLeuArg

Db

3148

CTGCTCCGACATCTCCCTGCTGCTCATTCACATCGTGGCTGAGCCCGGCTTCTCAGG

QY

106

SerValPheAlaSerLeuValTyrGlyAlaSerAspSerAsnValTyrAspLeuLeu

Db

3208

AGTGTCTTCCCAACAGCCCTGCTGTAAGGCGCTCTGACAGCAACGCTTATGACTCTTA

QY

126

LysAspLeuGluGlnGlyIleGlnThrLeuMetGlyArgLeuGluAspGlySerProArg

Db

3268

AAGGACTTACAGAGAGAGCATCCAAAGCTGATGGAGGCTGGAAGATGGACCCCGG

QY

146

ThrGlyGlnIlePheLeuGlnThrTyrSerLysPheAspThrAsnSerHisAsnAspAsp

Db

3328

ACTGGCAGATCTTCAAGACAGACTTACAGCAAGTTGACACAACTCACACAGATGAC

QY

166

AlaLeuLeuLysAsnTyrGlyLeuLeuTyrCysPheArgLysAspMetAspLysValGlu

Db

3388

GCACTACTCAAGAACTACAGGCGCTGCTACTCTCTCAGAAAGACATGACAGGTCAG

QY

186

ThrPheLeuArgIleValGlnCysArgSerValGlnGlySerCysGlyPhe

Db

3448

ACATTCCTGGCGCATCGTGCAGTGCCTCTGTGAGGGGACGCTGTGCTTC

3498

RESULT 4

US-09-949-016-2779

Sequence 2779, Application US/09949016

Patent No. 6812319

GENERAL INFORMATION:

APPLICANT: VENTER, J. Craig et al.

TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED

FILE REFERENCE: C1001307

CURRENT APPLICATION NUMBER: US/09/949,016

PRIOR FILING DATE: 2000-04-14

PRIOR APPLICATION NUMBER: 60/241,755

PRIOR FILING DATE: 2000-10-20

PRIOR APPLICATION NUMBER: 60/237,768

PRIOR FILING DATE: 2000-10-03

PRIOR APPLICATION NUMBER: 60/231,498

PRIOR FILING DATE: 2000-09-08

NUMBER OF SEQ ID NOS: 207012

SOFTWARE: PASCSEQ for Windows Version 4.0

SEQ ID NO 2779

LENGTH: 821

TYPE: DNA

ORGANISM: Human

US-09-949-016-2779

Alignment Scores:

Pred. No.:

Score:

Percent Similarity:

Best Local Similarity:

Query Match:

DB:

US-09-856-796B-2 (1-202) x US-09-949-016-2779 (1-821)

QY

1

MetalAlThrGlySerArgThrSerLeuLeuAlaPheGlyLeuLeuCysLeuProTyr

Db

63

ATGGCTACAGGCTCCGAGAGTCCCTGCTCTGCTTTGGCTTGGCTGCTGCTGCTG

QY

21

LeuGlnGluGlySerAlaPheProThrIleProLeuSerArgLeuPheAspAlaSer

Db

123

CTTCAAGAGGCGAGTCTCTCCACCATTCCTTATCCAGGCTTTTGAACAACGCTAAG

QY

41

LeuAlaGlyAlaHisArgLeuHisGlnLeuAlaPheAspThrTyrGlnGluPhe

Db

183

CTCCGCGCCCATCGTCTGACCACTGCGCTTTGACACCTACCAAGAGTTTGAAGAAGCC

242

QY

58

-----AsnProGlnThrSerLeuCysPhe

Db

3028

TATATCCCAAGAAAGAAATATTCTCTGACGAAGCCCAAGACCTCTCTGTTTC

3087

QY

66

SerGlnSerIleProThrProSerAsnArgGlnGluThrGlnGlnIlePheSerAsnLeuGlu

Db

3088

TCAAGCTTATATCCGACACCTCCCAACAGGAGGAGAAACAAAGAAATCCAACTAAG

3147

Db 243 TATATCCCAAGAGAGATTCATTCCTGACAGAACCCCAAGACCTCTCTGTTTC 302  
QY 66 SerGluSerIleProThrProSerAsnArgLugluThrgIngluInlySerAsnLeuGlu 85  
Db 303 TCAGAGTCATTCGACACCCCTCCCAACAGGAGAAACACAAAGAAATCCACCTAGAG 362  
QY 86 LeuLeuArgIleSerLeuLeuLeuIleGlnSerTrpLeuGluProValGlnPheLeuArg 105  
Db 363 CTGCTCCGATCTCCCTGCTGCTCATCTGAGTGGCTGAGCCCGTGCATTCCTCAGG 422  
QY 106 SerValPheAlaAsnSerLeuLeuIleGlnSerTrpLeuGluProValGlnPheLeuArg 125  
Db 423 AGTGCTTCGCCAAGACCTGCTGCTCATCTGAGTGGCTGAGCCCGTGCATTCCTCAGG 482  
QY 126 LysAspLeuGluGluGlyIleGlnThrLeuMetGlyArgLeuGluAspGlySerProArg 145  
Db 483 AAGGACCTAGAGAGAGGACATCAACGCTGATGGGGG--CTGGAGAGATGGAGCCCGCG 540  
QY 146 ThrGlyGlnIlePheLeuGlnThrTyrserysPheAspThrAsnSerHisAsnAsp 165  
Db 541 ACTGGGAGATCTTCAAGACGACCTACAGCAAGTTCGACAACTCACACAAAGATGAC 600  
QY 166 AlaLeuLeuLysAsnTrpGlyLeuLeuTrpCysPheArgLysAspMetAspLysValGlu 185  
Db 601 GCACTACTCAAGAACTACGGGCTGCTCTACTGCTTACAGAAAGACATGAGCAAGCTCAG 660  
QY 186 ThrPheLeuArgIleValGlnCysArgSerValGluGlySerCysGlyPhe 202  
Db 661 ACAATTCCTGGCATCTGCGAGTGGCGCTCTGTGAGGGAGGAGCTGTGGCTTC 711

RESULT 5  
US-09-949-016-2780  
Sequence 2780, Application US/09949016  
Patent No. 6812339  
GENERAL INFORMATION:  
APPLICANT: VENTER, J. Craig et al.  
TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED  
TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF  
FILE REFERENCE: CLO01307  
CURRENT APPLICATION NUMBER: US/09/949, 016  
CURRENT FILING DATE: 2000-04-14  
PRIOR APPLICATION NUMBER: 60/241,755  
PRIOR FILING DATE: 2000-10-20  
PRIOR FILING DATE: 2000-10-20  
PRIOR APPLICATION NUMBER: 60/237,768  
PRIOR FILING DATE: 2000-10-03  
PRIOR APPLICATION NUMBER: 60/231,498  
PRIOR FILING DATE: 2000-09-08  
NUMBER OF SEQ ID NOS: 207012  
SOFTWARE: FastSeq for Windows Version 4.0  
SEQ ID NO 2780  
LENGTH: 821  
TYPE: DNA  
ORGANISM: Human  
US-09-949-016-2780

Alignment Scores:  
Pred. No.: 2,15e-114 Length: 821  
Score: 996.00 Matches: 200  
Percent Similarity: 92.17% Conservative: 0  
Best Local Similarity: 92.17% Mismatches: 2  
Query Match: 95.13% Indels: 16  
Gaps: 1  
DB: 4

US-09-856-796b-2 (1-202) x US-09-949-016-2780 (1-821)

QY 1 MetAlaThrGlySerArgTrpSerLeuLeuAlaPheGlyLeuLeuCysLeuProTrp 20  
Db 63 ATGGCTACAGGCTCCCGAGCGCTGCTGCTGCTTTGGGCTGCTGCTGCTGCTGCTG 122  
QY 21 LeuGlnGluGlySerAlaPheProThrIleProLeuSerArgLeuPheAsnAlaSer 40  
Db 123 CTTCAAGAGGGAGGCGCTTCCCAACCAATTCCTTATCCAGGCTTTTGAACAAGCTATG 182

QY 41 LeuArgAlaHisArgLeuHisGlnLeuAlaPheAspThrTyrgIngluPhe----- 57  
Db 183 CTCGGGGCCATCGCTGACACAGCTGGCCCTTTGACACCTTACAGAGATTGGAAGAGCC 242  
QY 58 -----AsnProGlnThrSerLeuCysPhe 65  
Db 243 TATATCCCAAGAGAGAGATTCATTCCTGACAGAACCCCAAGACCTCTCTGTTTC 302  
QY 66 SerGluSerIleProThrProSerAsnArgLugluThrgIngluInlySerAsnLeuGlu 85  
Db 303 TCAGAGTCATTCGACACCCCTCCCAACAGGAGAAACACAAAGAAATCCACCTAGAG 362  
QY 86 LeuLeuArgIleSerLeuLeuLeuIleGlnSerTrpLeuGluProValGlnPheLeuArg 105  
Db 363 CTGCTCCGATCTCCCTGCTGCTCATCTGAGTGGCTGAGCCCGTGCATTCCTCAGG 422  
QY 106 SerValPheAlaAsnSerLeuLeuIleGlnSerTrpLeuGluProValGlnPheLeuArg 125  
Db 423 AGTGCTTCGCCAAGACCTGCTGCTCATCTGAGTGGCTGAGCCCGTGCATTCCTCAGG 482  
QY 126 LysAspLeuGluGluGlyIleGlnThrLeuMetGlyArgLeuGluAspGlySerProArg 145  
Db 483 AAGGACCTAGAGAGAGGACATCAACGCTGATGGGGG--CTGGAGATGGAGCCCGCG 540  
QY 146 ThrGlyGlnIlePheLeuGlnThrTyrserysPheAspThrAsnSerHisAsnAsp 165  
Db 541 ACTGGGAGATCTTCAAGACGACCTACAGCAAGTTCGACAACTCACACAAAGATGAC 600  
QY 166 AlaLeuLeuLysAsnTrpGlyLeuLeuTrpCysPheArgLysAspMetAspLysValGlu 185  
Db 601 GCACTACTCAAGAACTACGGGCTGCTCTACTGCTTACAGAAAGACATGAGCAAGCTCAG 660  
QY 186 ThrPheLeuArgIleValGlnCysArgSerValGluGlySerCysGlyPhe 202  
Db 661 ACAATTCCTGGCATCTGCGAGTGGCGCTCTGTGAGGGAGGAGCTGTGGCTTC 711

RESULT 6  
US-09-949-016-2781  
Sequence 2781, Application US/09949016  
Patent No. 6812339  
GENERAL INFORMATION:  
APPLICANT: VENTER, J. Craig et al.  
TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED  
TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF  
FILE REFERENCE: CLO01307  
CURRENT APPLICATION NUMBER: US/09/949, 016  
CURRENT FILING DATE: 2000-04-14  
PRIOR APPLICATION NUMBER: 60/241,755  
PRIOR FILING DATE: 2000-10-20  
PRIOR FILING DATE: 2000-10-20  
PRIOR APPLICATION NUMBER: 60/237,768  
PRIOR FILING DATE: 2000-10-03  
PRIOR APPLICATION NUMBER: 60/231,498  
PRIOR FILING DATE: 2000-09-08  
NUMBER OF SEQ ID NOS: 207012  
SOFTWARE: FastSeq for Windows Version 4.0  
SEQ ID NO 2781  
LENGTH: 821  
TYPE: DNA  
ORGANISM: Human  
US-09-949-016-2781

Alignment Scores:  
Pred. No.: 2,15e-114 Length: 821  
Score: 996.00 Matches: 200  
Percent Similarity: 92.17% Conservative: 0  
Best Local Similarity: 92.17% Mismatches: 2  
Query Match: 95.13% Indels: 16  
Gaps: 1  
DB: 4

US-09-856-796b-2 (1-202) x US-09-949-016-2781 (1-821)

QY 1 MetAlaThrGlySerArgTrpSerLeuLeuAlaPheGlyLeuLeuCysLeuProTrp 20

```

Length:      821
Matches:     200
Conservative: 0
Mismatch:    2

```

```

Query Match: 95.13% Indels: 16
DB: 4 Gaps: 1
US-09-856-796B-2 (1-202) x US-09-949-016-2782 (1-821)

QY 1 MetAlaThrGlySerArgThrSerLeuLeuAlaPheGlyLeuLeuCyLeuProTTP 20
DB 63 ATGGCTACAGGCTCCCGAGAGTCTCTGCTCTGCTTTGGCCGTGCTCTGCTCCGCTGG 122
QY 21 LeuGlnGlnGlySerAlaPheProThrIleProLeuSerArgLeuPheAspAlaSer 40
DB 123 CTTCAAGAGGGGAGTCTCTCTCCCAACCAATTCCTTATCCAGGCTTTTGAACAACGCTAG 182
QY 41 LeuArgAlaHisArgLeuHisGlnLeuAlaPheAspThrTyrlnglnPhe----- 57
DB 183 CTCGGCGCCCATGCTCTGCACAGAGCTGGCTTTGACACCTACAGAGATTGAAGAACC 242
QY 58 -----AsnProGlnThrSerLeuCyPhe 65
DB 243 TATATCCCAAGAAACAGAGATTAATTCATTCTGCAGAACCCCAAGACCTCCTGTTTC 302
QY 66 SerGlnSerIleProThrProSerAsnArgGlnGlnGlnGlnGlnGlnGlnGlnGln 85
DB 303 TCAGAGTCTATTCGACACCTCTCCAAACAGGAGGAGAAACACAAACAAATTCACCTAGAG 362
QY 86 LeuLeuAlaGlyIleSerLeuLeuLeuIleGlnSerIlePheGlnProValGlnPheLeuArg 105
DB 363 CTGCTCCGCATCTCTCTCTGCTCATTCAGTCGTGGCTGGAGCCCTGACGTTCTCGAG 422
QY 106 SerValPheAlaAsnSerLeuValTyrlGlyAlaSerAspSerAsnValTyrlAspLeuLeu 125
DB 423 AGTCTCTTCGCAACAGCTGGTGTATGCGCCCTCTGACAGCAACAGTCTAGACCTCTTA 482
QY 126 LysAspLeuGlnGlnGlyIleGlnThrLeuMetGlyArgLeuGlnAspGlySerProArg 145
DB 483 AAGGACCTAGAGAGAGAGCATTCACACCTGATGGGGG--CTGGAGAGATGGCAGCCCCGG 540
QY 146 ThrGlyGlnIlePheLeuGlnIleTyrlSerLysPheAspThrAsnSerHisAsnAspAsp 165
DB 541 ACTGGGAGATCTTCAAGACAGACCTTACAGAACTTGCACACAACTACACAAAGATGAC 600
QY 166 AlaLeuLeuLysAsnTyrlGlyLeuLeuTyrlCySPheArgLysAspMetAspLysValGlu 185
DB 601 GCACTACTCAAGAACTACAGGGCTGCTCTACTGCTTACAGAGAGACATGACAGAGTTCAG 660
QY 186 ThrPheLeuArgIleValGlnCySPheArgSerValGlnGlySerCyGlyPhe 202
DB 661 ACATTCTCGGAGTCGTGACAGTGCCTGCTGTGAGAGGAGAGCTGTGGCTTC 711

RESULT 8
US-09-949-016-2783
; Sequence 2783, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; WITH HUMAN DISEASE. METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: C1001307
; CURRENT APPLICATION NUMBER: US/09/949.016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 2783
; LENGTH: 821
; TYPE: DNA
; ORGANISM: Human

```



QY 181 LaspIysValGluThrPheLeuArgIleValGlnCysArgSerValGluGlySerCysG1 201  
 Db 957 GACAAAGTGCAGACATTCCTGCGCATGTCAGATGCGCTGTGTGAGAGGCGACGTGTGG 1016  
 QY 201 yphe 202  
 Db 1017 CTTC 1020

## RESULT 10

US-09-949-016-2790  
 ; Sequence 2790, Application US/09949016  
 ; Patent No. 6812339  
 ; GENERAL INFORMATION:  
 ; APPLICANT: VENTER, J. Craig et al.  
 ; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED  
 ; FILE REFERENCE: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF  
 ; FILE REFERENCE: CL001307  
 ; CURRENT APPLICATION NUMBER: US/09/949, 016  
 ; PRIOR FILING DATE: 2000-04-14  
 ; PRIOR APPLICATION NUMBER: 60/241,755  
 ; PRIOR FILING DATE: 2000-10-20  
 ; PRIOR APPLICATION NUMBER: 60/237,768  
 ; PRIOR FILING DATE: 2000-10-03  
 ; PRIOR APPLICATION NUMBER: 60/231,498  
 ; NUMBER OF SEQ ID NOS: 207012  
 ; SOFTWARE: FastSeq for Windows Version 4.0  
 ; SEQ ID NO 2790  
 ; LENGTH: 1132  
 ; TYPE: DNA  
 ; ORGANISM: Human  
 US-09-949-016-2790

## Alignment Scores:

Pred. No.: 1,25e-109 Length: 1132  
 Score: 959.50 Matches: 201  
 Percent Similarity: 66.56% Conservative: 0  
 Best Local Similarity: 66.56% Mismatches: 1  
 Query Match: 91.64% Indels: 100  
 DB: 4 Gaps: 2

US-09-856-796B-2 (1-202) x US-09-949-016-2790 (1-1132)

QY 1 MetAlaThrGlySerArgThrSerLeuLeuAlaPheGlyLeuLeuCysLeuProTrp 20  
 Db 117 ATGGCTACAGGCTCCGAGAGTCCCTGCTCTGCTTTGGCCCTGCTGCTGCTGCTGCTG 176  
 QY 21 LeuGlnGluGlySerAlaPheProThrIleProLeuSerArgLeuPheAspAlaSer 40  
 Db 177 CTTCAGAGGGGCGAGTGGCTTCCCAACCATTCCTTATTCAGAGGCTTTTGGCAACGCTATG 236  
 QY 41 LeuArgAlaHisArgLeuHisGlnLeuAlaPheAspThrTyrGlnGluPhe----- 57  
 Db 237 CTCGGGGCCCATCGTGCAGCAGCGTGGCTTTGACCTTACCAAGAGTTTGAAGAACCC 296  
 QY 58 -----AspProGlnThrSerLeuCysPhe 65  
 Db 297 TATATCCCAAGAGACAGATATTCATTCCTGCAGAACCCCGACACCTCCCTCTGTTTC 356  
 QY 66 SerGluSerIleProThrProSerAsnaArgGluGlnThrGlnGlnLysSerAsnLeuGlu 85  
 Db 357 TCGAGATCTATTCGACACCTTCCTCAACAGGAGAAACACACAGAAATCCAACTCAGAG 416  
 QY 86 LeuLeuArgIleSerLeuLeuLeuIleGlnSerTrpLeuGlnProValGlnPheLeuArg 105  
 Db 417 CTGCTCCGCGATCTCCTGCTCTCATCTGCTGAGCGTGGAGCCCGCTGAGATTCTCCAG 476  
 QY 106 SerValPheAlaAsnSerLeuValTyrGlyAlaSerAspSerAsnValTyrAspLeuLeu 125  
 Db 477 AGTGTCTTCGCAACAGCGCTGTGTATACGCGCTCTGCAGACAGACGTCTATACCTCTCA 536  
 QY 126 LysAspLeuGluGluGlyIleGlnThrLeuMet-Gly----- 137

Db 537 AAGGACCTAGAGAGAGGATCCAAACCGCTATGAGGGGTGAGGGTGGCGCCAGGGGTCC 596  
 QY 137 -----  
 Db 597 AATCTGAGAGCCCACTGACTTTGAGAGCTGTGTAGAGAAACACTGCTGCTTTT 656  
 QY 137 -----  
 Db 657 AGAGTCAGGCGCTGACCCCAAGAACTACCTTATTTCTTATTTCCCTGGAATCCT 716  
 QY 137 -----  
 Db 717 CAGGCTTTCTTACACCTTGAGAGGAGGAGGAGAAATGATGATGAGAAAGGAGG 776  
 QY 138 -----ArgLeuGluAs 141  
 Db 777 GAACGTACCCCAAGCGCTTGGCTCTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCT 836  
 QY 141 PGLYserProArgThrGlnIlePheLeuGlnThrTyrSerLysPheAspThrAsnSe 161  
 Db 837 TGGCAGCCCCCGAGCTGGGACATCTTCAAGACAGCTTACAGAGTTGACACAAATC 896  
 QY 161 rHisAsnAspAlaLeuLeuLysAsnTyrIleLeuLeuTyrCysPheArgLysAspSe 181  
 Db 897 ACACACAGTACGACGACTACTCAAGACTAGGGGCTGCTTCTTCTTCTTCTTCTTCTTCT 956  
 QY 181 LaspIysValGluThrPheLeuArgIleValGlnCysArgSerValGluGlySerCysG1 201  
 Db 957 GACAAAGTGCAGACATTCCTGCGCATGTCAGATGCGCTGTGTGAGAGGCGACGTGTGG 1016  
 QY 201 yphe 202  
 Db 1017 CTTC 1020

## RESULT 11

US-09-949-016-2791  
 ; Sequence 2791, Application US/09949016  
 ; Patent No. 6812339  
 ; GENERAL INFORMATION:  
 ; APPLICANT: VENTER, J. Craig et al.  
 ; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED  
 ; FILE REFERENCE: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF  
 ; FILE REFERENCE: CL001307  
 ; CURRENT APPLICATION NUMBER: US/09/949, 016  
 ; PRIOR FILING DATE: 2000-04-14  
 ; PRIOR APPLICATION NUMBER: 60/241,755  
 ; PRIOR FILING DATE: 2000-10-20  
 ; PRIOR APPLICATION NUMBER: 60/237,768  
 ; PRIOR FILING DATE: 2000-10-03  
 ; PRIOR APPLICATION NUMBER: 60/231,498  
 ; NUMBER OF SEQ ID NOS: 207012  
 ; SOFTWARE: FastSeq for Windows Version 4.0  
 ; SEQ ID NO 2791  
 ; LENGTH: 1132  
 ; TYPE: DNA  
 ; ORGANISM: Human  
 US-09-949-016-2791

Alignment Scores:  
 Pred. No.: 1,25e-109 Length: 1132  
 Score: 959.50 Matches: 201  
 Percent Similarity: 66.56% Conservative: 0  
 Best Local Similarity: 66.56% Mismatches: 1  
 Query Match: 91.64% Indels: 100  
 DB: 4 Gaps: 2

US-09-856-796B-2 (1-202) x US-09-949-016-2791 (1-1132)

QY 1 MetAlaThrGlySerArgThrSerLeuLeuAlaPheGlyLeuLeuCysLeuProTrp 20  
 Db 117 ATGGCTACAGGCTCCGAGAGTCCCTGCTCTGCTTTGGCCCTGCTGCTGCTGCTGCTG 176

```
OY 21 LeuGlnGluGlySerAlaPheProThrIleProLeuSerArgLeuPheAspAlaSer 40
DB 177 CTTCAAGAGGCGAGTCCCTCCCAACCATTCCTTATCCAGGCTTTTGACAAAGCTATG 236
OY 41 LeuArgAlaHisArgLeuHisGlnLeuAlaPheAspThrTyrGlnGluPhe----- 57
DB 237 CTCGGGCGCCATGCTGTGACACAGCTGGCTTTGACACTTACAGAGAGTTGAAAGAGCC 296
OY 58 -----AsnProGlnThrSerLeuCySphe 65
DB 297 TATATCCCAAGAACAGAAATATTCATTCCTGCAAGAACCCCAAGACTCCCTCTGTTTC 356
OY 66 SerGlnSerIleProThrProSerAsnArgGlnGluThrGlnGlnLeuSerAsnLeuGlu 85
DB 357 TCGAGGTATATTCGACACCTCCCAACAGGAGAAACAAACAAATCCAACTCAGAG 416
OY 86 LeuLeuArgIleSerLeuLeuLeuIleGlnSerTyrLeuGluProValGlnPheLeuArg 105
DB 417 CTGCTCCGCACTCTCCCTGCTGCTCATTCAGTGTGGTGGAGCCCGTGCAGTCTCTCAG 476
OY 106 SerValPheAlaAsnSerLeuValTyrGlnAlaSerAspSerAsnValTyrAspLeuLeu 125
DB 477 AGTGTCTTCGCAACAGCTGTGTAGAGCGGCTCTGACAGCAAGCTATGACCTCTCA 536
OY 126 LysAspLeuGlnGluGlyIleGlnThrLeuMet-Gly----- 137
DB 537 AAGGACCTAGAGAAAGGACATCCAAACGCTGATGGGGGTGAGGGTGGCCCAAGGGTCCCC 596
OY 137 ----- 137
DB 597 AATCTGGAGCCCACTGACTTTAGAGCTGTGTAGAGAAACACAGTGCCTCTTTT 656
OY 137 ----- 137
DB 657 AGCAGTCAAGCCCTGACCCCAAGAACTGACCTTATTTCCCTGTAATCCT 716
OY 137 ----- 137
DB 717 CCAGGCTTTTCTACACCTGAAAGGAGGAGGAAATGAAATGAAATGAGAAAGGAGG 776
OY 138 -----ArgLeuGluAs 141
DB 777 GAACAGTACCAAGCCCTTGCCCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 836
OY 141 PGLYSEPRQARGTHGVLGHNLEPHELYSGINTHRTYRSEIRYSPHEAPTHRANSE 161
DB 837 TGGCAGCCCCCGGACGTGGGAGATCTTCAAGCAGACCTTACAGCAAGTTGCAACAACCTC 896
OY 161 HisAsnAspAspAlaLeuLeuLysAsnTyrGlyLeuLeuTyrCysPheArgLysAspPhe 181
DB 897 ACAACAAGATGACGCACTACTCAAGAACTAGGGCTGTCTACTGCTTCAAGAAAGACAT 956
OY 181 LAspLysValGluThrPheLeuArgIleValGlnCysArgSerValGlnGlySerCysGln 201
DB 957 GGAACAAGTGAAGCATTCCTGCGCATGTGACAGTGGCGCTGTGTGAGGGGAGCTGTGG 1016
OY 201 YPHE 202
DB 1017 CTCCTC 1020
```

RESULT 12

US-09-949-016-2792

Sequence 2792, Application US/09949016

Patent No. 6812339

GENERAL INFORMATION:

APPLICANT: VENTER, J. Craig et al.

TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED

TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF

FILE REFERENCE: CLO01307

CURRENT APPLICATION NUMBER: US/09/949,016

CURRENT FILING DATE: 2000-04-14

PRIOR APPLICATION NUMBER: 60/241,755

PRIOR FILING DATE: 2000-10-20

```
;; PRIOR APPLICATION NUMBER: 60/237,768
;; PRIOR FILING DATE: 2000-10-03
;; PRIOR APPLICATION NUMBER: 60/231,498
;; PRIOR FILING DATE: 2000-09-08
;; NUMBER OF SEQ ID NOS: 207012
;; SOFTWARE: FastSeq for Windows Version 4.0
;; SEQ ID NO 2792
;; LENGTH: 1132
;; TYPE: DNA
;; ORGANISM: Human
US-09-949-016-2792
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## Alignment Scores:

	1,256-109	Length:	1132
Pred. No.:	959.50	Matches:	201
Score:	66.56%	Conservative:	0
Percent Similarity:	66.56%	Mismatches:	1
Best Local Similarity:	91.64%	Indels:	100
Query Match:	4	Gaps:	2

US-09-856-796B-2 (1-202) x US-09-949-016-2792 (1-1132)

```
OY 1 MetAlaThrGlySerArgThrSerLeuLeuLeuAlaPheGlyLeuLeuCySteuProTrp 20
DB 117 ATGGCTACAGGCTCCGGAAGTCCCTGCTCTGCTTTGGCTTGGCTGCTGCTGCTGCTG 176
OY 21 LeuGlnGluGlySerAlaPheProThrIleProLeuSerArgLeuPheAspAlaSer 40
DB 177 CTTCAAGAGGCGAGTCCCTCCCAACCATTCCTTATCCAGGCTTTTGACAAAGCTATG 236
OY 41 LeuArgAlaHisArgLeuHisGlnLeuAlaPheAspThrTyrGlnGluPhe----- 57
DB 237 CTCGGGCGCCATGCTGTGACACAGCTGGCTTTGACACTTACAGAGAGTTGAAAGAGCC 296
OY 58 -----AsnProGlnThrSerLeuCySphe 65
DB 297 TATATCCCAAGAACAGAAATATTCATTCCTGCAAGAACCCCAAGACTCCCTCTGTTTC 356
OY 66 SerGlnSerIleProThrProSerAsnArgGlnGluThrGlnGlnLeuSerAsnLeuGlu 85
DB 357 TCGAGGTATATTCGACACCTCCCAACAGGAGAAACAAACAAATCCAACTCAGAG 416
OY 86 LeuLeuArgIleSerLeuLeuLeuIleGlnSerTyrLeuGluProValGlnPheLeuArg 105
DB 417 CTGCTCCGCACTCTCCCTGCTGCTCATTCAGTGTGGTGGAGCCCGTGCAGTCTCTCAG 476
OY 106 SerValPheAlaAsnSerLeuValTyrGlnAlaSerAspSerAsnValTyrAspLeuLeu 125
DB 477 AGTGTCTTCGCAACAGCTGTGTAGAGCGGCTCTGACAGCAAGCTATGACCTCTCA 536
OY 126 LysAspLeuGlnGluGlyIleGlnThrLeuMet-Gly----- 137
DB 537 AAGGACCTAGAGAAAGGACATCCAAACGCTGATGGGGGTGAGGGTGGCCCAAGGGTCCCC 596
OY 137 ----- 137
DB 597 AATCTGGAGCCCACTGACTTTAGAGCTGTGTAGAGAAACACAGTGCCTCTTTT 656
OY 137 ----- 137
DB 657 AGCAGTCAAGCCCTGACCCCAAGAACTGACCTTATTTCCCTGTAATCCT 716
OY 137 ----- 137
DB 717 CCAGGCTTTTCTACACCTGAAAGGAGGAGGAAATGAAATGAAATGAGAAAGGAGG 776
OY 138 -----ArgLeuGluAs 141
DB 777 GAACAGTACCAAGCCCTTGCCCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 836
OY 141 PGLYSEPRQARGTHGVLGHNLEPHELYSGINTHRTYRSEIRYSPHEAPTHRANSE 161
DB 837 TGGCAGCCCCCGGACGTGGGAGATCTTCAAGCAGACCTTACAGCAAGTTGCAACAACCTC 896
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QY	161	THISANASPSAPALALEULEULEYASNTYCIYUULEUITYCSPHATGLYASPM	181
Db	897	ACACACCATGACGCACCTACMACAACTACGGGCTGCTACTCTCCAGGAGGACAT	956
QY	181	IASPIYVAIGLUTHRPHLEUARGILEVALGICNYARGSERVALGIUGLYSERCYSGI	201
Db	957	GGACAGGTGACGACATTCCTGCGCATGTGCAGTGGCTCTGTGGAGGGCAGCTGTGG	1016
QY	201	YFHE	202
Db	1017	CTTC	1020

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RESULT 13
US-09-949-016-2793
; Sequence 2793, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; PRIOR APPLICATION NUMBER: 2000-04-14
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq For Windows Version 4.0
; SEQ ID NO 2793
; LENGTH: 1132
; TYPE: DNA
; ORGANISM: Human
; US-09-949-016-2793

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Alignment Scores:	
Pred. No.:	1.25e-109
Score:	959.50
Percent Similarity:	66.56%
Best Local Similarity:	66.56%
Query Match:	91.64%
RB:	4
Length:	1132
Matches:	201
Conservative:	0
Mismatches:	1
Indels:	100

US-09-856-796B-2 (1-202) x US-09-949-016-2793 (1-1132)

QY 1 MetAlaThrGlySerArgThrSerLeuLeuLeuAlaPheGlyLeuLeuCysLeuProTrp 20  
Db 117 ATGGCTACAGGCGTCCCGAGCTCCCTCTGCTTGGCCGTGCTGCTGCCCTGG 176  
QY 21 LeuGlnGlnGlySerAlaPheProThrIleProLeuSerArgLeuPheAspAsnIleSer 40  
Db 177 CTTCAGAGGCGGAGTGGCTTCCCAACATTCCTTATCCAGGCTTTTGTGCAACAGCTATG 236  
QY 41 LeuAlaGlnAlaIleArgLeuIleGlnLeuAlaPheAspThrTyrGlnGlnIlePhe 57  
Db 237 CTCCGGGCCCATCGTCTGCACCCAGCTGGCTTTGACACCTACAGAGGATTTGAAGAAGCC 296  
QY 58 -----AsnProGlnThrSerLeuCysPhe 65  
Db 297 TATATCCCAAGGAACAGAAGTATTCATTCTCTGCAGAACCCCAAGACTCTCTGTTC 356  
QY 66 SerGlnSerIleProThrProSerAsnArgGlnGlnThrGlnGlnIleSerAsnLeuGln 85  
Db 357 TCAGAGCTATATCCACACCCCTCCAAACAGGAGGAACAACAAGAAATCCAACTCAAGG 416  
QY 86 LeuLeuArgIleSerLeuLeuLeuIleGlnSerTrpLeuGlnProValGlnPheLeuArg 105  
Db 417 CTGCTCCGCATCTCCCTGCTGCTCATTCACAGTGGTGGAGACCCGTGAGTTCCTCAAG 476  
QY 106 SerValPheAlaAsnSerLeuValTyrGlnValAlaSerAspSerAsnValTyrAspLeuLeu 125

Db 477 AGTCTCTTCCCAACACCCCTGGTGTATAGGGGCCCTTGACAGCAACGCTTATGACTCTTA 533

Qy 126 LysAspLeuGluGluGlyIleGlnThrLeuMet-Gly----- 137

Db 537 AAGGACTTAAGAGAGAGGACTTCAACGCGTATGGGGGTGAGGGTGGCCAGGGGTCCC 597

Qy 137 ----- 137

Db 597 AATCTGAGAGCCCACTGACTTTGAGAGCTGTGTATAGAAACACTGCTGCCCTTCTTTT 656

Qy 137 ----- 137

Db 657 AGCAGTCAGGCGCCTGACCCAGAGAACTCACTTATTCTTCATTTCCTCGTGAATCCT 716

Qy 137 ----- 137

Db 717 CCAGGCTTTCTTCTACACCTGAAGGGGAGGAGGAAAAATGAATGATAGAAAGGGAGG 776

Qy 138 ----- ArgLeuGluAs 141

Db 777 GAACAGTACCCAAAGCGCTTGCGCTTCTCTTCTTCACTTTCGACAGCGCTGGAAGA 836

Qy 141 PGIYserProaIrgThrgIyGlnIlePheIyGlnThrTyIserIyPheAspThrAsnSe 161

Db 837 TGGCAGCCCCCGGAGTGGGAGATCTTCACACAGACTCAAGCAAGTTCGACACAAATCC 896

Qy 161 rHisAsnAspAspAlaLeuLeuIyAsnTyIglyIleuLeuTyIcysPheargIyAspMe 181

Db 897 ACACAGCATATACGCACTACTCAAGAACTACGGGCTGCTTACGCTTCAGAGAGAGCAT 956

Qy 181 cAspIyValGlnThrPheLeuArgIleValGlnCysArgserValGluIySerYcgI 201

Db 957 GGAACAAGGTGAGACATTTCTCGCCCATCGTGCAGTGGCGCTGTGTGAGAGGCACTGTGG 1016

Qy 201 yPhe 202

Db 1017 CTTC 1020

RESULT 14  
US-08-187-756C-1  
Sequence 1, Application US/08187756C  
Patent No. 5597709  
GENERAL INFORMATION:  
APPLICANT: ROSEN, ET AL.  
TITLE OF INVENTION: Human Growth Hormone  
NUMBER OF SEQUENCES: 7  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: CARELLA, BYRNE, BAIN, GILFI  
ADDRESSEE: DECHT, STEWART & OLSTEIN  
STREET: 6 BECKER FARM ROAD  
CITY: ROSELAND  
STATE: NEW JERSEY  
COUNTRY: USA  
ZIP: 07068  
COMPUTER READABLE FORM:  
MEDIUM TYPE: 3.5 INCH DISKETTE  
COMPUTER: IBM PS/2  
OPERATING SYSTEM: MS-DOS  
SOFTWARE: WORD PERFECT 5.1  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/187, 756C  
FILING DATE: January 27, 1994  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER:  
FILING DATE:  
ATTORNEY/AGENT INFORMATION:  
NAME: FERRARO, GREGORY D.  
REGISTRATION NUMBER: 36,134  
REFERENCE/DOCKET NUMBER: 325800-55  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 201-994-1700

auProTrp 20  
|||  
|||  
GTGCTCG 60  
||||  
analaser 40  
|||||

----- 5'  
AAGAAGCC 18  
eucysphe 6:  
|||||  
TCTGCTTC 2

8  
 3  
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aspLeuLeu 1  
|||  
CGCCACCTG 4  
SerProArg 1

auProTrp 20  
|||  
|||  
GTGCTCG 60  
||||  
analaser 40  
|||||

----- 5'  
AAGAAGCC 18  
eucysphe 6:  
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TCTGCTTC 2

8  
 3  
 1  
 3

aspLeuLeu 1  
|||  
CGCCACCTG 4  
SerProArg 1



```

Db      421 AAGGACCTAGAGGAGGATCCAAAGCTGATGTGAGGCTGAAAGATGGCAGCCCGG 480
Qy      146 ThrGlnIlePheLysGlnThrTySerLysPheAspThrAsnSerHisAsnAspAsp 165
Db      481 ACTGGGAGATCTTCATCAATCAGTCTACAGCAAGTTTGACACAAATCGCACACGATGAC 540
Qy      166 AlaLeuLeuLysAsnTyGlyLeuLeuTyrcysPheArgLysAspMetAspLysValGlu 185
Db      541 GCACTGCTCAAGAACTACGGGCTGCTCTACTGCTTCAGGAAGGACATGGACAAAGTGGAG 600
Qy      186 ThrPheLeuArgIleValGlnCysArgSerValGluGlySerCysGlyPhe 202
Db      601 ACATTCTGCGGCATGTCAGAGTCCGCTGTGTGGAGGGCAGCTGTGGCTTC 651

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Search completed: February 7, 2005, 15:53:21  
 Job time : 188 secs

***This Page Blank (uspto)***

25-NOV-1998. 0852B-00014050

XX	RESULT 1
XX	AAAA6696
ID	AAAA6696 standard; DNA; 609 BP.
AC	AAAA6696;
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DT	25-SEP-2000 (first entry)
XX	
DE	DNA encoding a human growth hormone (hGH).
XX	
KW	Human; growth hormone; hGH; inhibitor; nuclear factor-kappaB; NF-kappaB;
KW	multi-drug resistance gene; malignant hemopathy; solid tumour;
KW	malignant blood disease; leukaemia; lymphoma; solid cancer; ds.
XX	
OS	Homo sapiens.
XX	
FH	Key
FT	Location/Qualifiers
CDS	1..609
FT	/*tag= a
FT	/product= "growth hormone"
XX	
PN	WO200030587-A2.
XX	
PD	02-JUN-2000.
XX	
PF	24-NOV-1999; 99WO-FR002897.
XX	
PR	25-NOV-1998; 98FR-00014858.
XX	

(CNRS ) CENT NAT RECH SCI.  
XX Hirsch F, Haeflner A;  
XX WPI: 2000-399901/34.  
XX P-PSDB; AAY93637.  
XX Treatment of hematological or solid tumors using an inhibitor of the  
XX activation of nuclear factor-kappaB, particularly to prevent development  
XX of resistance to chemotherapeutics.  
XX  
XX Claim 4; Page 26-27; 30pp; French.  
XX  
XX The present sequence encodes a human growth hormone (hGH). The human  
XX growth hormone protein is used as an inhibitor of the activation of  
XX nuclear factor-kappaB (NF-kappaB). The inhibitor inhibits activation of  
XX NF-kappaB, and thus transcription of the multi-drug resistance gene  
XX (which contains binding sites for NF-kappaB within its regulatory  
XX regions). The inhibitors are used to produce pharmaceuticals which may be  
XX used in the treatment of malignant hemopathy or solid tumours. The  
XX inhibitors are especially used to treat malignant blood diseases  
XX (leukaemia, lymphoma) and solid cancers (of breast or ovary)  
XX  
XX Sequence 609 BP; 133 A; 197 C; 151 G; 128 T; 0 U; 0 Other;  
XX  
XX Alignment Scores:  
XX Pred. No.: 3,34e-110 Length: 609  
XX Score: 1047.00 Matches: 202  
XX Percent Similarity: 100.00% Conservative: 0  
XX Best Local Similarity: 100.00% Mismatches: 0  
XX Query Match: 100.00% Indels: 0  
XX DB: 3 Gaps: 0  
XX  
XX US-09-856-796B-2 (1-202) x AAA46696 (1-609)  
XX  
XX 1 MetAlaThrGlySerArgThySerLeuLeuAlaPheGlyLeuLeuGlyLeuProTyr 20  
XX 1 ATGGCTAAGAGGCTCCCGAGCTGCTCCCTGCTGCTGCTTTGGCTGCTGCTGCTGCTG 60  
XX 21 LeuGlnGluGlySerAlaPheProThrIleProLeuSerArgLeuPheAspAlaSer 40  
XX 61 CTTCAGAGAGGAGGAGCTGCTCCCAACCATTCCTTATCCAGGCTTTTGACCAAGCTAGT 120  
XX 41 LeuAlaGAlaHisArgLeuHisGlnLeuAlaPheAspThrTyrGlnGluPheAsnProGln 60  
XX 121 CTCCGCGCCCATGCTGACACGCTGCTTGGACACCTACAGAGGATTAAACCCGAG 180  
XX 61 ThrSerLeuCyPheSerGluSerIleProThrProSerAsnArgGluGlnGln 80  
XX 181 ACCTCCCTCTGTTTCTCAGAGTCTATTCGACACCTCCAAAGAGGAGAAACACACAG 240  
XX 81 LysSerAsnLeuGlnLeuLeuArgIleSerLeuLeuLeuGlnSerTyrLeuGluPro 100  
XX 241 AATTCACACTAAGAGCTGCTCCGATCTCCCTGCTGCTATCCAGCTGAGCTGAGCC 300  
XX 101 ValGlnPheLeuArgSerValPheAlaAsnSerLeuValTyrGlyAlaSerAspSerAsn 120  
XX 301 GTGCAAGTTCCTCAGAGTGTCTTCCCAACAGCTGAGTACGCGGCTCTGACAGCAAC 360  
XX 121 ValTyrAspLeuLeuLeuAspLeuGluGluGlyIleGlnThrLeuMetGlyValArgLeuGlu 140  
XX 361 GTCTATGACCTCTTAAGAGACCTTGAGAGAGGATCCAAAGCTGATGGGAGGCTGGAA 420  
XX 141 AspGlySerProArgThrGlnGlnIlePheLeuGlnThrTyrSerLysPheAspPheAsn 160  
XX 421 GATGGCAGCCCGGAGCTGGGAGAGTCTTCAAGCAGACTTCAAGCAAGTTCAACCAAC 480  
XX 161 SerHisAsnAspAlaLeuLeuLeuValSerTyrGlyLeuLeuTyrCyPheArgLysAsp 180  
XX 481 TCCACACAGATGACGACACTTCAAGAACTACGAGGCTGCTTACGCTTCCAGAGGAC 540  
XX 181 MetAspLysValGluThrPheLeuArgIleValGlnCyArgSerValGluGlySerCys 200

Db 541 ATGACAAAGGTGAGACATTCTGCGCATGCTGACAGTGGCGGCTCTGTGAGAGGAGCTGT 600  
Oy 201 GlyPhe 202  
Db 601 GGCTTC 606  
RESULT 2  
AA518887  
ID AA518887 standard; cDNA; 654 BP.  
AC AA518887;  
XX 12-MAR-2002 (first entry)  
XX  
XX DNA encoding growth hormone 1 gene (GH1), major isoform.  
XX  
XX Growth hormone 1; GH1; osteopathic; gene therapy; protein therapy;  
XX diabetes; obesity; infection; acromegaly; gigantism; sodium retention;  
XX water retention; metabolic syndrome; mood disorder; sleep disorder;  
XX Growth hormone dysfunction; familial growth hormone deficiency;  
XX short stature; pituitary storage defect; human; chromosome 17q23; 88.  
XX  
XX Homo sapiens.  
XX  
XX Key location/Qualifiers  
XX CDS 1..654  
XX FT /tag= a  
XX FT /product= "GH1"  
XX PT /note= "Growth hormone 1"  
XX  
XX MO200185993-A2.  
XX  
XX 15-NOV-2001.  
XX  
XX 14-MAY-2001; 2001MO-GB002126.  
XX  
XX 12-MAY-2000; 2000GB-00011459.  
XX  
XX 14-JUL-2000; 2000EP-00306004.  
XX  
XX (UWMA-) UNIV WALES COLLEGE OF MEDICINE.  
XX  
XX Cooper DN, Procter AM, Gregory J, Millar DS;  
XX  
XX WPI: 2002-089798/12.  
XX  
XX P-PSDB; AAU11719.  
XX  
XX Detecting growth hormone variants (GH1), useful in screening patients for  
XX growth hormone irregularities, comprises comparing the nucleotide  
XX sequence of a GH1 gene from a test sample with that of a standard  
XX sequence of the human GH1.  
XX  
XX Disclosure; Fig 6; 95pp; English.  
XX  
XX The invention described a method of detecting variation in growth hormone  
XX 1 (GH1), and therefore GH dysfunction in an individual. The method  
XX comprises comparing the nucleotide sequence of GH1 gene obtained from the  
XX test sample with a standard human GH1 gene sequence, in order to identify  
XX variation (GH1 variant). The method is useful in screening patients for  
XX growth hormone irregularities or producing variant proteins for treating  
XX irregularities, and for the early detection and appropriate clinical  
XX management of familial GH deficiency. The GH1 variants are useful in  
XX therapeutic, diagnostic or detection method, particularly for determining  
XX binding defects and susceptibility to a disease such as diabetes, obesity  
XX or infection; for treating acromegaly or gigantism conditions associated  
XX with lactogenic, diabetogenic, lipolytic and protein anabolic effects,  
XX conditions associated with sodium and water retention, metabolic  
XX syndromes, mood and sleep disorders; diagnosing GH dysfunction and  
XX determining pituitary storage defects. The GH1 variants are especially  
XX useful in gene therapy or protein therapy. The GH1 or GH variant may also  
XX be used in the preparation of a medicament, diagnostic composition or  
XX kit, or detection kit. The method has the advantage of: expanding the  
XX know spectrum of GH1 gene mutations; evaluating the role of GH1 gene  
XX mutations in the etiology of short stature; identifying of the mode of

CC inheritance of novel lesions; evaluation the effects of GH1 mutations on  
 CC the structure and function of the GH molecule and development of rapid  
 CC diagnostic tests for inherited GH deficiency. This sequence encodes the  
 CC major isoform of human growth hormone 1 (GH1), located on chromosome  
 CC 17q23, used as a reference sequence for creating the mutants (AAU11721-  
 CC AAU11750 and AAU11901) described in the method of the invention

SQ Sequence 654 BP; 150 A; 207 C; 160 G; 137 T; 0 U; 0 Other;

# Alignment Scores:

Pred. No.:	Score:	3.73e-108	Length:	654
Percent Similarity:	1029.50		Matches:	202
Best Local Similarity:	93.09%		Conservative:	0
Query Match:	98.33%		Mismatches:	0
			Indels:	15
			Gaps:	1

US-09-856-796b-2 (1-202) x AAS18887 (1-654)

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QY 1 MetAlaThrGlySerArgThrSerLeuLeuAlaPheGlyLeuLeuCySleuProTyr 20
DB 1 ATGAGCTACAGAGCTCCGAGAGCTCCCTGCTGCTTTGGCTGCTGCTGCTGCTGCTG 60
QY 21 LeuGlnGluGlySerAlaPheProThrIleProLeuSerArgLeuPheAspAlaSer 40
DB 61 CTTCAGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 120
QY 41 LeuArgAlaHisArgLeuHisGlnLeuAlaPheAspThrIleGlnGluPhe----- 57
DB 121 CTCGGGCGCCATGATGTCGACAGCAGCTGCTTGGACACCTACAGAGGAGGAGGAGGAGG 180
QY 58 -----AsnProGlnThrSerLeuCySph 65
DB 181 TATATCCCAAGAGACAGAGATTCATCTCTGAGAGAGGAGGAGGAGGAGGAGGAGGAGG 240
QY 66 SerGluSerIleProThrProSerAsnArgGluGlnThrGlnGlnSerAsnLeuGln 85
DB 241 TCAGAGCTTATTCGACACCTCCACAGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 300
QY 86 LeuLeuArgIleSerLeuLeuLeuIleGlnSerTrpLeuGlnProValGlnPheLeuArg 105
DB 301 CTGCTCGGATCTCTCTGCTGCTCATCTGAGTCTGAGGAGGAGGAGGAGGAGGAGGAGG 360
QY 106 SerValPheAlaAsnSerLeuValIleGlnAlaSerAspSerAsnValIleAspLeuLeu 125
DB 361 AGTGTCTTGGCCAAAGCCGCTGCTGACGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 420
QY 126 LysAspLeuGluGlnIleGlnThrLeuMetGlyArgLeuGlnAspGlySerProArg 145
DB 421 AAGGAGCTAGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 480
QY 146 ThrGlyGlnIlePheLeuGlnThrIleSerIlePheAspThrAsnSerHisAsnAsp 165
DB 481 ACTGGGCAATCTTCAAGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 540
QY 166 AlaLeuLeuLysAsnTrpGlyLeuLeuTrpCySphArgIleAspMetAspLeuValGln 185
DB 541 GACACTACTAGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 600
QY 186 ThrPheLeuArgIleValGlnCySphSerValGlnGlySerCySphGlyPhe 202
DB 601 ACATTCCTGCGCATCTGAGAGTCCGCTCTGAGAGGAGGAGGAGGAGGAGGAGGAGG 651

```

## RESULT 3

AAS18888 standard; DNA; 654 BP.

XX AAS18888;

XX 12-MAR-2002 (first entry)

XX DNA encoding growth hormone 1 gene (GH1), E56G mutant.

XX

KW Growth hormone 1; GH1; osteopathic; gene therapy; protein therapy;  
 KW diabetes; obesity; infection; acromegaly; gigantism; sodium retention;  
 KW water retention; metabolic syndrome; mood disorder; sleep disorder;  
 KW Growth hormone dysfunction; familial growth hormone deficiency;  
 KW short stature; pituitary storage defect; human; mutant; ds.

OS Homo sapiens.  
 OS Synthetic.

FT Key Location/Qualifiers  
 FT CDS 1..654  
 FT /\*tag= a  
 FT /product= "GH1 mutant E56G"  
 FT /note= "Growth hormone 1 mutant E56G"

FT mutation replace(17..4,A)  
 FT /\*tag= c  
 FT /\*tag= b  
 FT mutation replace(17..3,A)  
 FT /\*tag= b

FT WO200185993-A2.

FT 15-NOV-2001.

FT 14-MAY-2001; 2001WO-GB002126.

FT 12-MAY-2000; 2000GB-00011459.

FT 14-JUL-2000; 2000EP-00306004.

FT (UYWA-) UNIV WALES COLLEGE OF MEDICINE.

FT Cooper DN, Procter AM, Gregory J, Millar DS;  
 FT WPI: 2002-089798/12.

FT P-PSDB; AAU11720.

PT Detecting growth hormone variants (GH1), useful in screening patients for  
 PT growth hormone irregularities, comprises comparing the nucleotide  
 PT sequence of a GH1 gene from a test sample with that of a standard  
 PT sequence of the human GH1.

PT Disclosure; Fig 7; 95pp; English.

CC The invention described a method of detecting variation in growth hormone  
 CC 1 (GH1), and therefore GH dysfunction in an individual. The method  
 CC comprises comparing the nucleotide sequence of GH1 gene obtained from the  
 CC test sample with a standard human GH1 gene sequence, in order to identify  
 CC variation (GH1 variant). The method is useful in screening patients for  
 CC growth hormone irregularities or producing variant proteins for treating  
 CC irregularities, and for the early detection and appropriate clinical  
 CC management of familial GH deficiency. The GH1 variants are useful in  
 CC therapeutic, diagnostic or detection method, particularly for determining  
 CC binding defects and susceptibility to a disease such as diabetes, obesity  
 CC or infection; for treating acromegaly or gigantism conditions associated  
 CC with lactogenic, diabetogenic, lipolytic and protein anabolic effects,  
 CC conditions associated with sodium and water retention, metabolic  
 CC syndromes, mood and sleep disorders; diagnosing GH dysfunction and  
 CC determining pituitary storage defects. The GH1 variants are especially  
 CC useful in gene therapy or protein therapy. The GH1 or GH variant may also  
 CC be used in the preparation of a medicament, diagnostics composition or  
 CC kit, or detection kit. The method has the advantage of: expanding the  
 CC know spectrum of GH1 gene mutations; evaluating the role of GH1 gene  
 CC mutations in the etiology of short stature; identifying the mode of  
 CC inheritance of novel lesions; evaluation the effects of GH1 mutations on  
 CC the structure and function of the GH molecule and development of rapid  
 CC diagnostic tests for inherited GH deficiency. This sequence encodes a  
 CC variant of human growth hormone 1 (GH1), created from the GH1 wild type  
 CC sequence (AAS18887) given in figure 6 and one of many variations of the  
 CC gene discussed in the method of the invention

SQ Sequence 654 BP; 148 A; 207 C; 162 G; 137 T; 0 U; 0 Other;

## Alignment Scores:

Pred. No.:	Score:	3.73e-108	Length:	654
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QY 106 SerValPheAlaAsnSerLeuValTyrGlyAlaSerAspSerAsnValTyrAspLeu 125  
 Db 422 AGTCTCTTCCCAACAGCTGTGTACGGCCCTCTGACACAACTGCTATGACTCTCTA 481  
 QY 126 LysAspLeuGluGluGlyIleGlnThrLeuMetGlyTyrGluGluAspGlySerProArg 145  
 Db 482 AAGGACCTAGAGAGAGAGCATCCAAACGCTGATGGGAGGCTGAGAGATGGCAGCCCGG 541  
 QY 146 ThrGlyGlnIlePheLeuSerGlnThrTyrSerIlePheAspThrAsnSerHisAsnAsp 165  
 Db 542 ACTGGGAGATCTTCAAGACAGACTTACAGCAAGTTCAACAACCTACACACAGATGAC 601  
 QY 166 AlaLeuLeuLysAsnTyrGlyLeuLeuTyrCysPheArgIleAspMetAspLeuValGlu 185  
 Db 602 GCACTACTCAAGAACTACAGGGCTGCTCTACTGCTTCAAGAGACATGACAAAGTCTGAG 661  
 QY 186 ThrPheLeuArgIleValGlnCysArgSerValGluGlySerCysGlyPhe 202  
 Db 662 ACATTCTCGGATCGTGCAGTCCGCTCTGTGAGAGGCGAGCTGTGGCTTC 712

RESULT 5  
 AAN60801  
 ID AAN60801 standard; DNA; 3557 BP.

AC AAN60801;  
 DT 24-OCT-1991 (first entry)  
 DE Human pro-growth hormone.  
 KM Pituitary gland; E.coli; ds.  
 OS Homo sapiens.  
 PN JF61202689-A.  
 PD 08-SEP-1986.  
 PF 04-MAR-1985; 85JP-00042404.  
 PR 04-MAR-1985; 85JP-00042404.  
 PA (NAKA/) NAKAJIMA K.  
 DR WPI; 1986-276387/42.  
 PS Plasmid for amplification of human growth hormone gene - derived from human pituitary gland tissue.  
 PT Disclosure; Table 1-9; 9pp; Japanese.  
 CC Sequence is derived from human pituitary gland tissue, and allows pro-growth hormone to be produced by a circular plasmid carrying an amp resistance gene, from a transformed E.coli expression system in an ampicillin containing medium. See also J61202690

SO Sequence 3557 BP; 927 A; 902 C; 897 G; 831 T; 0 U; 0 Other;  
 Alignment Scores:  
 Pred. No.: 8,58e-107  
 Score: 1026.50  
 Percent Similarity: 93.09%  
 Best Local Similarity: 92.63%  
 Query Match: 98.04%  
 DB: 1  
 Gaps: 1

US-09-856-796b-2 (1-202) x AAN60801 (1-3557)

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 Db 394 ATGGCTACAGGCTCCCGAGCGTCCCTGCTCTGCTTGGGCTTCTGCTGCTGCTG 453

QY 21 LeuGlnGluGlySerAlaPheProThrIleProLeuSerArgLeuPheAspAsnIleSer 40  
 Db 454 CTTCAGAGAGGAGAGTGGCTTCCCAACCATTCCTTATCCAGGCTTTTTCAGACGCTAGT 513  
 QY 41 LeuArgAlaHisArgLeuHISGlnLeuAlaPheAspThrTyrGlnGluPhe----- 57  
 Db 514 CTCCGCGCCCATGCTGTGCACACAGCTGGCTTTGACACCTACAGAGGTTTGAAGAGCC 573  
 QY 58 -----AsnProGlnThrSerLeuCysPhe 65  
 Db 574 TATATCCAAAGAGACAGAACTATTATTCCTGACAGAACCCCAAGACTCTCTGTTTC 633  
 QY 66 SerGluSerIleProThrProSerAsnArgGluGlnThrGlnGlnIleSerAsnLeuGlu 85  
 Db 634 TCAGACTCTATTCTCGACACCTCTCAACAGAGAGAAACAGAACAAATCCAACTTAGAG 693  
 QY 86 LeuLeuArgIleSerLeuLeuLeuIleGlnSerTyrLeuGluProValGlnPheLeuArg 105  
 Db 694 CTGCTCCGATCTCCCTGCTCTCATTCAGTGTGCTGAGGCCCTGCAAGTTCTCTAGG 753  
 QY 106 SerValPheAlaAsnSerLeuValTyrGlyAlaSerAspSerAsnValTyrAspLeuLeu 125  
 Db 754 AGTGTCTTGCACAGAGCTGTGTACGGCCCTCTGACAGACAGTCTATGACCTCTCA 813  
 QY 126 LysAspLeuGluGluGlyIleGlnThrLeuMetGlyArgLeuGluAspGlySerProArg 145  
 Db 814 AAGGACCTAGAGAGAGAGCTCAACAGCTGATGGGAGGCTGGAAGATGGCAGCCCGG 873  
 QY 146 ThrGlyGlnIlePheLeuSerGlnThrTyrSerIlePheAspThrAsnSerHisAsnAsp 165  
 Db 874 ACTGGGAGATCTTCAACAGACCTACAGCAAGTTGACACAACTACACAAACATGAC 933  
 QY 166 AlaLeuLeuLysAsnTyrGlyLeuLeuTyrCysPheArgIleAspMetAspLeuValGlu 185  
 Db 934 GCACACTCAAGAACTACGGGCTGCTCTACTGCTTCAAGAGACATGACAAAGTCTGAG 993  
 QY 186 ThrPheLeuArgIleValGlnCysArgSerValGluGlySerCysGlyPhe 202  
 Db 994 ACATTCTCGGATCGTGCAGTCCGCTCTGTGAGAGGCGAGCTGTGGCTTC 1044

RESULT 6  
 ABK90830  
 ID ABK90830 standard; DNA; 654 BP.

AC ABK90830;  
 DT 05-NOV-2002 (first entry)  
 DE DNA encoding human growth hormone (hGH).  
 KM Human; growth hormone; hGH; Turner's syndrome; achondroplasia;  
 KW growth hormone deficiency in adults; GHDA; chronic renal insufficiency;  
 KM renal failure in children; acquired immune deficiency syndrome; AIDS;  
 OS Homo sapiens.

Key Location/Qualifiers  
 FT sig\_peptide 1..80  
 FT /\*tag= a  
 FT CDS 81..654  
 FT /\*tag= b  
 FT /\*product= "human growth hormone"  
 FT mat\_peptide 81..651  
 FT /\*tag= c  
 FT /\*note= "Mature human growth hormone"

WO200255532-A2.

18-JUL-2002.

10-JAN-2002; 2002WO-DK000017.

11-JAN-2001; 2001DK-00000042.  
 11-JAN-2001; 2001US-0261411P.  
 (MAXY-) MAXYGEN APS.  
 (MAXY-) MAXYGEN HOLDINGS LTD.  
 Andersen KV, Drustup J, Christiansen J;  
 WPI; 2002-608345/65.  
 P-PSDB; ABG31857.  
 New conjugates exhibiting growth hormone activity, useful for treating a disease or for manufacturing a medicament for treating a disease, e.g. Turner's syndrome, growth hormone deficiency, achondroplasia, AIDS wasting or cachexia.

Claim 16; Page 73-74; 74pp; English.

The invention relates to new conjugates, which exhibit growth hormone (GH) activity and comprise at least one non-polypeptide group covalently attached to a GH polypeptide. The amino acid sequence of the conjugates differs from that of wild type human GH in at least one introduced and at least one removed amino acid residue comprising an attachment group for the first non-polypeptide group. The conjugate or pharmaceutical composition is useful for treating a disease or for manufacturing a medicament for treating a disease, e.g. Turner's syndrome, GH deficiency or in adults (i.e. GHDA), achondroplasia, chronic renal insufficiency or failure (including renal failure in children), acquired immune deficiency syndrome (AIDS) wasting, cachexia in AIDS patients, or cachexia associated with other diseases. The conjugates are useful for treating a variety of disorders caused by growth hormone inadequacy. The present sequence represents the coding sequence of human growth hormone

Sequence 654 BP; 150 A; 207 C; 160 G; 137 T; 0 U; 0 Other;

Alignment Scores:

Pred. No.: 1.39e-107 Length: 654  
 Score: 1024.50 Matches: 201  
 Percent Similarity: 92.63% Conservative: 0  
 Best Local Similarity: 92.63% Mismatches: 1  
 Query Match: 97.85% Indels: 15  
 DB: 6 Gaps: 1

US-09-856-796B-2 (1-202) x ABK90830 (1-654)

1 MetAlaThrGlySerArgThrSerLeuLeuAlaPheGlyLeuLeuCysLeuProTyr 20  
 1 ATGGCTACAGGCTCCCGAGAGCTCCGCTCTGCTTTGGCTCTGCTGCTGCTGCTG 60  
 21 LeuGlnGlnGlySerAlaPheProThrIleProLeuSerArgLeuPheAspAsnAlaSer 40  
 61 CTTCAGAGAGGCGAGTGGCTTCCCAACATTCCTTATCCAGGCTTTTGAACAGCTATG 120  
 41 LeuArgAlaHisArgLeuHisGlnLeuAlaPheAspThrTyrGlnGlnPhe 57  
 121 CTCGGGCGCCATGCTCTGCACACAGCTGAGCTTGAACCTACAGAGAGCTTTGAAGAACCC 180  
 58 -----AsnProGlnThrSerLeuCysPhe 65  
 181 TATATCCCAAGAAAGAAAGATATTCTCTGCAGAAACCCCAAGACCTCTCTGTTTC 240  
 66 SerGlnSerIleProThrProSerAsnArgGlnGlnGlnGlnGlnGlnGlnGlnGln 85  
 241 TCAGAGCTATTTCCGACACCTCCCAACAGGAGAAACACACAAATCCAACTAAGAG 300  
 86 LeuLeuArgIleSerLeuLeuLeuIleGlnSerTyrLeuGlnProValGlnPheLeuArg 105  
 301 CTGCTCCGCACTCTCCCTGCTGCTATTCAGTGTGGCTGAGACCCGTGCAAGTTCCACAG 360  
 106 SerValPheAlaAsnSerLeuValTyrGlnAlaSerAspSerAsnValTyrAspLeuLeu 125  
 361 AGTGTCTTCGCAACAGCTGCTGTATACGGCGCTCTGACAGCAACCTATATGACCTCTCA 420

126 LysAspLeuGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGln 145  
 421 AAGAGCTTACAGAGGAGCATCCAAACCTGATGGGAGCTGGAAATGGCAAGCCCGG 480  
 146 ThrGlyGlnIlePheLeuGlnThrTyrSerIleAspPheThrAsnSerHisAsnAspAsp 165  
 481 ACTGGGCGAGATCTTCAGACAGACCTTACAGAGATTCACACAACTCACAACAGATGAC 540  
 166 AlaLeuLeuLysAsnTyrGlyLeuLeuTyrCysPheArgIleAspMetAspLeuValGln 185  
 541 GCATCTCAAGAACTACAGGAGCTGCTCTACTGCTTCAGGAAGAGACATGACAGGTCCAG 600  
 186 ThrPheLeuArgIleValGlnCysArgSerValGlnGlySerCysGlyPhe 202  
 601 ACATTCCTCGCATGCTGCAAGTCCGCTCTGAGAGGCGAGCTGTGGCTTC 651

RESULT 7

ADCC61349 standard; DNA; 654 BP.

ADCC61349;

18-DEC-2003 (first entry)

Human Growth Hormone 1, GH1, coding sequence.

Growth Hormone; GH1; human; gene; chromosome 17q23; ds.

Homo sapiens.

Key Location/Qualifiers

FT CDS 1..654  
 /product= "Human growth hormone, GH1"

MO2003042408-A2.

22-MAY-2003:

12-NOV-2002; 2002MO-GB005103.

12-NOV-2001; 2001GB-00027213.

(UYWA-) UNIV WALES COLLEGE OF MEDICINE.

Cooper DN, Procter AM, Gregory J, Millar DS;

WPI; 2003-449578/42.

P-PSDB; ADCC61299.

Detecting a variation in pituitary-expressed growth hormone (GH1), useful as an indicator of growth hormone (GH) dysfunction comprises comparing the sequence obtained from the test sample with a standard sequence of the human GH1 gene.

Claim 1; Fig 6; 70pp; English.

The present invention relates to a method for detecting a variation in pituitary-expressed Growth Hormone (GH1) effective to act as an indicator of Growth Hormone (GH) dysfunction in an individual. The method comprises comparing the sequence obtained from the test sample with a standard sequence of the human GH1 gene. The present sequence is the coding sequence for human GH1, used to illustrate the method of the invention. The detection comprises PCR amplification of the GH1 gene of the individual using a GH1 gene-specific fragment that is unique to the GH1 gene whose sequence is not found in the four paralogous (non-GH1) genes in the GH cluster, and one or more GH1-gene specific primers that cannot bind to the homologous flanking regions in the four other paralogous (non-GH1) genes in the GH cluster (ADCC1308-). The gene encoding GH1 is located on chromosome 17q23 within a cluster of five related genes.

Sequence 654 BP; 150 A; 207 C; 160 G; 137 T; 0 U; 0 Other;



```

FT      FT      /product= "Human growth hormone"
FT      FT      1. .78
FT      FT      /*tag= b
FT      FT      mat_peptide 79. .651
FT      FT      /*tag= c
FT      FT      /product= "Human growth hormone"
PN      MO2003042245-A2.
XX      XX
XX      12-NOV-2002; 2002MO-GB005112.
XX      PF
XX      PD
XX      22-MAY-2003.
XX      XX
XX      12-NOV-2001; 2001GB-00027214.
XX      PR
XX      14-NOV-2001; 2001GB-00027328.
XX      XX
XX      (UYMA-) UNIV WALES COLLEGE OF MEDICINE.
PI      Cooper DN, Procter AM, Gregory J, Millar DS, Lewis M, Ulied A,
XX      WPI; 2003-449559/42.
XX      DR
XX      P-PSDB; ABR42662.
XX      XX
XX      New polynucleotide comprising a variant of the human growth hormone
XX      PT      nucleic acid sequence, GH1, useful for diagnosing or treating obesity,
XX      PT      diabetes, infection, cancer or cardiac conditions.
XX      PS      Disclosure; Fig 5; 62pp; English.
XX      PS
XX      CC
XX      CC      The present sequence is the coding sequence of the human growth hormone
XX      CC      GH1 gene. The invention relates to naturally-occurring mutations (see
XX      CC      ACC58424) that have been detected in a cohort of patients with short
XX      CC      stature. Methods are provided for detection of these variants, for screening
XX      CC      patients for growth hormone irregularities, and for producing variant
XX      CC      proteins for use in therapeutic, diagnostic or detection methods, e.g.
XX      CC      for determination of susceptibility of an individual to diabetes,
XX      CC      obesity, infection, cancer or a cardiac condition, and in gene therapy
XX      CC
XX      SQ      Sequence 654 BP; 150 A; 207 C; 160 G; 137 T; 0 U; 0 Other;

Alignment Scores:
Pred. No.:      1,39e-107      Length:      654
Score:          1024.50      Matches:      201
Percent Similarity: 92.63%      Conservative: 0
Best Local Similarity: 92.63%      Mismatches: 1
Query Match:      97.85%      Indels:      15
DB:              10      Gaps:      1

US-09-856-796B-2 (1-202) x ACC58425 (1-654)

QY      1 MetAlaThGlySerAArgThSeriLeuLeuAlaPheGlyLeuLeuCysLeuProTrp 20
DB      1 ATGGCTACACGGCTCCCGACGCTCCGCTCTGGCTTTTGCCCTGCTCTGCTGCTCGG 60
QY      21 LeuGInGInGlySerAlaPheProThrIleProLeuSerAArgLeuPheAspAsnAlaSer 40
DB      61 CTTCAAGAGGGCAGCGCTCTCCCAACCACTTCCTTATTCACAGCTTTTGAACAAGCTATG 120
QY      41 LeuAArgAlaHISarGLeuHISglLeuAlaPheAspThrTyArgInGInGluPhe----- 57
DB      121 CTCCGGCGCCATCGTCGACACACTGCGCTTTGACACCTACACGAGGATTGAAGAAGCC 180
QY      58 -----AsnProGInTrpSeriLeuCysPhe 65
DB      181 TATATCCCAAGAACAGAGTATTCATTCCTCGAGAACCCCAAGACTCTCTGTTTC 240
QY      66 SerGInSerIleProThrProSerAsnAArgGInGInThGInGInGlySerAsnLeuGlu 85
DB      241 TCGAGGCTATTCGACACCTCCCAACAGGAGGAACAACAAGAAATCAACCTTAAG 300
QY      86 LeuLeuAArgIleSerLeuLeuLeuIleGInSerTrpLeuGInProValGInGInGluGlu 300

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QY SerValPheAlaAsnSerLeuValTyrGlyAlaSerAspSerAsnValTyrAspLeu 125  
 Db AGGTCTTCGCAACAGCTGATGACGCGCTGACAGCAAGCTATGACCTCTTA 420  
 QY 126 LysAspLeuGluGluGlyTyrLeuMetGlyArgLeuGluAspGlySerProArg 145  
 Db 421 AAGGACCTAGAGGAAGGATCCAAAGCTGATGGGAGGCTGGAAGATGGCAGCCCG 480  
 QY 146 ThrGlyGlnIlePheLeuGlnThrTyrSerLysPheAspThrAsnSerHisAsnAsp 165  
 Db 481 ACTGGGAGATCTTCAGAGCAAGCTACAGCAAGTTCAGCAACAATCAGCAAGATGAC 540  
 QY 166 AlaLeuLeuLysAsnTyrGlyLeuLeuTyrCysPheArgLysAspMetAspLysValGlu 185  
 Db 541 GCACACTCAAGAACTACGAGGCTGCTCTACTGCTTCAAGAAAGCATGAGCAAGTCCAG 600  
 QY 186 ThrPheLeuArgIleValGlnCysArgSerValGluGlySerCysGlyPhe 202  
 Db 601 ACATTCTCGCATCGTCGAGTCCCGCTCTGTGAGGAGGAGCTGTGCTTC 651

RESULT 9  
 ADJ93049 ID ADJ93049 standard; DNA; 654 BP.

AC ADJ93049;  
 DT 06-MAY-2004 (first entry)  
 XX Human growth hormone DNA for stinging cell therapeutic system.  
 XX ds; dermatological; stinging cell; vaccination; epidermal mucosal;  
 XX membrane barrier; human growth hormone.  
 OS Homo sapiens.  
 XX MO2003079967-A2.  
 PN 02-OCT-2003.  
 PD 20-MAR-2003; 2003WO-IL000241.  
 PF 26-MAR-2002; 2002US-0367261P.  
 PR 26-MAR-2002; 2002US-0367261P.  
 PA (NANO-) NANOCYTE INC.  
 XX Lotan T, Eckhouse S, Shaoul E;  
 PI WPI; 2003-779171/73.  
 DR Novel stinging cell or stinging cell progenitor comprising exogenous  
 XX polynucleotide capable of expressing therapeutic, cosmetic or diagnostic  
 PT agent, useful for delivering therapeutic agents.  
 PS Example 1; SEQ ID NO 1; 58bp; English.  
 XX The invention relates to a stinging cell or a stinging cell progenitor  
 CC (I) comprising an exogenous polynucleotide capable of expressing a  
 CC therapeutic, cosmetic or diagnostic agent in the stinging cell. (I) is  
 CC useful for delivery a variety of therapeutic agents and for vaccination.  
 CC (II) provides a safe, efficient and contamination risk free method for  
 CC delivering agents across epidermal or mucosal or membranous barriers. This  
 CC sequence corresponds to a human growth hormone DNA used in the invention.  
 CC  
 SQ Sequence 654 BP; 150 A; 207 C; 160 G; 137 T; 0 U; 0 Other;

Alignment Scores: 1.39e-107 Length: 654  
 Pred. No.: 1024.50 Matches: 201  
 Score: 92.63% Conservative: 0  
 Percent Similarity: 92.63% Mismatches: 1  
 Best Local Similarity: 97.85% Indels: 15  
 Query Match: 97.85% Gaps: 1  
 DB: 10

us-09-856-796b-2 (1-202) x ADJ93049 (1-654)

QY 1 MetAlaThrGlySerArgThrSerLeuLeuAlaPheGlyLeuLeuCysLeuProTyr 20  
 Db 1 ATGGTCTTCGCAACAGCTGATGACGCGCTGACAGCAAGCTATGACCTCTTA 60  
 QY 21 LeuGlnGluGlySerAlaPheProThrIleProLeuSerArgLeuPheAspAlaSer 40  
 Db 61 CTCGAGGAGGAGGAGTGGCTTCCCAACATTCCTTATCCAGGCTTTTTCGCAAGCTTATG 120  
 QY 41 LeuArgAlaHisArgLeuHisGlnLeuAlaPheAspThrTyrGlnGluPhe 57  
 Db 121 CTCGCGCCCATCGCTCTGCAACAGCTGCGCTTTCAGCACTTACCGAGGATTGAAGAAC 180  
 QY 58 -----AsnProGlnThrSerLeuCysPhe 65  
 Db 181 TATATCCCAAGGAACAGAAATTCATTCCTGCAAGAACCCCGACCTCTCTGTTTC 240  
 QY 66 SerGluSerIleProThrProSerAsnArgGluGluThrGlnGlnLysSerAsnLeu 85  
 Db 241 TCAGAGTCTATTCGCAACCTCCCAACAGGAGGAGGAACACACAGAAATCCAGCTAGAG 300  
 QY 86 LeuLeuArgIleSerLeuLeuLeuIleGlnSerTyrLeuGluProValGlnPheLeuArg 105  
 Db 301 CTGCTCCGATCTCCCTGTGCTCTCATTCAGTGTGCTGAGCCCGCTGACAGTTCCTCAGG 360  
 QY 106 SerValPheAlaAsnSerLeuValTyrGlyAlaSerAspSerAsnValTyrAspLeu 125  
 Db 361 AGGTCTTCGCAACAGCTGATGACGCGCTGACAGCAAGCTATGACCTCTTA 420  
 QY 126 LysAspLeuGluGluGlyTyrLeuMetGlyArgLeuGluAspGlySerProArg 145  
 Db 421 AAGGACCTAGAGGAAGGATCCAAAGCTGATGGGAGGCTGGAAGATGGCAGCCCGG 480  
 QY 146 ThrGlyGlnIlePheLeuGlnThrTyrSerLysPheAspThrAsnSerHisAsnAsp 165  
 Db 481 ACTGGGAGATCTTCAGAGCAAGCTACAGCAAGTTCAGCAACAATCAGCAAGATGAC 540  
 QY 166 AlaLeuLeuLysAsnTyrGlyLeuLeuTyrCysPheArgLysAspMetAspLysValGlu 185  
 Db 541 GCACACTCAAGAACTACGAGGCTGCTCTACTGCTTCAAGAAAGCATGAGCAAGTCCAG 600  
 QY 186 ThrPheLeuArgIleValGlnCysArgSerValGluGlySerCysGlyPhe 202  
 Db 601 ACATTCTCGCATCGTCGAGTCCCGCTCTGTGAGGAGGAGCTGTGCTTC 651

RESULT 10  
 ADP19728 ID ADP19728 standard; cDNA; 654 BP.

AC ADP19728;  
 DT 12-AUG-2004 (first entry)  
 XX Human growth hormone 1 (GHI) encoding cDNA.  
 DE human; growth hormone; growth hormone variant; GH; GHI;  
 XX human; growth hormone; growth hormone variant; GH; GHI;  
 KW receptor-mediated cell signaling pathway activator; chromosome 17;  
 KW growth hormone dysfunction; growth hormone irregularity; chromosome 17;  
 OS gene; se.  
 XX Homo sapiens.  
 XX  
 FH Key Location/Qualifiers  
 FT 1..654  
 FT /tag= a  
 FT /product= "growth hormone 1 (GHI)"  
 PN MO2004044002-A1.  
 XX 27-MAY-2004.

PF 04-NOV-2003; 2003WO-GB004775.  
XX  
XX  
PR 12-NOV-2002; 2002GB-00026441.  
PR 12-NOV-2002; 2002WO-GB005112.  
PR 10-APR-2003; 2003GB-00008242.  
XX  
XX PA (UYMA-) UNIV WALES COLLEGE OF MEDICINE.  
XX  
P1 Cooper DN, Procter AM, Gregory J, Millar DS, Lewis M, Ulied A;  
XX  
XX WPI; 2004-411699/38.  
DR P-PSDB; ADP19729.  
DR  
XX  
PT Isolated variant of human growth hormone nucleic acid molecule, GH1  
PT useful for diagnosing growth hormone dysfunction or development of  
PT suitable therapies, comprises altered nitrogenous bases.  
XX  
PS Disclosure; Fig 5; 66pp; English.  
XX

CC present invention describes an isolated variant of a human growth  
CC hormone (GH) nucleic acid molecule (I), GH1, comprising the substitution:  
CC +191 cytosine substituted by guanine, wherein 191 refers to the  
CC position of the nucleotide with respect to this transcription initiation  
CC site which is designated 1 or comprises a nucleic acid molecule that  
CC encodes a protein, i.e. a GH protein, including the substitution  
CC Ile179Met. Also described: (1) a transcript of (I); (2) an isolated  
CC polypeptide encoded by (II); (3) an isolated polypeptide which is a  
CC variant of the growth hormone protein, GH, and which includes the  
CC substitution Ile179Met; (4) screening (M1) an individual suspected of  
CC having dysfunctional GH, involving: (a) obtaining a test sample  
CC comprising a nucleic acid molecule of human GH1 gene from an individual,  
CC sequencing the molecule, examining the sequence for a+1491 cytosine,  
CC substituted by guanine, and where the substitution exists comprising  
CC there is GH dysfunction; (b) obtaining a test sample comprising a growth  
CC hormone, GH, polypeptide from the individual, sequencing the polypeptide,  
CC examining the sequence for a Ile179Met substitution, and where the  
CC substitution exists concluding there is a GH dysfunction; or (c)  
CC obtaining a test sample from the individual comprising the individual's  
CC endogenous growth mitogen-activated protein kinases (MAPK) hormone,  
CC examining the growth hormone to determine whether and to what extent it  
CC will activate the receptor-mediated cell signaling pathway, and where  
CC there is a reduction in MAPK cell signaling, with respect to wild-type  
CC GH, concluding there is a GH dysfunction; (5) a kit suitable for carrying  
CC out M1; (6) an oligonucleotide suitable for use in (M1) and optionally,  
CC protein (II), containing an Ile179Met substitution and which further  
CC provides for differential activation of receptor-mediated cell signaling  
CC pathways or possessing a reduced ability to activate the MAP kinase  
CC pathway; (8) an antibody specific for (II); (9) pharmaceutical  
CC composition comprising (I) or (II) with a carrier; (10) vector (III)  
CC comprising (I); (11) host cell (IV) comprising (III); and (12) a  
CC polypeptide or protein produced by using (IV). (I) activates receptor-  
CC mediated cell signaling pathway. (I) and (II) are useful for the  
CC diagnosis of growth hormone dysfunction or the development of suitable  
CC therapies. (I) or (II) is useful as a pharmaceutical composition for  
CC treating growth hormone irregularities. (IV) is useful for preparing  
CC polypeptide or protein produced by the cell. The present sequence encodes  
CC human GH1 which is given in the exemplification of the present invention.  
CC Human GH1 is located on chromosome 17q23.

Alignment Scores:  
 sequence 654 BP; 150 A; 207 C; 160 G; 137 T; 0 U; 0 Other;

Pred. No.:	1,39e-107	Length:	654
Score:	1024.50	Matches:	201
Percent Similarity:	92.63%	Conservative:	0
Best Local Similarity:	92.63%	Mismatches:	1
Query Match:	97.85%	Indels:	15
EB:	12		

US-09-856-796B-2 (1-202) x ADP19728 (1-654)

QY	1	MetAlaThrGlySerArgThrSerLeuLeuAlaPheGlyLeuLeuCysLeuProTyr	20
Db	1	ATGGCTACAGAGCTCCCGGACGTCCTGCTCTGGCTTTGGCTGCTGCTGCTCCCTGG	60
QY	21	LeuGlnGlnGlySerAlaPheProThrIleProLeuSerArgLeuPheAspAlaSer	40
Db	61	CTTCAAGAGGGCAGGCTTCCCAACCATCTCCTTATTCAGAGGCTTTTGACACGCTATG	120
QY	41	LeuArgAlaHisArgLeuHisGlnLeuAlaPheAspThrTyrGlnGlnPhe-----	57
Db	121	CTCCGGCGCCCATCGCTGACACAGCTGGCTTTGACACCTTACACAGAGAGTTTGAAGAAGCC	180
QY	58	-----AsnProGlnThrSerLeuCysPhe	65
Db	181	TATATCCCAAGGAACAGAGTATTCATCTCTGACAGAACCCCAAGACTTCCCTCTGTTTC	240
QY	66	SerGlnSerIleProThrProSerAsnArgGlnGlnThrGlnGlnIlnYssSerAsnLeuGln	85
Db	241	TCGAAGCTTATTCGACACCCCTCCAAACAGGAGGAAGAACACAAAGAAATCCAACTTAGAG	300
QY	86	LeuLeuArgIleSerLeuLeuLeuIleGlnSerTyrLeuGlnProValGlnPheLeuArg	105
Db	301	CTGCTCCGCAATCTCCCTGCTGCTCATCTCCAGTCCGTGGCTGAGGCCGTGCAGTTCCCTCAGG	360
QY	106	SerValPheAlaAsnSerLeuValTyrGlnAlaSerAspSerAsnValTyrAspLeuLeu	125
Db	361	AGTGTCTTGGCCCAACAGCCCTGGGTGACGGGGCCCTGACAGAGACGCTTATGACCTCTCA	420
QY	126	LysAspLeuGlnGlnGlyIleGlnThrLeuMetGlyArgLeuGlnAspGlySerProArg	145
Db	421	AAGGACCTAGAGGAAGGACATCCAAAGCTGATGGGGAGGCTTGAAGATGGCAGCCCGGG	480
QY	146	ThrGlyGlnIlePheLeuGlnThrTyrSerIlyPheAspThrAsnSerHisAsnAspAsp	165
Db	481	ACTGGGCAGATCTTCACAGCAGACTTACAGCAAGTTGCACAAATCTCACACAGATGAC	540
QY	166	AlaLeuLeuLysAsnTyrGlyLeuLeuTyrCysPheArgLysAspMetAspLysValGln	185
Db	541	GACCTACTCAAGAACTACGGGCTGCTCTTACTGCTTCAGAGGAAGCATGACAAAGTGCAG	600
QY	186	ThrPheLeuArgIleValGlnCysArgSerValGlnGlySerCysGlyPhe	202
Db	601	ACATTCCTCGCATCGTCGATGCGCGCTCTGTGAGGGCAGCTGTGGCTTC	651
RESULT 11			
AAL46249			
ID AAL46249 standard; DNA; 769 BP.			
XX	AAL46249;		
XX			
DT	15-ADG-2002 (first entry)		
XX			
DE	Human growth hormone coding sequence SEQ ID NO: 29.		
XX			
OS	Homo sapiens.		
XX			
PN	MO200172119-A2.		
XX			
PD	04-OCT-2001.		
XX			
PF	02-APR-2001; 2001WO-EP003733.		
XX			
PR	31-MAR-2000; 2000DE-01016083.		
XX			
FA	(INGE-) INGENIUM PHARM AG.		
XX			
XX	Cornali E, Nehls MC, Schlueiter V, Wattler F, Wattler S, Wolf S;		

WPI: 2001-616425/71.  
P-PSDB: AAO17479.

New animal model expressing a modified growth hormone has reduced body weight and size and is useful to determine treatment for growth hormone, particularly IGF-1 related conditions and diseases.

Claim 13; Page 77; 93pp; English.

The present invention relates to a mouse model expressing a modified growth hormone and designated SWM1. The model is used to study diseases, test prospective treatments and identify early detection markers associated with abnormal growth hormone (GH) or IGF-1 activity, particularly dwarfism, Laron syndrome, illig-type deficiency, Kowarsky syndrome, pituitary gland deficiency, reduced bone mineral density, increased or insufficient body fat accumulation, diabetes, osteoporosis, glomerulosclerosis, gigantism, acromegaly, information processing and cognitive function defects, age-related memory and behaviour deficits, glucose metabolism disorders and cardiovascular disorders. The present invention is a coding sequence described in the exemplification of the

Sequence 769 BP; 167 A; 255 C; 188 G; 159 T; 0 U; 0 Other;

Alignment Scores:  
Pred. No.: 1.74e-107 Length: 769  
Score: 1024.50 Matches: 201  
Percent Similarity: 92.63% Conservative: 0  
Best Local Similarity: 92.63% Mismatches: 1  
Query Match: 97.85% Indels: 15  
DB: Gaps: 1

US-09-856-796B-2 (1-202) x AAL46249 (1-769)

1 MetAlaThrGlySerArgThrSerLeuLeuAlaPheGlyLeuLeuCysLeuProTIP 20  
56 ATGGCTACAGGCTCCGGACGTCCTGCTGCTTGGCTTGGCTGCTGCTGCTGCTG 115  
21 LeuGlnGluGlySerAlaPheProThrIleProLeuSerArgLeuPheAspAlaSer 40  
116 CTTCAAGAGGAGAGTCCCTTCCCAACATTCCTTATCCAGGCTTTTGAACAAGCTATG 175  
41 LeuArgAlaHisArgLeuHisGlnLeuAlaPheAspThrTyrGlnGluPhe----- 57  
176 CTCGGGGCCCATCGCTCGACCACTGGCCCTTGGACCTTACCAAGAGATTGAAAGAAC 235  
58 -----AspProGlnThrSerLeuCysPhe 65  
236 TATATCCCAAGAGACAGAAATTCATTCCTGACAAACCCCAAGCTCCTCTGTTTC 295  
66 SerGlnSerIleProThrProSerAsnArgGluGluThrGlnGlnIlySerAsnLeuGlu 85  
296 TCAGAGCTATATTCGACACCTCCACACGAGAGAAACAAAGAAATCCAAACCTAGAG 355  
86 LeuLeuArgGlyIleSerLeuLeuLeuIleGlnSerTyrLeuGluProValGlnPheLeuArg 105  
356 CTGCTCGGATCTCCCTGCTGCTCATCCAGTCGTGCTGAGACCCGTCAGATTCTCTAGG 415  
106 SerValPheAlaAsnSerLeuValTyrGlyAlaSerAspSerAsnValTyrAspLeuLeu 125  
416 AGTGCTTCCGCAACAGCTGCTGTAAGCGCTCTGACAGCAACGCTATATACCTCTTA 475  
126 LysAspLeuGluGluGlyIleGlnThrLeuMetGlyArgLeuGluLysAspIlySerProArg 145  
476 AAGGACCTAGAGAGAGGATCCAAACGCTGATGGAGAGGCTGAGAGATGAGACCCCGG 535  
146 ThrGlyGlnIlePheLeuGlnThrTyrSerIlyPheAspThrAsnSerHisAsnAspAsp 165  
536 ACTGGGAGATCTTCAACAGACCTTACAGACAGATTTCACAACTCACACAGATGAC 595  
166 AlaLeuLeuLysAsnTyrGlyLeuLeuTyrCysPheArgLysAspMetAspIlyValGlu 185  
596 GCACTACTCAAGAACTACGGGCTGCTCTACTGCTTCAAGAGAGCATGACAGAGCTGAG 655

OY 186 ThrPheLeuArgIleValGlnCysArgSerValGluGlySerCysGlyPhe 202  
DB 656 ACATTCTCGGCGCATCGTGAAGTGGCTCTGTGTGAGAGGACAGCTGTGGCTTC 706

RESULT 12  
AAO04700  
ID AAO04700 standard; DNA; 814 BP.

AC AAO04700;  
XX 25-MAR-2003 (revised)  
DT 10-OCT-1990 (first entry)  
XX

DE Sequence encoding human growth hormone (hGH) analogue.  
XX Human growth hormone; hGH; hypophyseal; dwarfism; insulin; ds.  
XX Homo sapiens.

OS Key Location/Qualifiers  
FH CDS 40..690  
FT /\*tag= a  
XX

PN MO9005185-A.

PD 17-MAY-1990.

XX 07-NOV-1988; 88FR-00014514.

PR 07-NOV-1988; 88FR-00014514.

XX (UYET-) UNIV ETAT LIEGE.  
PA (UYLI-) UNIV ETAT LIEGE.

PI Martial J, Lecomte C;

XX WPI: 1990-178826/23.

DR P-PSDB; AAR05169.

XX Modified human growth hormone - with N-terminal deletions to eliminate effects on sugar metabolism.

PT Disclosure; Page 7; -pp; French.

PS Proteins are useful in treating hypophyseal insufficiency, growth hormone deficiency, growth disorders obesity and the aging process whilst

CC avoiding associated side effects on the sugar metabolism. This is

CC especially useful in elderly or neonatal subjects. (Updated on 25-MAR-2003 to correct PA field.) (Updated on 25-MAR-2003 to correct PI field.)

CC 2003 to correct PA field.) (Updated on 25-MAR-2003 to correct PI field.)

XX Sequence 814 BP; 193 A; 259 C; 192 G; 170 T; 0 U; 0 Other;

Alignment Scores:

Pred. No.: 1.89e-107 Length: 814  
Score: 1024.50 Matches: 201  
Percent Similarity: 92.63% Conservative: 0  
Best Local Similarity: 92.63% Mismatches: 1  
Query Match: 97.85% Indels: 15  
DB: Gaps: 1

US-09-856-796B-2 (1-202) x AAO04700 (1-814)

OY 1 MetAlaThrGlySerArgThrSerLeuLeuAlaPheGlyLeuLeuCysLeuProTIP 20  
DB 40 ATGGCTACAGGCTCCGGACGTCCTGCTGCTTGGCTTGGCTGCTGCTGCTGCTG 99  
OY 21 LeuGlnGluGlySerAlaPheProThrIleProLeuSerArgLeuPheAspAlaSer 40  
DB 100 CTTCAAGAGGAGAGTCCCTTCCCAACATTCCTTATCCAGGCTTTTGAACAAGCTATG 159  
OY 41 LeuArgAlaHisArgLeuHisGlnLeuAlaPheAspThrTyrGlnGluPhe----- 57

Db 160 CTCGGGCCCCATGCTGCACACAGCTGCCTTTGACACCTACACAGAGTTTGAAGAGCC 219  
 QY 58 -----AspProGlnThrSerLeuCyPhe 65  
 Db 220 TATATCCCAAGAGACAGATATTCATTCTCCGACAAACCCCGACCTCCCTGTTTC 279  
 QY 66 SerGluSerIleProThrProSerAsnArgGluGlnThrGlnGlnLysSerAsnLeuGlu 85  
 Db 280 TCAGAGCTATTTCGACACCTTCACACAGGAGAGAAACACACAAATCCAACTCAGAG 339  
 QY 86 LeuLeuArgIleSerLeuLeuLeuIleGlnSerIlePheGluProValGlnPheLeuArg 105  
 Db 340 CTGCTCCGCATCTCCCTGCTCTCAATCCAGTGTGCTGAGCCCGTCAGTTCCTCAGG 399  
 QY 106 SerValPheAlaAsnSerLeuValTyrGlyAlaSerAspSerAsnValTyrAspLeuLeu 125  
 Db 400 AGTGTCTTCCGCAACAGCTGTGTACGGCCCTCTGACAGCAAGCTATACCTCCTTA 459  
 QY 126 LysAspLeuGluGluGlyIleGlnThrLeuMetGlyArgLeuGluAspGlySerProArg 145  
 Db 460 AAGGACCTAGAGAGAGCATCCAAACGCTGATGGGAGGCTGGAAGATGGAGCCCGCG 519  
 QY 146 ThrGlyGlnIlePheLeuGlnThrTyrSerIleAspPheAspThrAsnSerHisAsnAsp 165  
 Db 520 ACTGGGCGAGATCTTCAGACAGACCTACAGAGATTCCACAACTCACACAGATGAC 579  
 QY 166 AlaLeuLeuLysAsnTyrGlyLeuLeuTyrCysPheArgLysAspMetAspLysValGlu 185  
 Db 580 GCACCTACTCAAGAACTACGGGCTGCTCTACTGCTTCAGAGAGCATGACAGATGAG 639  
 QY 186 ThrPheLeuArgIleValGlnCysArgSerValGluGlySerCysGlyPhe 202  
 Db 640 ACATTCTCGCATCTGCGAGTGCCCTCTGTGAGAGGCGAGCTGTGCTTT 690  
 RESULT 13  
 AAV33629  
 ID AAV33629 standard; DNA; 5594 BP.  
 AC AAV33629;  
 XX  
 DT 29-DEC-1998 (first entry)  
 XX  
 DE GENSA 981, a monomeric DNA sequence produced by the invention.  
 XX  
 KW Class IIS restriction endonuclease recognition site;  
 KW hormone mouse promoter element; tissue-specific gene expression;  
 KW developmental-specific gene expression.  
 XX  
 OS Synthetic.  
 XX  
 PN MO9838326-A1.  
 XX  
 PD 03-SEP-1998.  
 XX  
 PF 28-FEB-1998; 98MO-US003918.  
 XX  
 PR 28-FEB-1997; 97US-0070910P.  
 XX  
 PA (NATU-) NATURE TECHNOLOGY CORP.  
 XX  
 PI Hodgson CP, Zink MA, Xu G;  
 XX  
 DR WPI; 1998-495399/42.  
 XX  
 PT Method for assembling gene or gene vector - comprises use of primers  
 XX containing class IIS restriction endonuclease recognition sites.  
 XX  
 PS Example 2; Page 107-110; 141pp; English.  
 CC  
 CC The invention provides a novel method for directing self-assembly of a  
 CC gene having three or more fragments in a directionally and spatially  
 CC ordered fashion to produce a gene or a gene vector. The method involves

CC usage of primers, containing class IIS restriction endonuclease  
 CC recognition sites, for isolation of these fragments. As described in the  
 CC disclosure, the method may also use a vector for the incorporation and  
 CC screening of endogenous mouse promoter elements for the identification of  
 CC cell specific promoters. In the example given, plasmids pK-CMV  
 CC (AAV33626), pVLM8 (AAV33623) and pVLOVGH-900 (AAV33621) were used as  
 CC templates from which six fragments were amplified. Each of the fragments  
 CC contained different regulatory sequences. The six PCR fragments were  
 CC designed to self-assemble into a retro-vector using the method of the  
 CC invention. The present sequence, designated as GENSA 981, represents the  
 CC monomeric DNA sequence of the six ligated fragments. In general, the  
 CC method is claimed to be useful for isolating and identifying regulatory  
 CC or tissue-specific, hormone-specific or developmental-specific gene  
 CC expression  
 SQ Sequence 5594 BP; 1232 A; 1519 C; 1518 G; 1325 T; 0 U; 0 Other;  
 Alignment Scores:  
 Pred. No.: 2,72e-106 Length: 5594  
 Score: 1024.50 Matches: 201  
 Percent Similarity: 92.63% Conservative: 0  
 Best Local Similarity: 92.63% Mismatches: 1  
 Query Match: 97.85% Indels: 15  
 DB: 2 Gaps: 1  
 US-09-856-796B-2 (1-202) x AAV33629 (1-5594)  
 QY 1 MetAlaThrGlySerArgThrSerLeuLeuAlaPheGlyLeuLeuCyLeuProTrp 20  
 Db 2270 ATGGCTTACAGGCTCCCGAGCTCCCTGCTCTGCTGCTTGGCTGCTCTGCTGCTG 2329  
 QY 21 LeuGlnGluGlySerAlaPheProThrIleProLeuSerArgLeuPheAsnAlaSer 40  
 Db 2330 CTTCAAGAGGCGAGTGCCTCCCAACCATTCCTTATCCAGCTTTTACAAACGCTTANG 2389  
 QY 41 LeuArgAlaHisArgLeuHisGlnLeuAlaPheAspThrTyrGlnGluPhe 57  
 Db 2390 CTCCGCGCCCATCGTCTGACACAGCTGGCTTTGACACTTACAGAGATTGAGAGAGCC 2449  
 QY 58 -----AspProGlnThrSerLeuCyPhe 65  
 Db 2450 TATATCCCAAGAGACAGATATTCATTCTCGCAAGACCCCGACCTCCCTGTTTC 2509  
 QY 66 SerGluSerIleProThrProSerAsnArgGluGlnThrGlnGlnLysSerAsnLeuGlu 85  
 Db 2510 TCAGAGCTATTTCGACACCTTCACACAGGAGAGAAACACAAATCCAACTCAGAG 2569  
 QY 86 LeuLeuArgIleSerLeuLeuLeuIleGlnSerIlePheGluProValGlnPheLeuArg 105  
 Db 2570 CTGCTCCGCATCTCCCTGCTCTCAATCCAGTGTGAGGCGCCGTCAGTTCCTCAGG 2629  
 QY 106 SerValPheAlaAsnSerLeuValTyrGlyAlaSerAspSerAsnValTyrAspLeuLeu 125  
 Db 2630 AGTGTCTTCCGCAACAGCTGTGTACGGGCGCTCTGACAGCAACGCTATGACCTCCTTA 2689  
 QY 126 LysAspLeuGluGluGlyIleGlnThrLeuMetGlyArgLeuGluAspGlySerProArg 145  
 Db 2690 AAGGACCTAGAGAGAGCATCCAAACGCTGATGGAGGCTGAGAAATGCGACCCCGG 2749  
 QY 146 ThrGlyGlnIlePheLeuGlnThrTyrSerIlePheAspThrAsnSerHisAsnAsp 165  
 Db 2750 ACTGGGCGAGATCTTCAGACAGACCTACAGCAAGTTGACACAACTCCACACAGTGCAG 2809  
 QY 166 AlaLeuLeuLysAsnTyrGlyLeuLeuTyrCysPheArgLysAspMetAspLysValGlu 185  
 Db 2810 GCACCTACTCAAGAACTACGGGCTGCTCTACTGCTTCAGGAGAGATGAGCAAGTGTGAG 2869  
 QY 186 ThrPheLeuArgIleValGlnCysArgSerValGluGlySerCysGlyPhe 202  
 Db 2870 ACATTCTCGCATCTGCGAGTGCCCTCTGTGAGAGGCGAGCTGTGCTTT 2920  
 RESULT 14





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GenCore version 5.1.6  
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OM protein - nucleic search, using frame\_plus\_p2n model

Run on: February 7, 2005, 12:30:50 ; Search time 4142 Seconds  
(without alignments)  
2363.098 Million cell updates/sec

Title: US-09-856-796b-2  
Perfect score: 1047  
Sequence: 1 MATGRTSLLAFLGLCPW.....KYETPLRIYQCRSVSGSGF 202

Scoring table: BLOSUM62  
Xgapop 10.0 , Xgapext 0.5  
Ygapop 10.0 , Ygapext 0.5  
Fgapop 6.0 , Fgapext 7.0  
Delop 6.0 , Delext 7.0

Searched: 4708233 seqs, 24227607955 residues  
Total number of hits satisfying chosen parameters: 9416466

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000  
Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

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-Q=/csg2.1/USPTO.spool.h/US09856796/runat.06022005.124442.2569/asp.query.fasta\_1.391  
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-OUTFMT=pcio -NORM=ext -HEAPSIZE=500 -MINLEN=0 -ALIGN=15 -MODE=LOCAL  
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-FGAPEXT=7 -XGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database :

GenEmbl:.\*  
1: gb\_ba.\*  
2: gb\_hgt.\*  
3: gb\_in.\*  
4: gb\_om.\*  
5: gb\_ov.\*  
6: gb\_pat.\*  
7: gb\_ph.\*  
8: gb\_pl.\*  
9: gb\_pr.\*  
10: gb\_ro.\*  
11: gb\_sts.\*  
12: gb\_sy.\*  
13: gb\_un.\*  
14: gb\_vl.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1047	100.0	609	BD270127	BD270127 NF-kappa
2	1047	100.0	609	AX025440	AX025440 Sequence
3	1047	100.0	3387	E00974	E00974 cDNA encodi
4	1042	99.5	777	EC062475	EC062475 Homo sapi

5	1029.5	98.3	654	6	AX300799	AX300799 Sequence
6	1029.5	98.3	807	6	AX149376	AX149376 Sequence
7	1029.5	98.3	807	6	AX149381	AX149381 Sequence
8	1029.5	98.3	3477	6	E00952	E00952 Plasmid DNA
9	1024.5	97.9	654	6	AX481369	AX481369 Sequence
10	1024.5	97.9	654	6	AX766683	AX766683 Sequence
11	1024.5	97.9	654	6	AX767319	AX767319 Sequence
12	1024.5	97.9	663	6	AR183901	AR183901 Sequence
13	1024.5	97.9	663	6	AX028861	AX028861 Sequence
14	1024.5	97.9	700	6	AI2770	AI2770 pre-hg gen
15	1024.5	97.9	725	9	BC075012	BC075012 Homo sapi
16	1024.5	97.9	725	9	BC075013	BC075013 Homo sapi
17	1024.5	97.9	725	9	AX262454	AX262454 Sequence
18	1024.5	97.9	769	6	A00469	A00469 H.sapiens m
19	1024.5	97.9	5594	6	AR214682	AR214682 Sequence
20	1024.5	97.9	7080	6	AR214674	AR214674 Sequence
21	1020.5	97.5	822	9	AY613431	AY613431 Homo sapi
22	1017.5	97.2	769	6	AX262456	AX262456 Sequence
23	1017.5	97.2	799	6	BD276310	BD276310 NOVEL NUC
24	1017.5	97.2	799	6	AR409781	AR409781 Sequence
25	1017.5	97.2	799	6	AX047457	AX047457 Sequence
26	1017.5	97.2	799	6	AX370182	AX370182 Sequence
27	1017.5	97.2	799	6	HSGROW1	V00519 Human messe
28	1016.5	97.1	651	6	AI5072	AI5072 H.sapiens g
29	1016.5	97.1	651	6	AI5074	AI5074 H.sapiens g
30	1016.5	97.1	651	6	E01424	E01424 DNA Sequence
31	1016.5	97.1	822	9	AY613432	AY613432 Homo sapi
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33	1013.5	96.8	11271	12	ECT7DN1	Z32691 Expression
34	1010.5	96.5	651	6	A03992	A03992 Synthetic g
35	1010.5	96.5	651	6	A03994	A03994 Synthetic g
36	1010.5	96.5	821	6	AX527631	AX527631 Sequence
37	1007.5	96.2	796	6	E00009	E00009 mRNA coding
38	989.5	94.5	812	6	AX149356	AX149356 Sequence
39	981.5	93.7	600	6	CO827137	CO827137 Sequence
40	976.5	93.3	600	6	CO827155	CO827155 Sequence
41	976.5	93.3	677	9	AF006060	AF006060 Homo sapi
42	957	91.4	808	6	AX149358	AX149358 Sequence
43	945.5	90.2	654	9	CR541902	CR541902 Homo sapi
44	945.5	90.2	609	6	AX659150	AX659150 Sequence
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ALIGNMENTS

RESULT 1	BD270127	609 bp	DNA	linear	PAT 17-JUL-2003
LOCUS	BD270127				
DEFINITION	NF-kappa B activation inhibitors and their uses as drug.				
ACCESSION	BD270127				
VERSION	BD270127.1 GI:33079895				
KEYWORDS	JP 2002537224-A/1.				
SOURCE	JP 2002537224-A/1.				
ORGANISM	unclassified.				
REFERENCE	1 (bases 1 to 609)				
AUTHORS	Hirsch, F. and Haeflner, A.				
TITLE	NF-kappa B activation inhibitors and their uses as drug				
JOURNAL	Patent: JP 2002537224-A 1 05-NOV-2002;				
COMMENT	CENTRE NATIONAL DE LA RECHERCHE SCIENTIFIQUE				
OS	Unidentified				
PN	JP 2002537224-A/1				
PD	05-NOV-2002				
PF	24-NOV-1999 JP 2000583472				
PR	25-NOV-1998 FR 98/14858				
PI	FRANCOIS HIRSCH,ASTRID HAEFFNER				
PC	AG1445/00,AG1K31/337,AG1K31/475,AG1K31/65,AG1K38/00,AG1K45/06,				
PC	AG1935/00//				
PC	CO7K14/505,CO7K14/52,CO7K14/61,C12N15/09,AG1K37/02,C12N15/00				
CC	Strandedness: Double;				
CC	Topology: Linear;				
CC	NF-kappa B activation inhibitors and their uses as drug FH				
Key	Location/Qualifiers				

FEATURES  
source  
FT CDS Location/Qualifiers  
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ALIGNMENT SCORES:

Alignment Scores: 1.3e-103 Length: 609  
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Score: 100.00% Conservative: 0  
Percent Similarity: 100.00% Mismatches: 0  
Best Local Similarity: 100.00% Indels: 0  
Query Match: 100.00% Gaps: 0  
DB: 6

US-09-856-796B-2 (1-202) x BD270127 (1-609)

QY 1 MetAlaThrGlySerArgThrSerLeuLeuAlaPheGlyLeuLeuCysLeuProTTP 20  
1 ATGGCTACAGAGCTCCCGACGCTCTGCTCTGCTTTGGCTTGCCTGCTGCTGCTGCTG 60  
QY 21 LeuGlnGluGlySerAlaPheProThrIleProLeuSerArgLeuPheAspAsnAlaSer 40  
61 CTTCAGAGGCGAGTGCCTTCCACACATTCCTTATCCAGGCTTTTGACACACCTTACT 120  
DB 41 LeuArgAlaHisArgLeuHisGlnLeuAlaPheAspThrTyrGlnGluPheAsnProGln 60  
121 CTCGGCGCCCATCTCTGACACAGCTGCGCTTGACACTTACAGAGTTTAAACCCCGAG 180  
QY 61 ThrSerLeuCysPheSerGluSerIleProThrProSerAsnArgGluGlnThrGlnGln 80  
181 ACCTCCCTCTGTTCTCAGAGTCTATTCGACACCTCCACAGGAGGAAACACACAG 240  
DB 81 LysSerAsnLeuGluLeuLeuArgIleSerLeuLeuLeuIleGlnSerTrpLeuGluPro 100  
241 AAATCCAACTTAGAGTGTCTGCGCATCTCCGCTCTCATCCAGTCGTGGTGGAGCCC 300  
QY 101 ValGlnPheLeuArgSerValPheAlaAsnSerLeuValTyrGlyAlaSerAspSerAsn 120  
301 GTGCGATTCCTCAGAGTGTCTTCCGACACGCTGCTGTAAGGCGCTCTGACAGCAAC 360  
DB 121 ValTyrAspLeuLeuLysAspLeuGluGluGlyIleGlnThrLeuMetGlyArgLeuGlu 140  
361 GTCATGACCTCTTAAGACCTAGAGGAGGATCCAAAGCTGAGAGGAGGCTGAA 420  
QY 141 AspGlySerProArgThrGlyGlnIlePheLeuGlnThrTyrSerIysPheAspThrAsn 160  
421 GATGCGAGCCCCCGAGCTGGGAGATCTTCAGACGACCTTACAGCAAGTTGACACAAAC 480  
DB 161 SerHisAsnAspAspAlaLeuLeuLysAsnTyrGlyLeuLeuTyrCysPheArgLysAsp 180  
481 TCACACAAAGATGACGACCTACTCAGAACTACGAGGCTGCTCTTCTTACAGAAAGAC 540  
QY 181 MetAspLysValGlnThrPheLeuArgIleValGlnCysArgSerValGluGlySerCys 200  
541 ATGGACAAGGTTCAGACATTCCTGCGCATCTGCGAGTGCAGTCCGCTGTGAGAGGCGAGTGT 600  
DB 201 GlyPhe 202  
601 GGCTTC 606

RESULT 2  
AX025440 609 bp DNA linear PART 16-SEP-2000  
DEFINITION  
Sequence 1 from Patent FR2786104.  
ACCESSION  
AX025440.1 GI:10187116  
VERSION  
KEYWORDS  
SOURCE  
ORGANISM  
Homo sapiens (human)  
Homo sapiens; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

REFERENCE  
AUTHORS  
JOURNAL  
CENTRE NAT RECH SCIENT (FR)  
FEATURES  
source  
Location/Qualifiers  
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CDS

Alignment Scores: 1.3e-103 Length: 609  
Pred. No.: 1047.00 Matches: 202  
Score: 100.00% Conservative: 0  
Percent Similarity: 100.00% Mismatches: 0  
Best Local Similarity: 100.00% Indels: 0  
Query Match: 100.00% Gaps: 0  
DB: 6

US-09-856-796B-2 (1-202) x AX025440 (1-609)

ALIGNMENT SCORES:

Alignment Scores: 1.3e-103 Length: 609  
Pred. No.: 1047.00 Matches: 202  
Score: 100.00% Conservative: 0  
Percent Similarity: 100.00% Mismatches: 0  
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Query Match: 100.00% Gaps: 0  
DB: 6

US-09-856-796B-2 (1-202) x AX025440 (1-609)

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1 ATGGCTACAGAGCTCCCGACGCTCTGCTCTGCTTTGGCTTGCCTGCTGCTGCTGCTG 60  
DB 21 LeuGlnGluGlySerAlaPheProThrIleProLeuSerArgLeuPheAspAsnAlaSer 40  
61 CTTCAGAGGCGAGTGCCTTCCACACATTCCTTATCCAGGCTTTTGACACACCTTACT 120  
QY 41 LeuArgAlaHisArgLeuHisGlnLeuAlaPheAspThrTyrGlnGluPheAsnProGln 60  
121 CTCGGCGCCCATCTCTGACACAGCTGCGCTTGACACTTACAGAGTTTAAACCCCGAG 180  
DB 61 ThrSerLeuCysPheSerGluSerIleProThrProSerAsnArgGluGlnThrGlnGln 80  
181 ACCTCCCTCTGTTCTCAGAGTCTATTCGACACCTTCCACAGGAGGAAACACACAG 240  
QY 81 LysSerAsnLeuGluLeuLeuArgIleSerLeuLeuLeuIleGlnSerTrpLeuGluPro 100  
241 AAATCCAACTTAGAGTGTCTGCGCATCTCCGCTCTCATCCAGTCGTGGTGGAGCCC 300  
DB 101 ValGlnPheLeuArgSerValPheAlaAsnSerLeuValTyrGlyAlaSerAspSerAsn 120  
301 GTGCGATTCCTCAGAGTGTCTTCCGACACGCTGCTGTAAGGCGCTCTGACAGCAAC 360  
QY 121 ValTyrAspLeuLeuLysAspLeuGluGluGlyIleGlnThrLeuMetGlyArgLeuGlu 140  
361 GTCATGACCTCTTAAGACCTAGAGGAGGATCCAAAGCTGAGAGGAGGCTGAA 420  
DB 141 AspGlySerProArgThrGlyGlnIlePheLeuGlnThrTyrSerIysPheAspThrAsn 160  
421 GATGCGAGCCCCCGAGCTGGGAGATCTTCAGACGACCTTACAGCAAGTTGACACAAAC 480  
QY 161 SerHisAsnAspAspAlaLeuLeuLysAsnTyrGlyLeuLeuTyrCysPheArgLysAsp 180  
481 TCACACAAAGATGACGACCTACTCAGAACTACGAGGCTGCTCTTCTTACAGAAAGAC 540  
DB 181 MetAspLysValGlnThrPheLeuArgIleValGlnCysArgSerValGluGlySerCys 200  
541 ATGGACAAGGTTCAGACATTCCTGCGCATCTGCGAGTGCAGTCCGCTGTGAGAGGCGAGTGT 600  
QY 201 GlyPhe 202  
601 GGCTTC 606





QY 86 LeuLeuArgIleSerIleuLeuIleGlnSerTTPLeuGlnProValGlnPheLeuArg 105  
 DB 301 CTGCTCCGATCTCCCTGCTGCTCATCCAGTGTGTGAGCCCGTGCAGTTCTCTCAGG 360  
 QY 106 SerValPheAlaAsnSerIleuValTyrGlyAlaSerAspSerAsnValTyrAspLeu 125  
 DB 361 AGTGCTTCGGCAACAGCCTGTGTACGGCGCTCTGACAGCAAGCTCATGACCTCTTA 420  
 QY 126 LysAspLeuGlnGlyIleGlnThrLeuMetGlyArgLeuGlnAspGlySerProArg 145  
 DB 421 AAGACCTAGAGAAAGGACATCCAAACGCTGATGGGAGCGCTGAAAGATGGAGCCCGG 480  
 QY 146 ThrGlyGlnIlePheIlePheIleThrTyrSerIlePheAspThrAsnSerHisAsnAspAsp 165  
 DB 481 ACTGGGAGATCTTCAAGACAGCCTACAGCAAGTTCCAGCAAACTCACAACAGATGAC 540  
 QY 166 AlaLeuLeuLysAsnTyrGlyLeuLeuTyrCysPheArgIleAspMetAspIleValGlu 185  
 DB 541 GCACACTCAAGAACTACGGGCTGCTCTACTGCTTTCAGAAAGCATGACAAAGTGTGAG 600  
 QY 186 ThrPheLeuArgIleValGlnCysArgSerValGlnGlySerCysGlyPhe 202  
 DB 601 ACATTCCTGGCATCGTCAGTCCGCTGTGTGAGGGGAGCTGTGTGCTTC 651  
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 AXI49376 807 bp DNA linear PAT 08-JUN-2001  
 LOCUS AXI49376  
 DEFINITION Sequence 25 from Patent WO0136635.  
 AXI49376  
 VERSION AXI49376.1 GI:14347892  
 KEYWORDS  
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 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.  
 REFERENCE 1 Majumder, K., Prayaga, S. K. and Burgess, C.  
 Neutrite outgrowth-promoting factor homologue and nucleic acids  
 encoding same  
 Patent: WO 0136635-A 25 25-MAY-2001;  
 Curagen Corporation (US)  
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 QY 41 LeuAlaGlnIleArgLeuHisGlnLeuAlaPheAspThrTyrGlnGlnPhe----- 57  
 DB 171 CTCGCGCCCATGCTGTGACACAGGCTGCTTGACACTTACAGAGATTAAAGAAAGCC 230  
 QY 58 -----AsnProGlnThrSerLeuCysPhe 65  
 DB 231 TATATCCAAAGAAAGAGATATTCAATCTGACAGAACCCCAACCTCCCTCTGTTTC 290

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 QY 86 LeuLeuArgIleSerIleuLeuIleGlnSerTTPLeuGlnProValGlnPheLeuArg 105  
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 QY 126 LysAspLeuGlnGlyIleGlnThrLeuMetGlyArgLeuGlnAspGlySerProArg 145  
 DB 471 AAGACCTAGAGAAAGGACATCCAAACGCTGATGGGAGCGCTGAAAGATGGCAGCCCGG 530  
 QY 146 ThrGlyGlnIlePheIlePheIleThrTyrSerIlePheAspThrAsnSerHisAsnAspAsp 165  
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 QY 186 ThrPheLeuArgIleValGlnCysArgSerValGlnGlySerCysGlyPhe 202  
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 AXI49381 807 bp DNA linear PAT 08-JUN-2001  
 LOCUS AXI49381  
 DEFINITION Sequence 30 from Patent WO0136635.  
 AXI49381  
 VERSION AXI49381.1 GI:14347893  
 KEYWORDS  
 SOURCE Homo sapiens (human)  
 ORGANISM Homo sapiens  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
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 REFERENCE 1 Majumder, K., Prayaga, S. K. and Burgess, C.  
 Neutrite outgrowth-promoting factor homologue and nucleic acids  
 encoding same  
 Patent: WO 0136635-A 30 25-MAY-2001;  
 Curagen Corporation (US)  
 JOURNAL Location/Qualifiers  
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 Score: 1029.50 Matches: 202  
 Percent Similarity: 93.09% Conservative: 0  
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66 SerGluSerIleProThrProSerAsnArgIleGluIleThrGlnIleGlnIleSerAsnLeuGlu 85  
291 TCAGAGCTTATTCGACACCTCTCCACAGAGAGAGAACACACAGAAATCCAACTTAGAG 350  
86 LeuLeuArgIleSerLeuLeuLeuIleGlnSerIleProGluIleProValGlnIleLeuArg 105  
351 CTGCTCCGATCTCCCTGCTGCTCATCTGAGTCCGTCGTCGAGCCCGGCGAGTTCTTAGG 410  
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471 AAGGACCTTAGAGAGAGAGCTACCAACGCTGATGGGAGGCTGGAAGAGTGGCAGCCCGG 530  
146 ThrGlyGlnIlePheLeuGlnThrIleTyrSerIleAspPheThrAsnSerIleAsnAspAsp 165  
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RESULT 8  
LOCUS E00952 3477 bp DNA linear PAT 29-SEP-1997  
DEFINITION Plasmid DNA for amplifying human growth factor gene in E.coli.  
ACCESSION E00952  
VERSION E00952.1 GI:2169213  
KEYWORDS JP 1986202689-A/1.  
SOURCE synthetic construct  
ORGANISM other sequences; artificial sequences.  
REFERENCE 1 (bases 1 to 3477)  
AUTHORS Nakajima, K. and Nagai, J.  
TITLE RECOMBINANT PLASMID OF ESCHERICHIA COLI FOR AMPLIFICATION OF HUMAN GROWTH HORMONE COMPLEMENTARY STRAND DNA  
JOURNAL Patent: JP 1986202689-A 1 08-SEP-1986;  
NAKAJIMA KUNIO  
COMMENT OS Artificial gene  
OC Artificial sequence; Genes.  
PN JP 1986202689-A/1  
PD 08-SEP-1986  
PF 04-MAR-1985 JP 1985042404  
PI NAKAJIMA KUNIO, NAGAI JUN  
PC C12N15/00//C12P21/02;  
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CC topology: linear;  
CC hypothetical: No;  
CC anti-sense: No;  
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ORIGIN

Alignment Scores:  
Pred. No.: 9,57e-101 Length: 3477  
Score: 1029.50 Matches: 202  
Percent Similarity: 93.09% Conservative: 0  
Best Local Similarity: 93.09% Mismatches: 0  
Query Match: 98.33% Indels: 15  
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US-09-856-796b-2 (1-202) x E00952 (1-3477)

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RESULT 9  
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DEFINITION Sequence 3 from Patent WO02055532.  
ACCESSION AX481369  
VERSION AX481369.1 GI:22316286  
KEYWORDS  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Homindae; Homo.  
REFERENCE 1  
AUTHORS Andersen, K.V., Drustup, J. and Christiansen, J.  
TITLE Improved growth hormone molecules  
JOURNAL Patent: WO 02055532-A 3 18-JUL-2002;  
Maxygen Ape (DK); Maxygen Holdings Ltd. (KV)  
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ORIGIN

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VERSION	AX6767319.1	GI:32260801	
KEYWORDS			
SOURCE	Homo sapiens (human)		
ORGANISM	Homo sapiens		





LOCUS	AX028861	663 bp	DNA	linear	PAT 16-SEP-2000
DEFINITION	Sequence 2 from Patent EP0952158.				
ACCESSION	AX028861				
VERSION	AX028861.1	GI:10189957			
KEYWORDS					
SOURCE					
ORGANISM	synthetic construct				
	synthetic construct				
	other sequences; artificial sequences.				
REFERENCE	1				
AUTHORS	Viader,S.J., Barrera,S.H. and Guerrero,O.M.				
TITLE	Modified methylotrophic p. Pastoris yeast which secretes human groch hormone				
JOURNAL	Patent: EP 0952158-A 2 27-OCT-1999;				
	UNIV AUTONOMA DE NUEVO LEON (MX)				
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ACCESSION MGC.  
VERSION Homo sapiens (human)  
KEYWORDS Homo sapiens  
SOURCE Homo sapiens  
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Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

REFERENCE 1 (bases 1 to 725)  
AUTHORS Strausberg, R.L., Feingold, E.A., Grouse, L.H., Derge, J.G.,  
Klausner, R.D., Collins, F.S., Wagner, K.H., Shenmen, C.M., Schuler, G.D.,  
Altschul, S.F., Zeeberg, B., Buetow, K.H., Schaefer, C.F., Bat, N.K.,  
Hopkins, R.F., Jordan, H., Moore, T., Max, S.I., Wang, J., Hsieh, F.,  
Diachenko, L., Marusina, K., Farmer, A.A., Rubin, G.M., Hong, L.,  
Scapleton, M., Soares, M.B., Bonaldo, M.F., Casavant, T.L.,  
Schaefer, T.E., Brownstein, M.J., Ustin, T.B., Toshiyuki, S.,  
Carninci, P., Prange, C., Raha, S., Loquellano, N.A., Peters, G.J.,  
Abramson, R.D., Mallory, S.J., Bosak, S.A., McMan, P.J.,  
McKernan, K.J., Malek, J.A., Gunaratne, P.H., Richards, S.,  
Worley, K.C., Hale, S., Garcia, A.M., Gay, L.J., Hult, S.W.,  
Villalón, D.K., Muzny, D.M., Sodergren, E.J., Lu, X., Gibbs, R.A.,  
Fahey, J., Helton, E., Kettelman, M., Madan, A., Young, A.C., Shevchenko, Y.,  
Sanchez, A., Whiting, M., Madan, A., Touchman, J.W., Green, E.D.,  
Bouffard, G.G., Blakeley, R.W., Touchman, J.W., Schmutz, J., Myers, R.M.,  
Dickson, M.C., Rodriguez, A.C., Grimwood, J., Schmutz, J., Myers, R.M.,  
Butterfield, Y.S., Krzywinski, M.I., Skalska, U., Smallus, D.E.,  
Schnerch, A., Schein, J.E., Jones, S.J., and Marra, M.A.  
Generation and initial analysis of more than 15,000 full-length  
human and mouse cDNA sequences  
Proc. Natl. Acad. Sci. U.S.A. 99 (26), 16899-16903 (2002)  
12477932  
2 (bases 1 to 725)  
DIRECTOR MGC Project.  
TITLE Direct Submission  
AUTHORS Submitted (25-JUN-2004) National Institutes of Health, Mammalian  
JOURNAL Gene Collection (MGC), Cancer Genomics Office, National Cancer  
Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,  
USA  
REMARK NIH-MGC Project URL: <http://mgc.ncl.nih.gov>  
COMMENT On Aug 4, 2004 this sequence version replaced gi:49901773.  
Contact: MGC help desk  
Tissue: Procurement: Genome Sequence Centre, British Columbia Cancer  
Center  
Email: [cgabs-remail.nih.gov](mailto:cgabs-remail.nih.gov)  
CDNA Library Preparation: British Columbia Cancer Research Center  
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)  
DNA Sequencing by: Genome Sequence Centre,  
BC Cancer Agency, Vancouver, BC, Canada

info@bcgsc.bc.ca  
Steve Jones, Sarah Barber, Mabel Brown-John, Yaron Butterfield,  
Andy Chan, Steve S. Chand, William Chow, Allison Cloutier, Ruth  
Featherstone, Malachi Griffith, Ohi Griffith, Ran Gull, Nancy Liao,  
Kim MacDonald, Amara Maasson, Mike R. Mayo, Josh Moran, Ryan Morin,  
Teika Olson, Diana Palmquist, Anca Petrescu, Anna Lissa Prabhu,  
Paraneh Saeedi, JR Santos, Angelique Schnerch, Ursula Skalska,  
Duane Smallus, Jeff Stott, Miranda Tsai, George Yang, Jacque  
Schein, Asim Siddiqui, Rob Holt, Marco Marra.  
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through the I.M.A.G.E. Consortium/LNL at: <http://image.lnl.gov>  
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Pred. No.: 4,39e-101 Length: 725  
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Best Local Similarity: 92.63% Mismatches: 15  
Query Match: 97.85% Indels: 1  
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88 CTTCAAGAGGAGAGGCTCTCCCAACATTCCTTATCAGAGCTTTTGACAAAGCTATG 147  
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GenCore version 5.1.6  
Copyright (c) 1993 - 2005 Compugen Ltd.

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Searched: 1373511 seqs, 325702437 residues

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  - 3: /cgnt\_6/ptodata/2/pubpaa/US06\_NEW\_PUB.pep.\*
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  - 8: /cgnt\_6/ptodata/2/pubpaa/US08\_NEW\_PUB.pep.\*
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  - 17: /cgnt\_6/ptodata/2/pubpaa/US10D\_PUBCOMB.pep.\*
  - 18: /cgnt\_6/ptodata/2/pubpaa/US11\_NEW\_PUB.pep.\*
  - 19: /cgnt\_6/ptodata/2/pubpaa/US11\_NEW\_PUB.pep.\*
  - 20: /cgnt\_6/ptodata/2/pubpaa/US60\_NEW\_PUBCOMB.pep.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1029.5	98.3	217	9	US-09-853-688-2
2	1029.5	98.3	217	9	US-09-853-688-2
3	1029.5	98.3	217	10	US-09-853-688-4
4	1029.5	98.3	217	16	US-10-788-318-2
5	1029.5	98.3	217	16	US-10-788-318-4
6	1024.5	97.9	217	9	US-09-929-918-9
7	1017.5	97.2	217	9	US-09-804-409A-16
8	1017.5	97.2	217	15	US-10-411-037-48
9	1017.5	97.2	217	15	US-10-411-026-48
10	1017.5	97.2	217	15	US-10-410-962-48
11	1017.5	97.2	217	15	US-10-411-049-48
12	1017.5	97.2	217	16	US-10-410-930-48
13	1017.5	97.2	217	16	US-10-410-997-48

14	1017.5	97.2	217	16	US-10-411-012-48	Sequence 48, Appl
15	1017.5	97.2	217	16	US-10-287-994-48	Sequence 48, Appl
16	1017.5	97.2	217	16	US-10-410-913-48	Sequence 48, Appl
17	1016.5	97.1	217	16	US-10-477-651-2	Sequence 2, Appl
18	1010.5	96.5	232	16	US-10-477-651-3	Sequence 3, Appl
19	898.5	85.8	197	15	US-10-621-693-47	Sequence 47, Appl
20	898.5	85.8	198	15	US-10-621-693-45	Sequence 45, Appl
21	898.5	85.8	391	15	US-10-621-693-51	Sequence 51, Appl
22	898.5	85.8	396	15	US-10-621-693-49	Sequence 49, Appl
23	898.5	85.8	412	15	US-10-621-693-74	Sequence 74, Appl
24	898.5	85.8	589	15	US-10-621-693-53	Sequence 53, Appl
25	898.5	85.8	786	15	US-10-621-693-55	Sequence 55, Appl
26	898.5	85.6	810	15	US-10-621-693-76	Sequence 76, Appl
27	896.5	85.6	313	15	US-10-311-473-5	Sequence 16, Appl
28	896.5	85.6	338	15	US-10-311-473-16	Sequence 5, Appl
29	895.5	85.5	214	14	US-10-153-207-6	Sequence 37, Appl
30	895.5	85.5	384	15	US-10-621-693-37	Sequence 37, Appl
31	895.5	85.5	574	15	US-10-621-693-32	Sequence 32, Appl
32	895.5	85.5	576	15	US-10-621-693-39	Sequence 39, Appl
33	892.5	85.2	192	15	US-10-621-693-66	Sequence 66, Appl
34	892.5	85.2	192	15	US-10-621-693-68	Sequence 68, Appl
35	892.5	85.2	206	15	US-10-621-693-70	Sequence 70, Appl
36	891.5	85.1	191	14	US-10-153-207-1	Sequence 1, Appl
37	891.5	85.1	191	14	US-10-400-377-1	Sequence 1, Appl
38	891.5	85.1	191	14	US-10-298-148-1	Sequence 1, Appl
39	891.5	85.1	191	14	US-10-646-798-2	Sequence 2, Appl
40	891.5	85.1	191	15	US-10-621-693-80	Sequence 80, Appl
41	891.5	85.1	191	15	US-10-621-693-82	Sequence 82, Appl
42	891.5	85.1	191	15	US-10-621-693-84	Sequence 84, Appl
43	891.5	85.1	191	15	US-10-773-939-1	Sequence 1, Appl
44	891.5	85.1	191	16		
45	891.5	85.1	191	16		

ALIGNMENTS

RESULT 1  
US-09-853-688-2  
; Sequence 2, Application US/09853688  
; Patent No. US20020081605A1  
; GENERAL INFORMATION:  
; APPLICANT: COOPER, DAVID N.  
; APPLICANT: PROCTER, ANNIE M.  
; APPLICANT: GREGORY, JOHN  
; APPLICANT: MILLAR, DAVID S.  
; TITLE OF INVENTION: METHOD FOR DETECTING GROWTH HORMONE VARIATIONS IN  
; FILE REFERENCE: WCM78  
; CURRENT APPLICATION NUMBER: US/09/853.688  
; CURRENT FILING DATE: 2001-05-14  
; NUMBER OF SEQ ID NOS: 66  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 2  
; LENGTH: 217  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-09-853-688-2

Query Match 98.3%; Score 1029.5; DB 9; Length 217;  
Best Local Similarity 93.1%; Pred. No. 1.1e-93;  
Matches 202; Conservative 0; Mismatches 0; Indels 15; Gaps 1;

QY 1 MATGRTSLILAFGLICLPWIOEGSAFPTIPSRLLFDNNSLRARHRLHOLAFPTQCF--- 57  
DB 1 MATGRTSLILAFGLICLPWIOEGSAFPTIPSRLLFDNNSLRARHRLHOLAFPTQCFEERA 60  
QY 58 -----NPTSLCFSESITPTPSNREHTQKSNLELRISLILIQSWLEBPVQFLR 105  
DB 61 YIPKQKYSFLONPOTSLCFSESITPTPSNREHTQKSNLELRISLILIQSWLEBPVQFLR 120  
QY 106 SVFANSLYGASDSNVVLLDLDEGIOTLWGRLEDGSPRTGQIFKQYKSTNTSHND 165

Db 121 SVFANSLVYGASDSNVYDLKDLKEBGIQTLMGRLDGSPTGQIFKQYTSKFDNTHND 180  
QY 166 ALKNYGLLYCPRKMDKXETFLRIYQCRSVESGCGF 202  
Db 181 ALKNYGLLYCPRKMDKXETFLRIYQCRSVESGCGF 217

RESULT 2  
US-09-853-688-4  
Sequence 4, Application US/09853688  
Patent No. US20020081605A1  
GENERAL INFORMATION:  
APPLICANT: COOPER, DAVID N.  
APPLICANT: PROCTER, ANNIE M.  
APPLICANT: GREGORY, JOHN  
APPLICANT: MILLAR, DAVID S.  
TITLE OF INVENTION: METHOD FOR DETECTING GROWTH HORMONE VARIATIONS IN  
FILE REFERENCE: WCM78  
CURRENT APPLICATION NUMBER: US/09/853,688  
CURRENT FILING DATE: 2001-05-14  
NUMBER OF SEQ ID NOS: 66  
SOFTWARE: PatentIn Ver. 2.1  
SEQ ID NO 4  
LENGTH: 217  
TYPE: PRT  
ORGANISM: Homo sapiens  
US-09-853-688-4

Query Match 98.3%; Score 1029.5; DB 9; Length 217;  
Best Local Similarity 93.1%; Pred. No. 1.1e-93;  
Matches 202; Conservative 0; Mismatches 0; Indels 15; Gaps 1;  
QY 1 MATGSRISLLAFGLCLPWLQEGSAFPTIPLSRLFDNASLRARHLQALADTYQEF--- 57  
Db 1 MATGSRISLLAFGLCLPWLQEGSAFPTIPLSRLFDNASLRARHLQALADTYQEFGEA 60  
QY 58 -----NPQTSLCFSESIPTPSNREBTOQKSNLELRISLLIQLSWLEPVQFLR 105  
Db 61 YIPKQKYSFLQNPQTSLCFSESIPTPSNREBTOQKSNLELRISLLIQLSWLEPVQFLR 120  
QY 106 SVFANSLVYGASDSNVYDLKDLKEBGIQTLMGRLDGSPTGQIFKQYTSKFDNTHND 165  
Db 121 SVFANSLVYGASDSNVYDLKDLKEBGIQTLMGRLDGSPTGQIFKQYTSKFDNTHND 180  
QY 166 ALKNYGLLYCPRKMDKXETFLRIYQCRSVESGCGF 202  
Db 181 ALKNYGLLYCPRKMDKXETFLRIYQCRSVESGCGF 217

RESULT 3  
US-09-969-748C-4  
Sequence 4, Application US/09969748C  
Publication No. US20030161809A1  
GENERAL INFORMATION:  
APPLICANT: ARIZKEB PHARMACEUTICALS, INC.  
APPLICANT: HOUSTON, Lou, L.  
APPLICANT: SHERIDAN, Philip, J.  
APPLICANT: HAWLEY, Stephen  
APPLICANT: GLYNN, Jacqueline, M.  
APPLICANT: CHAPIN, Steven  
APPLICANT: BASU, Amarendra  
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE TRANSPORT OF BIOLOGICALLY ACTIVE  
FILE REFERENCE: 057220-0303  
CURRENT APPLICATION NUMBER: US/09/969,748C  
CURRENT FILING DATE: 2002-12-10  
PRIOR APPLICATION NUMBER: US 60/267,601  
PRIOR FILING DATE: 2001-02-09  
PRIOR APPLICATION NUMBER: US 60/248,819  
PRIOR FILING DATE: 2000-11-14  
PRIOR APPLICATION NUMBER: US 60/248,478  
PRIOR FILING DATE: 2000-11-13

PRIOR APPLICATION NUMBER: US 60/237,929  
PRIOR FILING DATE: 2000-10-02  
NUMBER OF SEQ ID NOS: 115  
SOFTWARE: PatentIn version 3.0  
SEQ ID NO 4  
LENGTH: 217  
TYPE: PRT  
ORGANISM: Homo sapiens  
US-09-969-748C-4

Query Match 98.3%; Score 1029.5; DB 10; Length 217;  
Best Local Similarity 93.1%; Pred. No. 1.1e-93;  
Matches 202; Conservative 0; Mismatches 0; Indels 15; Gaps 1;  
QY 1 MATGSRISLLAFGLCLPWLQEGSAFPTIPLSRLFDNASLRARHLQALADTYQEF--- 57  
Db 1 MATGSRISLLAFGLCLPWLQEGSAFPTIPLSRLFDNASLRARHLQALADTYQEFGEA 60  
QY 58 -----NPQTSLCFSESIPTPSNREBTOQKSNLELRISLLIQLSWLEPVQFLR 105  
Db 61 YIPKQKYSFLQNPQTSLCFSESIPTPSNREBTOQKSNLELRISLLIQLSWLEPVQFLR 120  
QY 106 SVFANSLVYGASDSNVYDLKDLKEBGIQTLMGRLDGSPTGQIFKQYTSKFDNTHND 165  
Db 121 SVFANSLVYGASDSNVYDLKDLKEBGIQTLMGRLDGSPTGQIFKQYTSKFDNTHND 180  
QY 166 ALKNYGLLYCPRKMDKXETFLRIYQCRSVESGCGF 202  
Db 181 ALKNYGLLYCPRKMDKXETFLRIYQCRSVESGCGF 217

RESULT 4  
US-10-788-318-2  
Sequence 2, Application US/10788318  
Publication No. US20040137510A1  
GENERAL INFORMATION:  
APPLICANT: COOPER, DAVID N.  
APPLICANT: PROCTER, ANNIE M.  
APPLICANT: GREGORY, JOHN  
APPLICANT: MILLAR, DAVID S.  
TITLE OF INVENTION: METHOD FOR DETECTING GROWTH HORMONE VARIATIONS IN  
FILE REFERENCE: WCM78  
CURRENT APPLICATION NUMBER: US/10/788,318  
CURRENT FILING DATE: 2004-03-01  
NUMBER OF SEQ ID NOS: 66  
SOFTWARE: PatentIn Ver. 2.1  
SEQ ID NO 2  
LENGTH: 217  
TYPE: PRT  
ORGANISM: Homo sapiens  
US-10-788-318-2

Query Match 98.3%; Score 1029.5; DB 16; Length 217;  
Best Local Similarity 93.1%; Pred. No. 1.1e-93;  
Matches 202; Conservative 0; Mismatches 0; Indels 15; Gaps 1;  
QY 1 MATGSRISLLAFGLCLPWLQEGSAFPTIPLSRLFDNASLRARHLQALADTYQEF--- 57  
Db 1 MATGSRISLLAFGLCLPWLQEGSAFPTIPLSRLFDNASLRARHLQALADTYQEFGEA 60  
QY 58 -----NPQTSLCFSESIPTPSNREBTOQKSNLELRISLLIQLSWLEPVQFLR 105  
Db 61 YIPKQKYSFLQNPQTSLCFSESIPTPSNREBTOQKSNLELRISLLIQLSWLEPVQFLR 120  
QY 106 SVFANSLVYGASDSNVYDLKDLKEBGIQTLMGRLDGSPTGQIFKQYTSKFDNTHND 165  
Db 121 SVFANSLVYGASDSNVYDLKDLKEBGIQTLMGRLDGSPTGQIFKQYTSKFDNTHND 180  
QY 166 ALKNYGLLYCPRKMDKXETFLRIYQCRSVESGCGF 202  
Db 181 ALKNYGLLYCPRKMDKXETFLRIYQCRSVESGCGF 217

RESULT 5  
US-10-788-318-4  
; Sequence 4, Application US/10788318  
; Publication No. US20040137510A1  
; GENERAL INFORMATION:  
; APPLICANT: COOPER, DAVID N.  
; APPLICANT: PROCTOR, ANNIE M.  
; APPLICANT: GREGORY, JOHN M.  
; APPLICANT: MILLAR, DAVID S.  
; TITLE OF INVENTION: METHOD FOR DETECTING GROWTH HORMONE VARIATIONS IN  
; FILE REFERENCE: WCM78  
; CURRENT APPLICATION NUMBER: US/10/788,318  
; CURRENT FILING DATE: 2004-03-01  
; NUMBER OF SEQ ID NOS: 66  
; SOFTWARE: Patent In Ver. 2.1  
; SEQ ID NO 4  
; LENGTH: 217  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-10-788-318-4

Query Match 98.3%; Score 1029.5; DB 16; Length 217;  
Best Local Similarity 93.1%; Pred. No. 1.1e-93;  
Matches 202; Conservative 0; Mismatches 0; Indels 15; Gaps 1;  
QY 1 MATGSRISLLAFGLCLPWLQEGSAFPTTILSRFPDNASLRARHLQALFDTYQEF--- 57  
1 MATGSRISLLAFGLCLPWLQEGSAFPTTILSRFPDNASLRARHLQALFDTYQEFEEA 60  
DB 1 YIPKEQKYSFLQNPQTSICFSESIPTPSNREETOQKSNLELRISLLIOSWLEPVQFLR 105  
61 YIPKEQKYSFLQNPQTSICFSESIPTPSNREETOQKSNLELRISLLIOSWLEPVQFLR 120  
QY 106 SVFANSILVYGASDSNVYDLKDLKEGIIQTLMGRLLEDGSPRTGQIFKQYTSKFDPTNSHND 165  
121 SVFANSILVYGASDSNVYDLKDLKEGIIQTLMGRLLEDGSPRTGQIFKQYTSKFDPTNSHND 180  
DB 166 ALKNYGLLYCFRKMDKVEFLRIYQCRSVGSGCF 202  
181 ALKNYGLLYCFRKMDKVEFLRIYQCRSVGSGCF 217

RESULT 6  
US-09-929-918-9  
; Sequence 9, Application US/09929918  
; Patent No. US20020090678A1  
; GENERAL INFORMATION:  
; APPLICANT: Kordyum, Vitaliy A.  
; APPLICANT: Chernykh, Svetlana I.  
; APPLICANT: Slavenko, Iryna Yu.  
; APPLICANT: Vozianov, Oleksandr  
; TITLE OF INVENTION: PHAGE-DEPENDENT SUPER PRODUCTION OF  
; FILE REFERENCE: BIOLOGICALLY ACTIVE PROTEIN AND PEPTIDES  
; CURRENT APPLICATION NUMBER: US/09/929,918  
; CURRENT FILING DATE: 2001-08-15  
; PRIOR APPLICATION NUMBER: 09/318,288  
; NUMBER OF SEQ ID NOS: 11  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 9  
; LENGTH: 217  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-09-929-918-9

Query Match 97.9%; Score 1024.5; DB 9; Length 217;  
Best Local Similarity 92.6%; Pred. No. 3.5e-93;  
Matches 201; Conservative 0; Mismatches 1; Indels 15; Gaps 1;  
QY 1 MATGSRISLLAFGLCLPWLQEGSAFPTTILSRFPDNASLRARHLQALFDTYQEF--- 57

DB 1 MATGSRISLLAFGLCLPWLQEGSAFPTTILSRFPDNASLRARHLQALFDTYQEFEEA 60  
QY 58 -----NPQTSICFSESIPTPSNREETOQKSNLELRISLLIOSWLEPVQFLR 105  
61 YIPKEQKYSFLQNPQTSICFSESIPTPSNREETOQKSNLELRISLLIOSWLEPVQFLR 120  
QY 106 SVFANSILVYGASDSNVYDLKDLKEGIIQTLMGRLLEDGSPRTGQIFKQYTSKFDPTNSHND 165  
121 SVFANSILVYGASDSNVYDLKDLKEGIIQTLMGRLLEDGSPRTGQIFKQYTSKFDPTNSHND 180  
DB 166 ALKNYGLLYCFRKMDKVEFLRIYQCRSVGSGCF 202  
181 ALKNYGLLYCFRKMDKVEFLRIYQCRSVGSGCF 217

RESULT 7  
US-09-804-409A-16  
; Sequence 16, Application US/09804409A  
; Patent No. US20020155100A1  
; GENERAL INFORMATION:  
; APPLICANT: KIEFER, TIMOTHY J.  
; APPLICANT: CHEUNG, ANTHONY T.  
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR REGULATED PROTEIN  
; FILE REFERENCE: 02996/027 8721  
; CURRENT APPLICATION NUMBER: US/09/804,409A  
; CURRENT FILING DATE: 2001-03-12  
; NUMBER OF SEQ ID NOS: 18  
; SOFTWARE: Patent In Ver. 2.1  
; SEQ ID NO 16  
; LENGTH: 217  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-09-804-409A-16

Query Match 97.2%; Score 1017.5; DB 9; Length 217;  
Best Local Similarity 92.2%; Pred. No. 1.7e-92;  
Matches 200; Conservative 0; Mismatches 2; Indels 15; Gaps 1;  
QY 1 MATGSRISLLAFGLCLPWLQEGSAFPTTILSRFPDNASLRARHLQALFDTYQEF--- 57  
1 MATGSRISLLAFGLCLPWLQEGSAFPTTILSRFPDNASLRARHLQALFDTYQEFEEA 60  
DB 1 YIPKEQKYSFLQNPQTSICFSESIPTPSNREETOQKSNLELRISLLIOSWLEPVQFLR 105  
61 YIPKEQKYSFLQNPQTSICFSESIPTPSNREETOQKSNLELRISLLIOSWLEPVQFLR 120  
QY 106 SVFANSILVYGASDSNVYDLKDLKEGIIQTLMGRLLEDGSPRTGQIFKQYTSKFDPTNSHND 165  
121 SVFANSILVYGASDSNVYDLKDLKEGIIQTLMGRLLEDGSPRTGQIFKQYTSKFDPTNSHND 180  
DB 166 ALKNYGLLYCFRKMDKVEFLRIYQCRSVGSGCF 202  
181 ALKNYGLLYCFRKMDKVEFLRIYQCRSVGSGCF 217

RESULT 8  
US-10-411-037-48  
; Sequence 48, Application US/10411037  
; Publication No. US20040043446A1  
; GENERAL INFORMATION:  
; APPLICANT: Neose Technologies, Inc.  
; APPLICANT: DePrees, Shawn  
; APPLICANT: Zopf, David  
; APPLICANT: Bayer, Robert  
; APPLICANT: Hakes, David  
; APPLICANT: Chen, Xi  
; APPLICANT: Bove, Caryn  
; TITLE OF INVENTION: ALPHA GALACTOSIDASE A  
; FILE REFERENCE: 040853-01-5082  
; CURRENT APPLICATION NUMBER: US/10/411,037

Query Match 97.2%; Score 1017.5; DB 9; Length 217;  
Best Local Similarity 92.2%; Pred. No. 1.7e-92;  
Matches 200; Conservative 0; Mismatches 2; Indels 15; Gaps 1;  
QY 1 MATGSRISLLAFGLCLPWLQEGSAFPTTILSRFPDNASLRARHLQALFDTYQEF--- 57  
1 MATGSRISLLAFGLCLPWLQEGSAFPTTILSRFPDNASLRARHLQALFDTYQEFEEA 60  
DB 1 YIPKEQKYSFLQNPQTSICFSESIPTPSNREETOQKSNLELRISLLIOSWLEPVQFLR 105  
61 YIPKEQKYSFLQNPQTSICFSESIPTPSNREETOQKSNLELRISLLIOSWLEPVQFLR 120  
QY 106 SVFANSILVYGASDSNVYDLKDLKEGIIQTLMGRLLEDGSPRTGQIFKQYTSKFDPTNSHND 165  
121 SVFANSILVYGASDSNVYDLKDLKEGIIQTLMGRLLEDGSPRTGQIFKQYTSKFDPTNSHND 180  
DB 166 ALKNYGLLYCFRKMDKVEFLRIYQCRSVGSGCF 202  
181 ALKNYGLLYCFRKMDKVEFLRIYQCRSVGSGCF 217

CURRENT FILING DATE: 2003-04-09  
PRIOR APPLICATION NUMBER: US 60/328,523  
PRIOR FILING DATE: 2001-10-10  
PRIOR APPLICATION NUMBER: US 60/344,692  
PRIOR FILING DATE: 2001-10-19  
PRIOR APPLICATION NUMBER: US 60/387,292  
PRIOR FILING DATE: 2002-06-07  
PRIOR APPLICATION NUMBER: US 60/391,777  
PRIOR FILING DATE: 2002-06-25  
PRIOR APPLICATION NUMBER: US 60/396,594  
PRIOR FILING DATE: 2002-07-17  
PRIOR APPLICATION NUMBER: US 60/404,249  
PRIOR FILING DATE: 2002-08-16  
PRIOR APPLICATION NUMBER: US 60/407,527  
PRIOR FILING DATE: 2002-08-28  
NUMBER OF SEQ ID NOS: 75  
SOFTWARE: PatentIn version 3.2  
SEQ ID NO 48  
LENGTH: 217  
TYPE: PRT  
ORGANISM: Homo sapiens  
US-10-411-037-48

Query Match 97.2%; Score 1017.5; DB 15; Length 217;  
Best Local Similarity 92.2%; Pred. No. 1.7e-92;  
Matches 200; Conservative 0; Mismatches 2; Indels 15; Gaps 1;

Db 1 MATGRTSLILAFGLICLPMLQGSAPPTIPLSRLFDNLSLRHRLHQLAFDTYQEF--- 57  
1 MATGRTSLILAFGLICLPMLQGSAPPTIPLSRPFDMMLRAHRLHQLAFDTYQEFEEA 60  
QY 58 -----NPQTSICFSESIPTPSNEETQOKSNLELRISLLIQSWLEPVQFLR 105  
61 YIPKQKYSFLQNPQTSICFSESIPTPSNEETQOKSNLELRISLLIQSWLEPVQFLR 120  
Db 106 SVFANSIYVYASDSNVYDLKDLKEGIQTLMGRLDGSPTGQIFKQYKSKFDINSHND 165  
121 SVFANSIYVYASDSNVYDLKDLKEGIQTLMGRLDGSPTGQIFKQYKSKFDINSHND 180  
QY 166 ALLKNYGLLYCFKMDKVEFTFLRIYVQCRSVESGCGF 202  
Db 181 ALLKNYGLLYCFKMDKVEFTFLRIYVQCRSVESGCGF 217

RESULT 9  
US-10-411-026-48  
Sequence 48, Application US/10411026  
Publication No. US20040063911A1  
GENERAL INFORMATION:  
APPLICANT: Neose Technologies, Inc.  
APPLICANT: Deftrees, Shawn  
APPLICANT: Zopf, David  
APPLICANT: Bayer, Robert  
APPLICANT: Hakes, David  
APPLICANT: Chen, Xi  
TITLE OF INVENTION: PROTEIN REMODELING METHODS AND PROTEINS/PEPTIDES PRODUCED BY THE  
FILE OF INVENTION: METHODS  
FILE REFERENCE: 040853-01-5053  
CURRENT APPLICATION NUMBER: US/10/411,026  
CURRENT FILING DATE: 2003-04-09  
PRIOR APPLICATION NUMBER: US 60/328,523  
PRIOR FILING DATE: 2001-10-10  
PRIOR APPLICATION NUMBER: US 60/344,692  
PRIOR FILING DATE: 2001-10-19  
PRIOR APPLICATION NUMBER: US 60/387,292  
PRIOR FILING DATE: 2002-06-07  
PRIOR APPLICATION NUMBER: US 60/391,777  
PRIOR FILING DATE: 2002-06-25  
PRIOR APPLICATION NUMBER: US 60/396,594  
PRIOR FILING DATE: 2002-07-17  
PRIOR APPLICATION NUMBER: US 60/404,249  
PRIOR FILING DATE: 2002-08-16  
PRIOR APPLICATION NUMBER: US 60/407,527

PRIOR FILING DATE: 2002-08-28  
NUMBER OF SEQ ID NOS: 75  
SOFTWARE: PatentIn version 3.2  
SEQ ID NO 48  
LENGTH: 217  
TYPE: PRT  
ORGANISM: Homo sapiens  
US-10-411-026-48

Query Match 97.2%; Score 1017.5; DB 15; Length 217;  
Best Local Similarity 92.2%; Pred. No. 1.7e-92;  
Matches 200; Conservative 0; Mismatches 2; Indels 15; Gaps 1;

QY 1 MATGRTSLILAFGLICLPMLQGSAPPTIPLSRLFDNLSLRHRLHQLAFDTYQEF--- 57  
1 MATGRTSLILAFGLICLPMLQGSAPPTIPLSRPFDMMLRAHRLHQLAFDTYQEFEEA 60  
Db 58 -----NPQTSICFSESIPTPSNEETQOKSNLELRISLLIQSWLEPVQFLR 120  
61 YIPKQKYSFLQNPQTSICFSESIPTPSNEETQOKSNLELRISLLIQSWLEPVQFLR 120  
QY 106 SVFANSIYVYASDSNVYDLKDLKEGIQTLMGRLDGSPTGQIFKQYKSKFDINSHND 165  
121 SVFANSIYVYASDSNVYDLKDLKEGIQTLMGRLDGSPTGQIFKQYKSKFDINSHND 180  
QY 166 ALLKNYGLLYCFKMDKVEFTFLRIYVQCRSVESGCGF 202  
Db 181 ALLKNYGLLYCFKMDKVEFTFLRIYVQCRSVESGCGF 217

RESULT 10  
US-10-410-962-48  
Sequence 48, Application US/10410962  
Publication No. US2004007836A1  
GENERAL INFORMATION:  
APPLICANT: Neose Technologies, Inc.  
APPLICANT: Deftrees, Shawn  
APPLICANT: Zopf, David  
APPLICANT: Bayer, Robert  
APPLICANT: Hakes, David  
APPLICANT: Chen, Xi  
TITLE OF INVENTION: GLYCOCONJUGATE COLONY STIMULATING FACTOR: REMODELING AND  
FILE REFERENCE: 040853-01-5054  
CURRENT APPLICATION NUMBER: US/10/410,962  
CURRENT FILING DATE: 2003-04-09  
PRIOR APPLICATION NUMBER: US 60/328,523  
PRIOR FILING DATE: 2001-10-10  
PRIOR APPLICATION NUMBER: US 60/344,692  
PRIOR FILING DATE: 2001-10-19  
PRIOR APPLICATION NUMBER: US 60/387,292  
PRIOR FILING DATE: 2002-06-07  
PRIOR APPLICATION NUMBER: US 60/391,777  
PRIOR FILING DATE: 2002-06-25  
PRIOR APPLICATION NUMBER: US 60/396,594  
PRIOR FILING DATE: 2002-07-17  
PRIOR APPLICATION NUMBER: US 60/404,249  
PRIOR FILING DATE: 2002-08-16  
PRIOR APPLICATION NUMBER: US 60/407,527  
PRIOR FILING DATE: 2002-08-28  
NUMBER OF SEQ ID NOS: 75  
SOFTWARE: PatentIn version 3.2  
SEQ ID NO 48  
LENGTH: 217  
TYPE: PRT  
ORGANISM: Homo sapiens  
US-10-410-962-48

Query Match 97.2%; Score 1017.5; DB 15; Length 217;  
Best Local Similarity 92.2%; Pred. No. 1.7e-92;  
Matches 200; Conservative 0; Mismatches 2; Indels 15; Gaps 1;



QY 1 MATGSRSTLLAFGLCLPWLQSGSAFPTPLSRFPDNASLRARHLQALFDYQOE--- 57  
DB 1 MATGSRSTLLAFGLCLPWLQSGSAFPTPLSRFPDNASLRARHLQALFDYQOE 60  
QY 58 -----NPTSICFSESIPTPSNEETQOKSNELRLISLLIQSWLEPYQFLR 105  
DB 61 YIPKEQKYSFLQNPQTSICFSESIPTPSNEETQOKSNELRLISLLIQSWLEPYQFLR 120  
QY 106 SVFANSILVYGASDSNVYDLKDLKEGIIQTLMGRLLEGSPRTGOIFKQYTSKEDTNSHND 165  
DB 121 SVFANSILVYGASDSNVYDLKDLKEGIIQTLMGRLLEGSPRTGOIFKQYTSKEDTNSHND 180  
QY 166 ALKKNYGLLYCPRKMDKXETFLRLIVQCRSVGSGCF 202  
DB 181 ALKKNYGLLYCPRKMDKXETFLRLIVQCRSVGSGCF 217

RESULT 11  
US-10-411-049-48  
Sequence 48, Application US/10411049  
Publication No. US20040082026A1  
GENERAL INFORMATION:  
APPLICANT: Neose Technologies, Inc.  
APPLICANT: Defrees, Shawn  
APPLICANT: Zopf, David  
APPLICANT: Bayer, Robert  
APPLICANT: Hakes, David  
APPLICANT: Chen, Xi  
APPLICANT: Bove, Caryn  
TITLE OF INVENTION: INTERFERON ALPHA: REMODELING AND GLYCOCONJUGATION OF INTERFERON  
FILE REFERENCE: 040853-01-5055  
CURRENT APPLICATION NUMBER: US/10/411, 049  
PRIOR FILING DATE: 2003-04-09  
PRIOR APPLICATION NUMBER: US 60/328, 523  
PRIOR FILING DATE: 2001-10-10  
PRIOR APPLICATION NUMBER: US 60/344, 692  
PRIOR FILING DATE: 2001-10-19  
PRIOR APPLICATION NUMBER: US 60/387, 292  
PRIOR FILING DATE: 2002-06-07  
PRIOR APPLICATION NUMBER: US 60/391, 777  
PRIOR FILING DATE: 2002-06-25  
PRIOR APPLICATION NUMBER: US 60/396, 594  
PRIOR FILING DATE: 2002-07-17  
PRIOR APPLICATION NUMBER: US 60/404, 249  
PRIOR FILING DATE: 2002-08-16  
PRIOR APPLICATION NUMBER: US 60/407, 527  
NUMBER OF SEQ ID NOS: 75  
SOFTWARE: PatentIn version 3.2  
SEQ ID NO 48  
LENGTH: 217  
TYPE: PR1  
ORGANISM: Homo sapiens  
US-10-411-049-48

Query Match 97.2%; Score 1017.5; DB 15; Length 217;  
Best Local Similarity 92.2%; Pred. No. 1,7e-92;  
Matches 200; Conservative 0; Mismatches 2; Indels 15; Gaps 1;

QY 1 MATGSRSTLLAFGLCLPWLQSGSAFPTPLSRFPDNASLRARHLQALFDYQOE--- 57  
DB 1 MATGSRSTLLAFGLCLPWLQSGSAFPTPLSRFPDNASLRARHLQALFDYQOE 60  
QY 58 -----NPTSICFSESIPTPSNEETQOKSNELRLISLLIQSWLEPYQFLR 105  
DB 61 YIPKEQKYSFLQNPQTSICFSESIPTPSNEETQOKSNELRLISLLIQSWLEPYQFLR 120  
QY 106 SVFANSILVYGASDSNVYDLKDLKEGIIQTLMGRLLEGSPRTGOIFKQYTSKEDTNSHND 165  
DB 121 SVFANSILVYGASDSNVYDLKDLKEGIIQTLMGRLLEGSPRTGOIFKQYTSKEDTNSHND 180  
QY 166 ALKKNYGLLYCPRKMDKXETFLRLIVQCRSVGSGCF 202  
DB 181 ALKKNYGLLYCPRKMDKXETFLRLIVQCRSVGSGCF 217

DB 181 ALKKNYGLLYCPRKMDKXETFLRLIVQCRSVGSGCF 217

RESULT 12  
US-10-410-930-48  
Sequence 48, Application US/10410930  
Publication No. US20040115168A1  
GENERAL INFORMATION:  
APPLICANT: Neose Technologies, Inc.  
APPLICANT: Defrees, Shawn  
APPLICANT: Zopf, David  
APPLICANT: Bayer, Robert  
APPLICANT: Hakes, David  
APPLICANT: Chen, Xi  
APPLICANT: Bove, Caryn  
TITLE OF INVENTION: INTERFERON BETA: REMODELING AND GLYCOCONJUGATION OF INTERFERON  
FILE REFERENCE: 040853-01-5056  
CURRENT APPLICATION NUMBER: US/10/410, 930  
PRIOR FILING DATE: 2003-04-09  
PRIOR APPLICATION NUMBER: US 60/328, 523  
PRIOR FILING DATE: 2001-10-10  
PRIOR APPLICATION NUMBER: US 60/344, 692  
PRIOR FILING DATE: 2001-10-19  
PRIOR APPLICATION NUMBER: US 60/387, 292  
PRIOR FILING DATE: 2002-06-07  
PRIOR APPLICATION NUMBER: US 60/391, 777  
PRIOR FILING DATE: 2002-06-25  
PRIOR APPLICATION NUMBER: US 60/396, 594  
PRIOR FILING DATE: 2002-07-17  
PRIOR APPLICATION NUMBER: US 60/404, 249  
PRIOR FILING DATE: 2002-08-16  
PRIOR APPLICATION NUMBER: US 60/407, 527  
NUMBER OF SEQ ID NOS: 75  
SOFTWARE: PatentIn version 3.2  
SEQ ID NO 48  
LENGTH: 217  
TYPE: PR1  
ORGANISM: Homo sapiens  
US-10-410-930-48

Query Match 97.2%; Score 1017.5; DB 16; Length 217;  
Best Local Similarity 92.2%; Pred. No. 1,7e-92;  
Matches 200; Conservative 0; Mismatches 2; Indels 15; Gaps 1;

QY 1 MATGSRSTLLAFGLCLPWLQSGSAFPTPLSRFPDNASLRARHLQALFDYQOE--- 57  
DB 1 MATGSRSTLLAFGLCLPWLQSGSAFPTPLSRFPDNASLRARHLQALFDYQOE 60  
QY 58 -----NPTSICFSESIPTPSNEETQOKSNELRLISLLIQSWLEPYQFLR 105  
DB 61 YIPKEQKYSFLQNPQTSICFSESIPTPSNEETQOKSNELRLISLLIQSWLEPYQFLR 120  
QY 106 SVFANSILVYGASDSNVYDLKDLKEGIIQTLMGRLLEGSPRTGOIFKQYTSKEDTNSHND 165  
DB 121 SVFANSILVYGASDSNVYDLKDLKEGIIQTLMGRLLEGSPRTGOIFKQYTSKEDTNSHND 180  
QY 166 ALKKNYGLLYCPRKMDKXETFLRLIVQCRSVGSGCF 202  
DB 181 ALKKNYGLLYCPRKMDKXETFLRLIVQCRSVGSGCF 217

RESULT 13  
US-10-410-997-48  
Sequence 48, Application US/10410997  
Publication No. US20040126838A1  
GENERAL INFORMATION:  
APPLICANT: Neose Technologies, Inc.  
APPLICANT: Defrees, Shawn  
APPLICANT: Zopf, David  
APPLICANT: Bayer, Robert

APPLICANT: Hakes, David  
APPLICANT: Chen, Xi  
APPLICANT: Bower, Caryn  
TITLE OF INVENTION: FOLICLE STIMULATING HORMONE: REMODELING AND GLYCOCONJUGATION OF  
TITLE OF INVENTION: FSH  
FILE REFERENCE: 040853-01-5059  
CURRENT APPLICATION NUMBER: US/10/410,997  
PRIOR FILING DATE: 2003-04-09  
PRIOR APPLICATION NUMBER: US 60/328,523  
PRIOR FILING DATE: 2001-10-10  
PRIOR APPLICATION NUMBER: US 60/344,692  
PRIOR FILING DATE: 2001-10-19  
PRIOR APPLICATION NUMBER: US 60/387,292  
PRIOR FILING DATE: 2002-06-07  
PRIOR APPLICATION NUMBER: US 60/391,777  
PRIOR FILING DATE: 2002-06-25  
PRIOR APPLICATION NUMBER: US 60/396,594  
PRIOR FILING DATE: 2002-07-17  
PRIOR APPLICATION NUMBER: US 60/404,249  
PRIOR FILING DATE: 2002-08-16  
PRIOR APPLICATION NUMBER: US 60/407,527  
PRIOR FILING DATE: 2002-08-28  
NUMBER OF SEQ ID NOS: 75  
SOFTWARE: PatentIn version 3.2  
SEQ ID NO 48  
LENGTH: 217  
TYPE: PRT  
ORGANISM: Homo sapiens  
US-10-410-997-48

Query Match 97.2%; Score 1017.5; DB 16; Length 217;  
Best Local Similarity 92.2%; Pred. No. 1,7e-92; Indels 15; Gaps 1;  
Matches 200; Conservative 0; Mismatches 2;

QY 1 MATGRTSLIAFGILCLPWLQEGSAFPTPLSLFDNASIRARHLQAFDTYQEF--- 57  
1 MATGRTSLIAFGILCLPWLQEGSAFPTPLSLFDNASIRARHLQAFDTYQEF 60  
DB 1 MATGRTSLIAFGILCLPWLQEGSAFPTPLSLFDNASIRARHLQAFDTYQEF 60

QY 58 -----NPTSLCFSESIPTPSNREPTQKSNLELRISILLIQSWLEPVOFLR 105  
1 YIPKQKXSLFQNPQTSICFSESIPTPSNREPTQKSNLELRISILLIQSWLEPVOFLR 120

DB 61 YIPKQKXSLFQNPQTSICFSESIPTPSNREPTQKSNLELRISILLIQSWLEPVOFLR 120

QY 106 SVFANSILVYGASDSNVYDLKDLKEGIIQTLWGRLEDGSPRTGQIFKQYTSKPTNSHND 165  
121 SVFANSILVYGASDSNVYDLKDLKEGIIQTLWGRLEDGSPRTGQIFKQYTSKPTNSHND 180

DB 121 SVFANSILVYGASDSNVYDLKDLKEGIIQTLWGRLEDGSPRTGQIFKQYTSKPTNSHND 180

QY 166 ALLKNYGLLYCPRKMDKVEFLRIYQCSVSGSGF 202  
181 ALLKNYGLLYCPRKMDKVEFLRIYQCSVSGSGF 217

DB 181 ALLKNYGLLYCPRKMDKVEFLRIYQCSVSGSGF 217

RESULT 14  
US-10-411-012-48  
Sequence 48, Application US/10411012  
Publication No. US20040132640A1  
GENERAL INFORMATION:  
APPLICANT: Neose Technologies, Inc.  
APPLICANT: Defrees, Shawn  
APPLICANT: Zopf, David  
APPLICANT: Bayer, Robert  
APPLICANT: Hakes, David  
APPLICANT: Chen, Xi  
APPLICANT: Bower, Caryn  
TITLE OF INVENTION: GLYCOPREGULATION METHODS AND PROTEINS/PEPTIDES PRODUCED BY THE  
TITLE OF INVENTION: METHODS  
FILE REFERENCE: 040853-01-5051  
CURRENT APPLICATION NUMBER: US/10/411,012  
PRIOR FILING DATE: 2003-04-09  
PRIOR APPLICATION NUMBER: US 60/328,523  
PRIOR FILING DATE: 2001-10-10  
PRIOR APPLICATION NUMBER: US 60/344,692  
PRIOR FILING DATE: 2001-10-19  
PRIOR APPLICATION NUMBER: US 60/387,292

PRIOR FILING DATE: 2002-06-07  
PRIOR APPLICATION NUMBER: US 60/391,777  
PRIOR FILING DATE: 2002-06-25  
PRIOR APPLICATION NUMBER: US 60/396,594  
PRIOR FILING DATE: 2002-07-17  
PRIOR APPLICATION NUMBER: US 60/404,249  
PRIOR FILING DATE: 2002-08-16  
PRIOR APPLICATION NUMBER: US 60/407,527  
PRIOR FILING DATE: 2002-08-28  
NUMBER OF SEQ ID NOS: 75  
SOFTWARE: PatentIn version 3.2  
SEQ ID NO 48  
LENGTH: 217  
TYPE: PRT  
ORGANISM: Homo sapiens  
US-10-411-012-48

Query Match 97.2%; Score 1017.5; DB 16; Length 217;  
Best Local Similarity 92.2%; Pred. No. 1,7e-92; Indels 15; Gaps 1;  
Matches 200; Conservative 0; Mismatches 2;

QY 1 MATGRTSLIAFGILCLPWLQEGSAFPTPLSLFDNASIRARHLQAFDTYQEF--- 57  
1 MATGRTSLIAFGILCLPWLQEGSAFPTPLSLFDNASIRARHLQAFDTYQEF 60  
DB 1 MATGRTSLIAFGILCLPWLQEGSAFPTPLSLFDNASIRARHLQAFDTYQEF 60

QY 58 -----NPTSLCFSESIPTPSNREPTQKSNLELRISILLIQSWLEPVOFLR 105  
61 YIPKQKXSLFQNPQTSICFSESIPTPSNREPTQKSNLELRISILLIQSWLEPVOFLR 120

DB 61 YIPKQKXSLFQNPQTSICFSESIPTPSNREPTQKSNLELRISILLIQSWLEPVOFLR 120

QY 106 SVFANSILVYGASDSNVYDLKDLKEGIIQTLWGRLEDGSPRTGQIFKQYTSKPTNSHND 165  
121 SVFANSILVYGASDSNVYDLKDLKEGIIQTLWGRLEDGSPRTGQIFKQYTSKPTNSHND 180

DB 121 SVFANSILVYGASDSNVYDLKDLKEGIIQTLWGRLEDGSPRTGQIFKQYTSKPTNSHND 180

QY 166 ALLKNYGLLYCPRKMDKVEFLRIYQCSVSGSGF 202  
181 ALLKNYGLLYCPRKMDKVEFLRIYQCSVSGSGF 217

DB 181 ALLKNYGLLYCPRKMDKVEFLRIYQCSVSGSGF 217

RESULT 15  
US-10-287-994-48  
Sequence 48, Application US/10287994  
Publication No. US20040137557A1  
GENERAL INFORMATION:  
APPLICANT: Neose Technologies, Inc.  
APPLICANT: Defrees, Shawn  
APPLICANT: Zopf, David  
APPLICANT: Bayer, Robert  
APPLICANT: Bower, Caryn  
APPLICANT: Hakes, David  
APPLICANT: Chen, Xi  
TITLE OF INVENTION: REMODELING AND GLYCOCONJUGATION OF PEPTIDES  
FILE REFERENCE: 040853-01-5052-00  
CURRENT APPLICATION NUMBER: US/10/287,994  
PRIOR FILING DATE: 2002-11-05  
PRIOR APPLICATION NUMBER: US 60/328,523  
PRIOR FILING DATE: 2001-10-10  
PRIOR APPLICATION NUMBER: US 60/344,692  
PRIOR FILING DATE: 2001-10-19  
PRIOR APPLICATION NUMBER: US 60/387,292  
PRIOR FILING DATE: 2002-06-07  
PRIOR APPLICATION NUMBER: US 60/391,777  
PRIOR FILING DATE: 2002-06-25  
PRIOR APPLICATION NUMBER: US 60/396,594  
PRIOR FILING DATE: 2002-07-17  
PRIOR APPLICATION NUMBER: US 60/404,249  
PRIOR FILING DATE: 2002-08-16  
PRIOR APPLICATION NUMBER: US 60/407,527  
PRIOR FILING DATE: 2002-08-28  
NUMBER OF SEQ ID NOS: 62  
SOFTWARE: PatentIn version 3.1  
SEQ ID NO 48  
LENGTH: 217  
TYPE: PRT

ORGANISM: Homo sapiens  
US-10-287-994-48

Query Match 97.2%; Score 1017.5; DB 16; Length 217;  
Best Local Similarity 92.2%; Pred. No. 1.7e-92;  
Matches 200; Conservative 0; Mismatches 2; Indels 15; Gaps 1;

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Qy 1 MATGRTSLLAFLGLCPMLQEGSAFPTIPISRLFDNASSLRHRLHQAFTTYQEF--- 57
Db 1 MATGRTSLLAFLGLCPMLQEGSAFPTIPISRLFDNASSLRHRLHQAFTTYQEF--- 57
Qy 58 -----NPQTSICFSESITPTPSNRRETOOKSNLELRISLLLIQSWLEPVQFLR 105
Db 61 YIPKEQKYSFIQNPQTSICFSESITPTPSNRRETOOKSNLELRISLLLIQSWLEPVQFLR 120
Qy 106 SVFANSIYVGASDSNVYDLKDLKEGIQTLMGRLSDGSPRTGOIFKQYSKFTDTSNND 165
Db 121 SVFANSIYVGASDSNVYDLKDLKEGIQTLMGRLSDGSPRTGOIFKQYSKFTDTSNND 180
Qy 166 ALKNYGLLYCFRKMDKVFETFLRIYQCRSVGSGCGF 202
Db 181 ALKNYGLLYCFRKMDKVFETFLRIYQCRSVGSGCGF 217

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Search completed: February 6, 2005, 13:17:03  
Job time : 133 secs

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GenCore version 5.1.6  
Copyright (c) 1993 - 2005 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: February 6, 2005, 12:55:48 ; Search time 43 Seconds  
(without alignments)  
350,677 Million cell updates/sec

Title: US-09-856-796B-2  
Perfect score: 1047  
Sequence: 1 MATGSRRLAFLGLCLPW.....KVFPLRIVQCRSEVSGSGR 202

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 513545 seqs, 74649064 residues

Total number of hits satisfying chosen parameters: 513545

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database :  
1: /cgn2\_6/ptodata/1/1aa/5A\_COMB.pep:\*  
2: /cgn2\_6/ptodata/1/1aa/5B\_COMB.pep:\*  
3: /cgn2\_6/ptodata/1/1aa/6A\_COMB.pep:\*  
4: /cgn2\_6/ptodata/1/1aa/6B\_COMB.pep:\*  
5: /cgn2\_6/ptodata/1/1aa/6C\_COMB.pep:\*  
6: /cgn2\_6/ptodata/1/1aa/backfill1.pep:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1029.5	98.3	217	1 US-08-469-486-51	Sequence 51, Appl
2	1029.5	98.3	217	2 US-08-469-658-51	Sequence 51, Appl
3	1024.5	97.9	217	3 US-08-589-028-10	Sequence 10, Appl
4	1024.5	97.9	217	3 US-08-784-582-10	Sequence 10, Appl
5	1024.5	97.9	217	3 US-08-785-271-10	Sequence 10, Appl
6	1024.5	97.9	217	3 US-08-759-628-11	Sequence 11, Appl
7	1024.5	97.9	217	3 US-09-284-878-11	Sequence 11, Appl
8	1024.5	97.9	217	4 US-09-929-918-9	Sequence 9, Appl
9	1016.5	97.1	217	2 US-08-187-756C-4	Sequence 4, Appl
10	1016.5	97.1	217	2 US-08-710-324A-4	Sequence 4, Appl
11	1016.5	97.1	217	4 US-09-411-657-4	Sequence 5, Appl
12	999	95.4	198	1 US-08-187-756C-5	Sequence 5, Appl
13	999	95.4	198	2 US-08-710-324A-5	Sequence 5, Appl
14	999	95.4	198	2 US-08-710-324A-5	Sequence 5, Appl
15	926.5	88.5	360	3 US-09-411-657-5	Sequence 5, Appl
16	924.5	88.3	274	3 US-08-784-582-73	Sequence 73, Appl
17	914	87.3	176	3 US-08-784-582-71	Sequence 71, Appl
18	914	87.3	176	3 US-08-791-728-2	Sequence 2, Appl
19	909	86.8	176	3 US-08-990-774-2	Sequence 1, Appl
20	909	86.8	176	3 US-08-791-728-1	Sequence 1, Appl
21	896.5	85.6	191	3 US-08-990-774-1	Sequence 1, Appl
22	891.5	85.1	191	3 US-09-465-461-1	Sequence 5, Appl
23	891.5	85.1	191	4 US-09-284-878-5	Sequence 1, Appl
24	891.5	85.1	192	1 US-09-462-941-1	Sequence 1, Appl
25	891.5	85.1	194	2 US-08-093-383-1	Sequence 1, Appl
26	891.5	85.1	194	2 US-08-383-621-4	Sequence 4, Appl
27	891.5	85.1	241	3 US-08-459-906-4	Sequence 25, Appl
				US-09-424-620B-25	

28	891.5	85.1	245	4 US-09-280-030-66	Sequence 66, Appl
29	891.5	85.1	448	4 US-09-916-229A-2	Sequence 2, Appl
30	888.5	84.9	197	4 US-09-949-016-8655	Sequence 8655, Ap
31	888.5	84.9	197	4 US-09-949-016-8656	Sequence 8656, Ap
32	888.5	84.9	197	4 US-09-949-016-8657	Sequence 8657, Ap
33	888.5	84.9	197	4 US-09-949-016-8658	Sequence 8658, Ap
34	888.5	84.9	197	4 US-09-949-016-8659	Sequence 8659, Ap
35	884.5	84.5	401	4 US-09-420-819-36	Sequence 36, Appl
36	881.5	84.2	191	4 US-09-554-451-1	Sequence 1, Appl
37	880.5	84.1	177	2 US-08-187-756C-6	Sequence 6, Appl
38	880.5	84.1	177	2 US-08-710-324A-6	Sequence 6, Appl
39	880.5	84.1	177	4 US-09-411-657-6	Sequence 6, Appl
40	876.5	83.9	400	4 US-09-420-819-37	Sequence 37, Appl
41	876.5	83.7	191	3 US-08-800-215C-16	Sequence 16, Appl
42	871.5	83.2	191	4 US-09-554-451-3	Sequence 3, Appl
43	867.5	82.9	191	3 US-08-800-215C-18	Sequence 18, Appl
44	867.5	82.9	191	3 US-08-800-215C-20	Sequence 20, Appl
45	772.5	73.8	168	6 5424199-3	Patent No. 5424199

## ALIGNMENTS

RESULT 1  
US-08-469-486-51  
Sequence 51, Application US/08469486  
Patent No. 5739281  
GENERAL INFORMATION:  
APPLICANT: Thoesersen, Hans Christian  
APPLICANT: Hollet, Thor Las  
TITLE OF INVENTION: Improved method for the refolding of  
NUMBER OF SEQUENCES: 58  
CORRESPONDENCE ADDRESS:  
ADDRESS: Fish & Richardson  
STREET: 225 Franklin Street  
CITY: Boston  
STATE: Massachusetts  
COUNTRY: USA  
ZIP: 02110-2804  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version  
SOFTWARE: #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/469,486  
FILING DATE:  
CLASSIFICATION: 530  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/192,060  
FILING DATE: February 4, 1994  
ATTORNEY/AGENT INFORMATION:  
NAME: Paul T. Clark  
REGISTRATION NUMBER: 30,162  
REFERENCE/DOCKET NUMBER: 06363/002001  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 617 542 5070  
TELEFAX: 617 542 8906  
TELEX: 200154  
INFORMATION FOR SEQ ID NO: 51:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 217 amino acids  
TYPE: amino acid  
STRANDEDNESS:  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-08-469-486-51

Query Match 98.3% Score 1029.5, DB 1, Length 217;  
Best Local Similarity 93.1%, Pred. No. 1.9e-108;

Matches 202; Conservative 0; Mismatches 0; Indels 15; Gaps 1;

QY 1 MATGRTSLLAFLGCLPWLQGSAPPTPLSRFLPDNASLRARHLQALFDTYOEF--- 57

Db 1 MATGRTSLLAFLGCLPWLQGSAPPTPLSRFLPDNASLRARHLQALFDTYOEFEEA 60

QY 58 -----NPOTSLCFSESIPTPSNREETOQKSNLELRISLLLIQSWLEPVQFLR 105

Db 61 YIPKQKYSFLONQOTSLCFSESIPTPSNREETOQKSNLELRISLLLIQSWLEPVQFLR 120

QY 106 SVFANSIYVAGSDSNVYDLKDLKEGIQTLMGRLDSSPRTGQIFKQYKSFDTNSHND 165

Db 121 SVFANSIYVAGSDSNVYDLKDLKEGIQTLMGRLDSSPRTGQIFKQYKSFDTNSHND 180

QY 166 ALLKNYGLLYCFRKMDKVFETFLRVQCRSVGSCGF 202

Db 181 ALLKNYGLLYCFRKMDKVFETFLRVQCRSVGSCGF 217

RESULT 2

US-08-469-658-51

Sequence 51, Application US/08469658

Patent No. 5917018

GENERAL INFORMATION:

APPLICANT: Th egeresen, Hans Christian

APPLICANT: Hollet, Thor Las

APPLICANT: Etzerodt, Michael

TITLE OF INVENTION: IMPROVED METHOD FOR THE REFOLDING OF

TITLE OF INVENTION: PROTEINS

NUMBER OF SEQUENCES: 58

CORRESPONDENCE ADDRESS:

ADDRESSEE: Fish & Richardson P.C.

STREET: 225 Franklin Street

CITY: Boston

STATE: Massachusetts

COUNTRY: USA

ZIP: 02110-2804

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patent in Release #1.0, Version

SOFTWARE: #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/469,658

FILING DATE: June 5, 1995

CLASSIFICATION: 530

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 08/192,060

FILING DATE: February 4, 1994

CLASSIFICATION: 530

ATTORNEY/AGENT INFORMATION:

NAME: Paul T. Clark

REGISTRATION NUMBER: 30,162

REFERENCE/DOCKET NUMBER: 06363/002002

TELECOMMUNICATION INFORMATION:

TELEPHONE: 617 542 5070

TELEFAX: 617 542 8906

TELEX: 200154

INFORMATION FOR SEQ ID NO: 51:

SEQUENCE CHARACTERISTICS:

LENGTH: 217 amino acids

TYPE: amino acid

STRANDEDNESS:

TOPOLOGY: linear

MOLECULE TYPE: protein

US-08-469-658-51

Query Match

Best Local Similarity 98.3%; Score 1029.5; DB 2; Length 217;

Matches 202; Conservative 0; Mismatches 0; Indels 15; Gaps 1;

QY 1 MATGRTSLLAFLGCLPWLQGSAPPTPLSRFLPDNASLRARHLQALFDTYOEF--- 57

Db 1 MATGRTSLLAFLGCLPWLQGSAPPTPLSRFLPDNASLRARHLQALFDTYOEFEEA 60

QY 58 -----NPOTSLCFSESIPTPSNREETOQKSNLELRISLLLIQSWLEPVQFLR 105

Db 61 YIPKQKYSFLONQOTSLCFSESIPTPSNREETOQKSNLELRISLLLIQSWLEPVQFLR 120

QY 106 SVFANSIYVAGSDSNVYDLKDLKEGIQTLMGRLDSSPRTGQIFKQYKSFDTNSHND 165

Db 121 SVFANSIYVAGSDSNVYDLKDLKEGIQTLMGRLDSSPRTGQIFKQYKSFDTNSHND 180

QY 166 ALLKNYGLLYCFRKMDKVFETFLRVQCRSVGSCGF 202

Db 181 ALLKNYGLLYCFRKMDKVFETFLRVQCRSVGSCGF 217

RESULT 3

US-08-589-028-10

Sequence 10, Application US/08589028

Patent No. 6087129

GENERAL INFORMATION:

APPLICANT: Newgard, Christopher B.

APPLICANT: Halban, Philippe

APPLICANT: No. 6087129mington, Karl D.

APPLICANT: Clark, Samuel A.

APPLICANT: Thigpen, Antice E.

APPLICANT: Quade, Christian

TITLE OF INVENTION: Recombinant Expression of Proteins From

TITLE OF INVENTION: Secretory Cell Lines

NUMBER OF SEQUENCES: 50

CORRESPONDENCE ADDRESS:

ADDRESSEE: Arnold, White & Durkee

STREET: P. O. Box 4433

CITY: Houston

STATE: TX

COUNTRY: USA

ZIP: 77210-4433

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patent in Release #1.0, Version #1.30

SOFTWARE: #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/589,028

FILING DATE: Concurrently Herewith

CLASSIFICATION: 435

ATTORNEY/AGENT INFORMATION:

NAME: Highlander, Steven L.

REGISTRATION NUMBER: 47,642

REFERENCE/DOCKET NUMBER: UTSD:426\HYL

TELECOMMUNICATION INFORMATION:

TELEPHONE: (512) 474-7577

TELEFAX: (512) 418-3000

INFORMATION FOR SEQ ID NO: 10:

SEQUENCE CHARACTERISTICS:

LENGTH: 217 amino acids

TYPE: amino acid

STRANDEDNESS:

TOPOLOGY: linear

US-08-589-028-10

Query Match

Best Local Similarity 97.9%; Score 1024.5; DB 3; Length 217;

Matches 201; Conservative 0; Mismatches 1; Indels 15; Gaps 1;

QY 1 MATGRTSLLAFLGCLPWLQGSAPPTPLSRFLPDNASLRARHLQALFDTYOEF--- 57

Db 1 MATGRTSLLAFLGCLPWLQGSAPPTPLSRFLPDNASLRARHLQALFDTYOEFEEA 60

QY 58 -----NPOTSLCFSESIPTPSNREETOQKSNLELRISLLLIQSWLEPVQFLR 105

Db 61 YIPKQKYSFLONQOTSLCFSESIPTPSNREETOQKSNLELRISLLLIQSWLEPVQFLR 120

QY 106 SVFANSIYVGASDSNVYDLKDLKEGIQTLMGRLDGSPTGQIFKQYSKFDJNSHND 165  
DB 121 SVFANSIYVGASDSNVYDLKDLKEGIQTLMGRLDGSPTGQIFKQYSKFDJNSHND 180  
QY 166 ALLKNYGLLYCFKRMKMDKVEFLRIYQCRSVGSGCF 202  
DB 181 ALLKNYGLLYCFKRMKMDKVEFLRIYQCRSVGSGCF 217

## RESULT 4

US-08-784-582-10  
; Sequence 10, Application US/08784582  
; Patent No. 6110707  
; GENERAL INFORMATION:  
; APPLICANT: Newgard, Christopher B.  
; APPLICANT: Halban, Philippe A.  
; APPLICANT: No. 6110707mington, Karl D.  
; APPLICANT: Clark, Samuel A.  
; APPLICANT: Thigpen, Anice E.  
; APPLICANT: Quaade, Christian  
; APPLICANT: Kruse, Fred  
; APPLICANT: McGarry, Dennis  
; TITLE OF INVENTION: RECOMBINANT EXPRESSION OF PROTEINS FROM  
; TITLE OF INVENTION: SECRETORY CELL LINES  
; NUMBER OF SEQUENCES: 79  
; CORRESPONDENCE ADDRESSES:  
; ADDRESSEE: Arnold, White & Durkee  
; STREET: P.O. Box 4433  
; CITY: Houston  
; STATE: Texas  
; COUNTRY: USA  
; ZIP: 77210  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patentin Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/784,582  
; FILING DATE: Concurrently Herewith  
; CLASSIFICATION: 435  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 60/028,427  
; FILING DATE: 15-OCT-1996  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/589,028  
; FILING DATE: 19-JAN-1996  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Highlander, Steven L.  
; REGISTRATION NUMBER: 37,642  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 512/418-3000  
; TELEFAX: 512/474-7577  
; INFORMATION FOR SEQ ID NO: 10:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 217 amino acids  
; TYPE: amino acid  
; STRANDEDNESS:  
; TOPOLOGY: linear  
US-08-784-582-10

Query Match 97.9%; Score 1024.5; DB 3; Length 217;  
Best Local Similarity 92.6%; Pred. No. 7.2e-108;  
Matches 201; Conservative 0; Mismatches 1; Indels 15; Gaps 1;

QY 1 MATGRTSLLAFLGLCLPWLQEGSAFPTIPISRLFDNASLRAHRLHQLAFTTYOEF--- 57  
DB 1 MATGRTSLLAFLGLCLPWLQEGSAFPTIPISRLFDNASLRAHRLHQLAFTTYOEFBEA 60  
QY 58 -----NPTSICFSESIPTPSNRRETOOKSNLELRISLLLIQSWLEFVQFLR 105  
|||||

DB 61 YIPKQKXSFLQNPQTSICFSESIPTPSNRRETOOKSNLELRISLLLIQSWLEFVQFLR 120  
QY 106 SVFANSIYVGASDSNVYDLKDLKEGIQTLMGRLDGSPTGQIFKQYSKFDJNSHND 165  
DB 121 SVFANSIYVGASDSNVYDLKDLKEGIQTLMGRLDGSPTGQIFKQYSKFDJNSHND 180  
QY 166 ALLKNYGLLYCFKRMKMDKVEFLRIYQCRSVGSGCF 202  
DB 181 ALLKNYGLLYCFKRMKMDKVEFLRIYQCRSVGSGCF 217

## RESULT 5

US-08-785-271-10  
; Sequence 10, Application US/08785271  
; Patent No. 6194176  
; GENERAL INFORMATION:  
; APPLICANT: Newgard, Christopher B.  
; APPLICANT: Halban, Philippe A.  
; APPLICANT: No. 6194176mington, Karl D.  
; APPLICANT: Clark, Samuel A.  
; APPLICANT: Thigpen, Anice E.  
; APPLICANT: Quaade, Christian  
; APPLICANT: Kruse, Fred  
; TITLE OF INVENTION: RECOMBINANT EXPRESSION OF PROTEINS FROM  
; TITLE OF INVENTION: SECRETORY CELL LINES  
; NUMBER OF SEQUENCES: 56  
; CORRESPONDENCE ADDRESSES:  
; ADDRESSEE: Arnold, White & Durkee  
; STREET: P.O. Box 4433  
; CITY: Houston  
; STATE: Texas  
; COUNTRY: USA  
; ZIP: 77210  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patentin Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/785,271  
; FILING DATE: Concurrently Herewith  
; CLASSIFICATION: 435  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: US 08/589,028  
; FILING DATE: 19-JAN-1996  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Highlander, Steven L.  
; REGISTRATION NUMBER: 37,642  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 512/418-3000  
; TELEFAX: 512/474-7577  
; INFORMATION FOR SEQ ID NO: 10:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 217 amino acids  
; TYPE: amino acid  
; STRANDEDNESS:  
; TOPOLOGY: linear  
US-08-785-271-10

Query Match 97.9%; Score 1024.5; DB 3; Length 217;  
Best Local Similarity 92.6%; Pred. No. 7.2e-108;  
Matches 201; Conservative 0; Mismatches 1; Indels 15; Gaps 1;

QY 1 MATGRTSLLAFLGLCLPWLQEGSAFPTIPISRLFDNASLRAHRLHQLAFTTYOEF--- 57  
DB 1 MATGRTSLLAFLGLCLPWLQEGSAFPTIPISRLFDNASLRAHRLHQLAFTTYOEFBEA 60  
QY 58 -----NPTSICFSESIPTPSNRRETOOKSNLELRISLLLIQSWLEFVQFLR 105  
DB 61 YIPKQKXSFLQNPQTSICFSESIPTPSNRRETOOKSNLELRISLLLIQSWLEFVQFLR 120  
QY 106 SVFANSIYVGASDSNVYDLKDLKEGIQTLMGRLDGSPTGQIFKQYSKFDJNSHND 165  
|||||

Db 121 SVFANSIVYGASDSNVYDLKDLBEGIQTLMGRLDGSPTGQIFKQYSKFDNNSHND 180  
166 ALKNYGLLYCFRDMKVEFLRIVQCRSVGSGCF 202  
181 ALKNYGLLYCFRDMKVEFLRIVQCRSVGSGCF 217

## RESULT 6

US-08-759-628-11  
Sequence 11, Application US/08759628  
Patent No. 6225446

## GENERAL INFORMATION:

APPLICANT: Altman, Scott W.  
APPLICANT: Rock, Fernando L.  
APPLICANT: Bazan, J. Fernando  
APPLICANT: Kastelein, Robert A.  
TITLE OF INVENTION: MUTATIONAL VARIANTS OF MAMMALIAN PROTEINS  
NUMBER OF SEQUENCES: 11  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: DNAX Research Institute  
STREET: 901 California Avenue  
CITY: Palo Alto  
STATE: California  
COUNTRY: USA  
ZIP: 94304-1104

## COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/759,628  
FILING DATE: 05-DEC-1996  
CLASSIFICATION: 435

## PRIOR APPLICATION DATA:

PRIOR APPLICATION NUMBER: US 60/008,574  
FILING DATE: 06-DEC-1995  
ATTORNEY/AGENT INFORMATION:  
NAME: Ching, Edwin P.

REGISTRATION NUMBER: 34,090  
REFERENCE/DOCKET NUMBER: DX05520  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 415-852-9196  
TELEFAX: 415-496-1200

## INFORMATION FOR SEQ ID NO: 11:

SEQUENCE CHARACTERISTICS:

LENGTH: 217 amino acids

TYPE: amino acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: protein

FEATURE:

NAME/KEY: Peptide

LOCATION: 32..53

FEATURE:

NAME/KEY: Peptide

LOCATION: 94..115

FEATURE:

NAME/KEY: Peptide

LOCATION: 133..153

FEATURE:

NAME/KEY: Peptide

LOCATION: 192..210

OTHER INFORMATION:

OTHER INFORMATION: depicted in Figure 1"

US-08-759-628-11

Query Match 97.9%; Score 1024.5; DB 3; Length 217;

Best Local Similarity 92.6%; Pred. No. 7.2e-108; Indels 15; Gaps 1;

Matches 201; Conservative 0; Mismatches 1; Indels 15; Gaps 1;

1 MATGSRISLLAFGLICLFWLOEGSAFPTIPLSRFLPDNMSLRARHLHQLAFDTYOEF--- 57

Db 1 MATGSRISLLAFGLICLFWLOEGSAFPTIPLSRFLPDNMSLRARHLHQLAFDTYOEF 60  
58 -----NPQTSICFSESIPTPSNRETOQKSNLELRISLLIQSWLEPVQFLR 105  
61 YIPKQKSFLONPQTSICFSESIPTPSNRETOQKSNLELRISLLIQSWLEPVQFLR 120  
106 SVFANSIVYGASDSNVYDLKDLBEGIQTLMGRLDGSPTGQIFKQYSKFDNNSHND 165  
121 SVFANSIVYGASDSNVYDLKDLBEGIQTLMGRLDGSPTGQIFKQYSKFDNNSHND 180

166 ALKNYGLLYCFRDMKVEFLRIVQCRSVGSGCF 202  
181 ALKNYGLLYCFRDMKVEFLRIVQCRSVGSGCF 217

## RESULT 7

US-09-284-878-1  
Sequence 1, Application US/09284878  
Patent No. 6342375

## GENERAL INFORMATION:

APPLICANT: Olazaran, Martha Guerrero

APPLICANT: Salgado, Jose Maria Viader

TITLE OF INVENTION: Genetically Modified Methylotrophic P. pastoris Yeast for the

TITLE OF INVENTION: Production and Secretion of the Human Growth Hormone

FILE REFERENCE: 1829, 0010000

CURRENT APPLICATION NUMBER: US/09/284,878

CURRENT FILING DATE: 1999-07-21

PRIOR APPLICATION NUMBER: PCT/MK97/00033

PRIOR FILING DATE: 1997-10-24

NUMBER OF SEQ ID NOS: 9

SOFTWARE: Patentin Ver. 2.1

SEQ ID NO 1

LENGTH: 217

TYPE: PRT

ORGANISM: Homo sapiens

US-09-284-878-1

Query Match 97.9%; Score 1024.5; DB 3; Length 217;

Best Local Similarity 92.6%; Pred. No. 7.2e-108; Indels 15; Gaps 1;

Matches 201; Conservative 0; Mismatches 1; Indels 15; Gaps 1;

1 MATGSRISLLAFGLICLFWLOEGSAFPTIPLSRFLPDNMSLRARHLHQLAFDTYOEF--- 57

1 MATGSRISLLAFGLICLFWLOEGSAFPTIPLSRFLPDNMSLRARHLHQLAFDTYOEF 60

58 -----NPQTSICFSESIPTPSNRETOQKSNLELRISLLIQSWLEPVQFLR 105

61 YIPKQKSFLONPQTSICFSESIPTPSNRETOQKSNLELRISLLIQSWLEPVQFLR 120

106 SVFANSIVYGASDSNVYDLKDLBEGIQTLMGRLDGSPTGQIFKQYSKFDNNSHND 165

121 SVFANSIVYGASDSNVYDLKDLBEGIQTLMGRLDGSPTGQIFKQYSKFDNNSHND 180

166 ALKNYGLLYCFRDMKVEFLRIVQCRSVGSGCF 202

181 ALKNYGLLYCFRDMKVEFLRIVQCRSVGSGCF 217

## RESULT 8

US-09-929-918-9  
Sequence 9, Application US/09929918  
Patent No. 6773899

## GENERAL INFORMATION:

APPLICANT: Kordyum, Vitaliy A.

APPLICANT: Chernykh, Svetlana I.

APPLICANT: Slavchenko, Iryna Yu.

APPLICANT: Vozianov, Oleksandr

TITLE OF INVENTION: PHAGE-DEPENDENT SUPER PRODUCTION OF

TITLE OF INVENTION: BIOLOGICALLY ACTIVE PROTEIN AND PEPTIDES

FILE REFERENCE: PHAGE.006A

CURRENT APPLICATION NUMBER: US/09/929,918



CURRENT FILING DATE: 2001-08-15  
PRIOR APPLICATION NUMBER: 09/318,288  
PRIOR FILING DATE: 1999-05-25  
NUMBER OF SEQ ID NOS: 11  
SOFTWARE: FASTSEQ for Windows Version 4.0  
SEQ ID NO 9  
LENGTH: 217  
TYPE: PRT  
ORGANISM: Homo sapiens  
US-09-929-918-9

Query Match  
Best Local Similarity 97.1%; Score 1024.5; DB 4; Length 217;  
Matches 201; Conservative 0; Mismatches 1; Indels 15; Gaps 1;

QY 1 MATGSRISLLAFGLCLPWLQEGSAFPTTIPLSRLFDNASLRARHLQADTYQEF--- 57  
DB 1 MATGSRISLLAFGLCLPWLQEGSAFPTTIPLSRLFDNASLRARHLQADTYQEFEEA 60  
QY 58 -----NQTSLCFSESIPTPSNREETOQKSNLELRISLLIOSWLEPVOFLR 105  
DB 61 YIPKQKYSFLQNPQTSLCFSESIPTPSNREETOQKSNLELRISLLIOSWLEPVOFLR 120  
QY 106 SVFANSIVYGASNSNYVDLKDLEEGIQTLMGRLDGSPTTGOIFKQYKSKPTNSHND 165  
DB 121 SVFANSIVYGASNSNYVDLKDLEEGIQTLMGRLDGSPTTGOIFKQYKSKPTNSHND 180  
QY 166 ALIKNYGLYCFRKMDKXETFLRIYQCRSVSGSCGF 202  
DB 181 ALIKNYGLYCFRKMDKXETFLRIYQCRSVSGSCGF 217

## RESULT 9

US-08-187-756C-4  
Sequence 4, Application US/08187756C  
Patent No. 5597709  
GENERAL INFORMATION:  
APPLICANT: ROSEN, ET AL.  
TITLE OF INVENTION: Human Growth Hormone  
NUMBER OF SEQUENCES: 7  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: CARELLA, BYRNE, BAIN, GILFILLAN,  
STREET: 6 BECKER FARM ROAD  
CITY: ROSELAND  
STATE: NEW JERSEY  
COUNTRY: USA  
ZIP: 07068  
COMPUTER READABLE FORM:  
MEDIUM TYPE: 3.5 INCH DISKETTE  
COMPUTER: IBM PS/2  
OPERATING SYSTEM: MS-DOS  
SOFTWARE: WORD PERFECT 5.1  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/187,756C  
FILING DATE: January 27, 1994  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER:  
FILING DATE:  
ATTORNEY/AGENT INFORMATION:  
NAME: FERRARO, GREGORY D.  
REGISTRATION NUMBER: 36,134  
REFERENCE/DOCKET NUMBER: 325800-55  
TELEPHONE: 201-994-1700  
TELEFAX: 201-994-1744  
INFORMATION FOR SEQ ID NO: 4:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 217 AMINO ACIDS  
TYPE: AMINO ACID  
STRANDEDNESS:  
TOPOLOGY: LINEAR

MOLECULE TYPE: PROTEIN  
US-08-187-756C-4

Query Match  
Best Local Similarity 97.1%; Score 1016.5; DB 1; Length 217;  
Matches 200; Conservative 0; Mismatches 2; Indels 15; Gaps 1;

QY 1 MATGSRISLLAFGLCLPWLQEGSAFPTTIPLSRLFDNASLRARHLQADTYQEF--- 57  
DB 1 MAAGSRISLLAFGLCLPWLQEGSAFPTTIPLSRLFDNASLRARHLQADTYQEFEEA 60  
QY 58 -----NQTSLCFSESIPTPSNREETOQKSNLELRISLLIOSWLEPVOFLR 105  
DB 61 YIPKQKYSFLQNPQTSLCFSESIPTPSNREETOQKSNLELRISLLIOSWLEPVOFLR 120  
QY 106 SVFANSIVYGASNSNYVDLKDLEEGIQTLMGRLDGSPTTGOIFKQYKSKPTNSHND 165  
DB 121 SVFANSIVYGASNSNYVDLKDLEEGIQTLMGRLDGSPTTGOIFKQYKSKPTNSHND 180  
QY 166 ALIKNYGLYCFRKMDKXETFLRIYQCRSVSGSCGF 202  
DB 181 ALIKNYGLYCFRKMDKXETFLRIYQCRSVSGSCGF 217

## RESULT 10

US-08-710-324A-4  
Sequence 4, Application US/08710324A  
Patent No. 5962411  
GENERAL INFORMATION:  
APPLICANT: ROSEN, et al.  
TITLE OF INVENTION: Human Growth Factor  
NUMBER OF SEQUENCES: 7  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Human Genome Sciences, Inc.  
STREET: 9410 Key West Avenue  
CITY: Rockville  
STATE: MD  
COUNTRY: USA  
ZIP: 20850  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/710,324A  
FILING DATE: 16-SEP-1996  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/187,756  
FILING DATE: 27-JAN-1994  
ATTORNEY/AGENT INFORMATION:  
NAME: Brookes, A. Anders  
REGISTRATION NUMBER: 36,373  
REFERENCE/DOCKET NUMBER: PF104D1.SXB  
TELEPHONE: 301-309-8504  
TELEFAX: 301-309-8439  
INFORMATION FOR SEQ ID NO: 4:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 217 AMINO ACIDS  
TYPE: AMINO ACID  
STRANDEDNESS:  
TOPOLOGY: LINEAR  
MOLECULE TYPE: PROTEIN  
US-08-710-324A-4

Query Match  
Best Local Similarity 97.1%; Score 1016.5; DB 2; Length 217;  
Matches 200; Conservative 0; Mismatches 2; Indels 15; Gaps 1;

QY 1 MATGSRISLLAFGLCLPWLQEGSAFPTTIPLSRLFDNASLRARHLQADTYQEF--- 57  
DB 1 MATGSRISLLAFGLCLPWLQEGSAFPTTIPLSRLFDNASLRARHLQADTYQEFEEA 60  
QY 58 -----NQTSLCFSESIPTPSNREETOQKSNLELRISLLIOSWLEPVOFLR 105  
DB 61 YIPKQKYSFLQNPQTSLCFSESIPTPSNREETOQKSNLELRISLLIOSWLEPVOFLR 120  
QY 106 SVFANSIVYGASNSNYVDLKDLEEGIQTLMGRLDGSPTTGOIFKQYKSKPTNSHND 165  
DB 121 SVFANSIVYGASNSNYVDLKDLEEGIQTLMGRLDGSPTTGOIFKQYKSKPTNSHND 180  
QY 166 ALIKNYGLYCFRKMDKXETFLRIYQCRSVSGSCGF 202  
DB 181 ALIKNYGLYCFRKMDKXETFLRIYQCRSVSGSCGF 217

Db 1 MAAGSRTSLLAFAGLLCTLSWLOEGSAFPTIPLSRLEFDNASLRARHLHQAFLPTTQEFEEA 60  
QY 58 -----NPTSLCFSESIPTPSNREETOQKSNLELRISLLIQLSWLEPVQFLR 105  
Db 61 YIPKQKYSFLONPQTSICFSESIPTPSNREETOQKSNLELRISLLIQLSWLEPVQFLR 120  
QY 106 SVFANSIYVGASDSNVYDLKDLKEGIQTLMGRLDEGSPRTGOIFKQYTSKFDTNSHND 165  
Db 121 SVFANSIYVGASDSNVYDLKDLKEGIQTLMGRLDEGSPRTGOIFKQYTSKFDTNSHND 180  
QY 166 ALKNYGLLYCFRKMDKXETFLRIYQCRSVESGCGF 202  
Db 181 ALKNYGLLYCFRKMDKXETFLRIYQCRSVESGCGF 217  
RESULT 11  
US-09-411-657-4  
Sequence 4, Application US/09411657  
Patent No. 6566328  
GENERAL INFORMATION:  
APPLICANT: ROSEN, et al.  
TITLE OF INVENTION: Human Growth Factor  
NUMBER OF SEQUENCES: 7  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Human Genome Sciences, Inc.  
STREET: 9410 Key West Avenue  
CITY: Rockville  
STATE: MD  
COUNTRY: USA  
ZIP: 20850  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/411,657  
FILING DATE:  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/710,324  
FILING DATE:  
ATTORNEY/AGENT INFORMATION:  
NAME: Brookes, A. Anders  
REGISTRATION NUMBER: 36,373  
REFERENCE/DOCKET NUMBER: PF104D1.SKB  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 301-309-8504  
TELEFAX: 301-309-8439  
INFORMATION FOR SEQ ID NO: 4:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 217 AMINO ACIDS  
TYPE: AMINO ACID  
STRANDEDNESS:  
TOPOLOGY: LINEAR  
MOLECULE TYPE: PROTEIN  
US-09-411-657-4  
Query Match 97.1%; Score 1016.5; DB 4; Length 217;  
Best Local Similarity 92.2%; Pred. No. 5,8e-107;  
Matches 200; Conservative 0; Mismatches 2; Indels 15; Gaps 1;  
QY 1 MATGSRISLLAFAGLLCTLSWLOEGSAFPTIPLSRLEFDNASLRARHLHQAFLPTTQEFEEA 57  
Db 1 MATGSRISLLAFAGLLCTLSWLOEGSAFPTIPLSRLEFDNASLRARHLHQAFLPTTQEFEEA 60  
QY 58 -----NPTSLCFSESIPTPSNREETOQKSNLELRISLLIQLSWLEPVQFLR 105  
Db 61 YIPKQKYSFLONPQTSICFSESIPTPSNREETOQKSNLELRISLLIQLSWLEPVQFLR 120  
QY 106 SVFANSIYVGASDSNVYDLKDLKEGIQTLMGRLDEGSPRTGOIFKQYTSKFDTNSHND 165  
Db 121 SVFANSIYVGASDSNVYDLKDLKEGIQTLMGRLDEGSPRTGOIFKQYTSKFDTNSHND 180

QY 166 ALKNYGLLYCFRKMDKXETFLRIYQCRSVESGCGF 202  
Db 181 ALKNYGLLYCFRKMDKXETFLRIYQCRSVESGCGF 217  
RESULT 12  
US-08-187-756C-5  
Sequence 5, Application US/08187756C  
Patent No. 5597709  
GENERAL INFORMATION:  
APPLICANT: ROSEN, ET AL.  
TITLE OF INVENTION: Human Growth Hormone  
NUMBER OF SEQUENCES: 7  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: CARELLA, BYRNE, BAIN, GILFILLAN,  
ADDRESSEE: CECCHI, STEWART & OLSTEIN  
STREET: 6 BECKER FARM ROAD  
CITY: ROSELAND  
STATE: NEW JERSEY  
COUNTRY: USA  
ZIP: 07068  
COMPUTER READABLE FORM:  
MEDIUM TYPE: 3.5 INCH DISKETTE  
COMPUTER: IBM PS/2  
OPERATING SYSTEM: MS-DOS  
SOFTWARE: WORD PERFECT 5.1  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/187,756C  
FILING DATE: January 27, 1994  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER:  
FILING DATE:  
ATTORNEY/AGENT INFORMATION:  
NAME: FERRARO, GREGORY D.  
REGISTRATION NUMBER: 36,134  
REFERENCE/DOCKET NUMBER: 325800-55  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 201-994-1700  
TELEFAX: 201-994-1744  
INFORMATION FOR SEQ ID NO: 5:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 198 AMINO ACIDS  
TYPE: AMINO ACID  
STRANDEDNESS:  
TOPOLOGY: LINEAR  
MOLECULE TYPE: PROTEIN  
US-08-187-756C-5  
Query Match 95.4%; Score 999; DB 1; Length 198;  
Best Local Similarity 97.0%; Pred. No. 4.9e-105;  
Matches 196; Conservative 0; Mismatches 2; Indels 4; Gaps 1;  
QY 1 MATGSRISLLAFAGLLCTLSWLOEGSAFPTIPLSRLEFDNASLRARHLHQAFLPTTQEFEEA 57  
Db 1 MATGSRISLLAFAGLLCTLSWLOEGSAFPTIPLSRLEFDNASLRARHLHQAFLPTTQEFEEA 60  
QY 61 TSLCFSESIPTPSNREETOQKSNLELRISLLIQLSWLEPVQFLRSVFANSIYVGASDSN 116  
Db 58 -SLCFSESIPTPSNREETOQKSNLELRISLLIQLSWLEPVQFLRSVFANSIYVGASDSN 120  
QY 121 VYDLKDLKEGIQTLMGRLDEGSPRTGOIFKQYTSKFDTNSHNDALLKNYGLLYCFRFD 180  
Db 117 VYDLKDLKEGIQTLMGRLDEGSPRTGOIFKQYTSKFDTNSHNDALLKNYGLLYCFRFD 176  
QY 181 MDKXETFLRIYQCRSVESGCGF 202  
Db 177 MDKXETFLRIYQCRSVESGCGF 198  
RESULT 13  
US-08-710-324A-5

Sequence 5, Application US/08710324A  
Patent No. 5862411  
GENERAL INFORMATION:  
APPLICANT: Rosen, et al.  
TITLE OF INVENTION: Human Growth Factor  
NUMBER OF SEQUENCES: 7  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Human Genome Sciences, Inc.  
STREET: 9410 Key West Avenue  
CITY: Rockville  
STATE: MD  
COUNTRY: USA  
ZIP: 20850  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent in Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/710,324A  
FILING DATE: 16-SEP-1996  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/187,756  
FILING DATE: 27-JAN-1994  
ATTORNEY/AGENT INFORMATION:  
NAME: Brookes, A. Anders  
REGISTRATION NUMBER: 36,373  
REFERENCE/DOCKET NUMBER: PF104D1.SKB  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 301-309-8504  
TELEFAX: 301-309-8439  
INFORMATION FOR SEQ ID NO: 5:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 198 AMINO ACIDS  
TYPE: AMINO ACID  
STRANDEDNESS:  
TOPOLOGY: LINEAR  
MOLECULE TYPE: PROTEIN  
US-08-710-324A-5

Query Match 95.4%; Score 999; DB 2; Length 198;  
Best Local Similarity 97.0%; Pred. No. 4.9e-105;  
Matches 196; Conservative 0; Mismatches 2; Indels 4; Gaps 1;

QY 1 MATGSRSLAFLGCLPMTQEGSAFPTTIPLSRLFDNASLRARHLQALADTYOEFNPQ 60  
DB 1 MAAGSRSLAFLGCLPMTQEGSAFPTTIPLSRLFDNASLRARHLQALADTYOEFNPQ 57  
QY 61 TSLCFSESIPTPSRRETOOKSNLELRISILLIQSWLEPVQFLRSVFANSVLYGASDSN 120  
DB 58 -SLCFSESIPTPSRRETOOKSNLELRISILLIQSWLEPVQFLRSVFANSVLYGASDSN 116  
QY 121 VYDLKDLREGIQTLMGRLEDGSPRTGQIFKQYKSKEDTNSHNDALLKNYGLYCPRKD 180  
DB 117 VYDLKDLREGIQTLMGRLEDGSPRTGQIFKQYKSKEDTNSHNDALLKNYGLYCPRKD 176  
QY 181 MDKVEFLRIVQCRSVGSGCF 202  
DB 177 MDKVEFLRIVQCRSVGSGCF 198

RESULT 14  
US-09-411-657-5  
Sequence 5, Application US/09411657  
Patent No. 6566328  
GENERAL INFORMATION:  
APPLICANT: Rosen, et al.  
TITLE OF INVENTION: Human Growth Factor  
NUMBER OF SEQUENCES: 7  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Human Genome Sciences, Inc.  
STREET: 9410 Key West Avenue

CITY: Rockville  
STATE: MD  
COUNTRY: USA  
ZIP: 20850  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent in Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/411,657  
FILING DATE:  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/710,324  
FILING DATE:  
ATTORNEY/AGENT INFORMATION:  
NAME: Brookes, A. Anders  
REGISTRATION NUMBER: 36,373  
REFERENCE/DOCKET NUMBER: PF104D1.SKB  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 301-309-8504  
TELEFAX: 301-309-8439  
INFORMATION FOR SEQ ID NO: 5:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 198 AMINO ACIDS  
TYPE: AMINO ACID  
STRANDEDNESS:  
TOPOLOGY: LINEAR  
MOLECULE TYPE: PROTEIN  
US-09-411-657-5

Query Match 95.4%; Score 999; DB 4; Length 198;  
Best Local Similarity 97.0%; Pred. No. 4.9e-105;  
Matches 196; Conservative 0; Mismatches 2; Indels 4; Gaps 1;

QY 1 MATGSRSLAFLGCLPMTQEGSAFPTTIPLSRLFDNASLRARHLQALADTYOEFNPQ 60  
DB 1 MAAGSRSLAFLGCLPMTQEGSAFPTTIPLSRLFDNASLRARHLQALADTYOEFNPQ 57  
QY 61 TSLCFSESIPTPSRRETOOKSNLELRISILLIQSWLEPVQFLRSVFANSVLYGASDSN 120  
DB 58 -SLCFSESIPTPSRRETOOKSNLELRISILLIQSWLEPVQFLRSVFANSVLYGASDSN 116  
QY 121 VYDLKDLREGIQTLMGRLEDGSPRTGQIFKQYKSKEDTNSHNDALLKNYGLYCPRKD 180  
DB 117 VYDLKDLREGIQTLMGRLEDGSPRTGQIFKQYKSKEDTNSHNDALLKNYGLYCPRKD 176  
QY 181 MDKVEFLRIVQCRSVGSGCF 202  
DB 177 MDKVEFLRIVQCRSVGSGCF 198

RESULT 15  
US-08-784-582-73  
Sequence 73, Application US/08784582  
Patent No. 6110707  
GENERAL INFORMATION:  
APPLICANT: Newgard, Christopher B.  
APPLICANT: Halban, Philippe A.  
APPLICANT: No. 6110707mington, Karl D.  
APPLICANT: Clark, Samuel A.  
APPLICANT: Thigpen, Anice B.  
APPLICANT: Quade, Christian  
APPLICANT: Kruse, Fred  
APPLICANT: McGarity, Dennis  
TITLE OF INVENTION: RECOMBINANT EXPRESSION OF PROTEINS FROM  
NUMBER OF SEQUENCES: 79  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Arnold, White & Durkee  
STREET: P.O. Box 4433  
CITY: Houston

STATE: Texas  
COUNTRY: USA  
ZIP: 77210  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/784,582  
FILING DATE: Concurrently Herewith  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 60/028,427  
FILING DATE: 15-OCT-1996  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 08/589,028  
FILING DATE: 19-JAN-1996  
ATTORNEY/AGENT INFORMATION:  
NAME: Highlander, Steven L.  
REGISTRATION NUMBER: 37,642  
REFERENCE/DOCKET NUMBER: UTSD:514  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 512/418-3000  
TELEFAX: 512/474-7577  
INFORMATION FOR SEQ ID NO: 73:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 360 amino acids  
TYPE: amino acid  
STRANDEDNESS:  
TOPOLOGY: linear  
US-08-784-582-73

Query Match 88.5%; Score 926.5; DB 3; Length 360;  
Best Local Similarity 87.6%; Pred. No. 2e-96;  
Matches 184; Conservative 4; Mismatches 7; Indels 15; Gaps 1;

QY 1 MATGSRISLLAFGLICLPWLEQGSAPFTIPLSRLLFDNASTRAHRLHQLAFDTYQEF--- 57  
DB 1 MATGSRISLLAFGLICLPWLEQGSAPFTIPLSRLLFDNASTRAHRLHQLAFDTYQEF 60  
QY 58 -----NPQTSICFSESIPTPSNREETOQKSNLELRISLLLIQSWLEPVQFLR 105  
DB 61 YIPKQKYSFLNPQTSICFSESIPTPSNREETOQKSNLELRISLLLIQSWLEPVQFLR 120  
QY 106 SYFANSIVYGAGDSNVYDLIKDLBEGIQTLMGRLDEGSPRTGQIFKQTSKFDTNSHND 165  
DB 121 SYFANSIVYGAGDSNVYDLIKDLBEGIQTLMGRLDEGSPRTGQIFKQTSKFDTNSHND 180  
QY 166 ALKXNYGLYCFKMDKVEFLRIVOCRS 195  
DB 181 ALKXNYGLYCFKMDKMQRSLODTREKS 210

Search completed: February 6, 2005, 13:06:01  
Job time : 44 secs

GenCore version 5.1.6  
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OM nucleic - protein search, using frame\_plus\_n2p model

Run on: February 6, 2005, 13:05:19 ; Search time 129.5 Seconds

(without alignments)  
3637.638 Million cell updates/sec

Title: US-09-856-796B-1

Perfect score: 1112

Sequence: 1 atggctacagctcccgagc.....agggcagctgtgcttctag 609

Scoring table:

BLOSUM62  
Xgapop 10.0 , Xgapext 0.5  
Ygapop 10.0 , Ygapext 0.5  
Fgapop 6.0 , Fgapext 7.0  
Delop 6.0 , Delext 7.0

Searched: 2105692 seqs, 386760381 residues

Total number of hits satisfying chosen parameters: 4211384

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%

Listing first 45 summaries

Command line parameters:  
-MODEL=frame+ n2p.model -DEV=x1p  
-O/cgmr2.1/USPRO.spool\_p/US09856796/runat\_06022005\_124619\_3477/bpp\_query.fasta\_1.775  
-DB=A Geneseq.16Dec04 -OPMT=fastan -SUFFIX=rag -MINMATCH=0.1 -LOOPCL=0  
-LOOEXT=0 -UNITS=bits -START=1 -END=-1 -MATRIX=blonum62 -TRANS=human40.cdi  
-LIST=45 -DOCALL=200 -THR SCORE=pct -THR MAX=100 -THR MIN=0 -ALIGN=15  
-MODE=LOCAL -OUTFMT=pco -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=2000000000  
-USER=US09856796 @CGM 1.1 224 @runat\_06022005\_124619\_3477 -NCPU=6 -ICPU=3  
-NO MMAP -LARGEOUTERY -NEG\_SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG  
-DEV TIMEOUT=120 -MARK TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6  
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database :

1: Geneseq.16Dec04:\*  
2: Geneseqp19808:\*  
3: Geneseqp19908:\*  
4: Geneseqp20008:\*  
5: Geneseqp20028:\*  
6: Geneseqp20038:\*  
7: Geneseqp20038s:\*  
8: Geneseqp20048s:\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1047	94.2	202	3	AA93637
2	1042	93.7	202	8	ADQ39295
3	1042	93.7	202	8	ADQ39284
4	1029.5	92.6	217	2	AA860516
5	1029.5	92.6	217	5	AAU11731
6	1029.5	92.6	217	5	AAU11719
7	1029.5	92.6	217	5	AAU11720
8	1029.5	92.6	217	5	AAU11730
9	1029.5	92.6	217	5	ABG60633
10	1028.5	92.5	217	5	AAU11742

11	1028.5	92.5	217	5	AAU11726	AAU11726 Growth ho
12	1026.5	92.3	217	5	AAU11746	AAU11746 Growth ho
13	1025.5	92.2	217	5	AAU11747	AAU11747 Growth ho
14	1025.5	92.2	217	5	AAU11735	AAU11735 Growth ho
15	1025.5	92.2	217	5	AAU11744	AAU11744 Growth ho
16	1025.5	92.2	217	5	AAU11722	AAU11722 Growth ho
17	1025.5	92.2	217	5	AAU11728	AAU11728 Growth ho
18	1024.5	92.1	217	3	AA805169	AA805169 Human gro
19	1024.5	92.1	217	2	AA826769	AA826769 Secretory
20	1024.5	92.1	217	4	AA017479	AA017479 Human gro
21	1024.5	92.1	217	4	AA835428	AA835428 Secretory
22	1024.5	92.1	217	5	AAU11741	AAU11741 Growth ho
23	1024.5	92.1	217	5	AAU11727	AAU11727 Growth ho
24	1024.5	92.1	217	5	AAU11748	AAU11748 Growth ho
25	1024.5	92.1	217	5	AAU11736	AAU11736 Growth ho
26	1024.5	92.1	217	5	AAU11750	AAU11750 Growth ho
27	1024.5	92.1	217	5	AAU11743	AAU11743 Growth ho
28	1024.5	92.1	217	5	AAU11740	AAU11740 Growth ho
29	1024.5	92.1	217	5	AAU11721	AAU11721 Growth ho
30	1024.5	92.1	217	5	AA019993	AA019993 Protein o
31	1024.5	92.1	217	6	ABR42662	ABr42662 Human gro
32	1024.5	92.1	217	7	AA029552	AA029552 Human gro
33	1024.5	92.1	217	7	ADG61299	ADG61299 Human gro
34	1024.5	92.1	217	7	ADG17923	ADG17923 Protein o
35	1024.5	92.1	217	8	ADP19729	ADP19729 Human gro
36	1024.5	92.1	217	8	ADQ39285	ADQ39285 Human gro
37	1024.5	92.1	407	4	AA849195	AA849195 Human myo
38	1023.5	92.0	217	5	AAU11725	AAU11725 Growth ho
39	1023.5	92.0	217	5	AAU11734	AAU11734 Growth ho
40	1022.5	92.0	217	5	AAU11738	AAU11738 Growth ho
41	1022.5	92.0	217	5	AAU11739	AAU11739 Growth ho
42	1022.5	92.0	217	5	AAU11723	AAU11723 Growth ho
43	1022.5	92.0	217	5	AAU11724	AAU11724 Growth ho
44	1022.5	92.0	217	5	AAU11745	AAU11745 Growth ho
45	1022.5	92.0	217	5	AAU11901	AAU11901 Growth ho

## ALIGNMENTS

RESULT 1  
AA93637  
ID AA93637 standard; protein; 202 AA.

AC	AA93637;	
XX		
DT	25-SEP-2000 (first entry)	
XX		
DE	Amino acid sequence of a human growth hormone (hGH).	
XX		
KW	Human; growth hormone; hGH; inhibitor; nuclear factor-kappaB; NF-kappaB;	
KW	multi-drug resistance gene; malignant hemopathy; solid tumour;	
KW	malignant blood disease; leukaemia; lymphoma; solid cancer.	
XX		
OS	Homo sapiens.	
XX		
PN	WO200030587-A2.	
XX		
PD	02-JUN-2000.	
XX		
PF	24-NOV-1999; 99MO-FR002897.	
XX		
PR	25-NOV-1998; 98FR-00014858.	
XX		
XX	(CNRS ) CENT NAT RECH SCI.	
XX		
PI	Hirsch F, Haeflner A;	
XX		
DR	WPI; 2000-399901/34.	
XX		
DR	N-PSDB; AAA46696.	
XX		
PT	Treatment of hematological or solid tumors using an inhibitor of the	
PT	activation of nuclear factor-kappaB, particularly to prevent development	
PT	of resistance to chemotherapeutics.	

Score:	1042.00	Matches:	201
Percent Similarity:	99.50%	Conservative:	0
Best Local Similarity:	99.50%	Mismatches:	1
Query Match:	99.71%	Indels:	0
DB:	8	Gaps:	0



Db ValGlnPheLeuAsgSerValPheHlaAsnSerLeuValTyrGlyAlaSerAspSerAsn 120  
 101 ValGlnPheLeuAsgSerValPheHlaAsnSerLeuValTyrGlyAlaSerAspSerAsn 120  
 361 GTCTATGACCTCTTAAAGACCTTAAGCAAGGCAAGCTGAATGGGAGGCTGGA 420  
 121 ValTyrAspLeuLeuValAspLeuGluGluGlyIleGlnThrLeuMetGlyArgLeuGlu 140  
 421 GATGGCAGCCCCCGGACCTGGGAGAGATCTTCAAGCAGACCTTACAGCAAGTTGACACAAAC 480  
 141 AspGlySerProValTyrThrGlyGlnIlePheLeuGlnThrTyrSerIleAspPheAsn 160  
 481 TCACACAAAGATGAGCAGCACTACTCAAGAACTACGGGCTGCTCTACTGCTTACAGAAAGAC 540  
 161 SerHisAsnAspAspAlaLeuLeuValSerTyrGlyLeuLeuTyrCysPheArgLysAsp 180  
 541 ATGCAACAAGTGCAGACATCTCTCGCATCTGTCAGATGTCAGCCGCTCTGTGAGAGGAGCTGT 600  
 181 MetAspLysValGlnThrPheLeuArgIleValGlnCysArgSerValGluGlySerCys 200  
 601 GGCTTC 606  
 201 GlyPhe 202

## RESULT 4

AA60516 standard; protein: 217 AA.

AA60516:

25-MAR-2003 (revised)  
 22-MAR-1995 (first entry)

Human somatotropin.

Serine protease; Factor-Xa; recognition site; fusion protein cleavage;  
 protein folding; growth hormone; somatotropin; primer;

polymerase chain reaction; amplification.

Homo sapiens.

MO9418227-A2.

18-AUG-1994.

04-FEB-1994; 94MO-DK000054.

04-FEB-1993; 93DK-00000130.

05-FEB-1993; 93DK-00000139.

03-DEC-1993; 93MO-GB002492.

(DENZ-) DENZYME APS.

Thogersen HC, Holtet TL, Etzerodt M;

WPI; 1994-279681/34.

Refolding of polypeptide molecules - using a cyclic process involving  
 denaturing and renaturing conditions to produce a correctly folded prod.

Disclosure; Page 129-30; 202pp; English.

cDNA encoding human somatotropin (aa sequence given in AA60516) was PCR  
 amplified using primers given in AA071248-49. Amplified cDNA was linked  
 to a sequence encoding the Factor-Xa cleavage site (given in AA60503),  
 subcloned in vector pTH6 so that it was N-terminally linked to a  
 hexahistidine-encoding sequence and expressed in E. coli BL21. The  
 resulting fusion protein included an affinity tag (AA60513) that  
 facilitated purification on Ni2+-activated NTA-agarose. A cyclic  
 procedure was used to obtain correctly folded recombinant protein.  
 (Updated on 25-MAR-2003 to correct PN field.)

Sequence 217 AA;

Sequence 217 AA;

Alignment Scores:  
 Pred. No.: 5.28e-89 Length: 217  
 Score: 1029.50 Matches: 202  
 Percent Similarity: 93.09% Conservative: 0  
 Best Local Similarity: 93.09% Mismatches: 15  
 Query Match: 92.58% Indels: 1  
 DB: 2 Gaps: 1

US-09-856-796B-1 (1-609) x AA60516 (1-217)

QY 1 ATGGCTTACAGGCTCCGGAGAGCTCCCTGCTCTGAGCTTTGAGCTGCTGCTGCTGCTG 60  
 Db 1 MetAlaThrGlySerArgTyrThrSerLeuLeuAlaPheGlyLeuLeuValProTyr 20  
 QY 61 CTTCAGAGGGCAGTGGCTTCCCAACCAATTCCTTATCCAGGCTTTTGACAGCTAGT 120  
 Db 21 LeuGlnGluGlySerAlaPheProThrIleProLeuSerArgLeuPheAspAlaSer 40  
 QY 121 CTCCGCGCCCATCGTCTGCACCAAGCTGGCCCTTGACACCTTACAGAGATT----- 171  
 Db 41 LeuArgAlaHisArgLeuHisGlnLeuAlaPheAspThrTyrGlnGluPheGluAla 60  
 QY 172 -----AACCCCAAGACCTCCCTGTTTC 195  
 Db 61 TyrIleProLysGluGlnLysTyrSerPheLeuGlnAsnProGlnThrSerLeuValPhe 80  
 QY 196 TCAGAGCTATTCGAGACACCTCCCAAGAGGAGAGAAACAACAAGAAATCCAACTAGAG 255  
 Db 81 SerGlnSerIleProThrProSerAsnArgGluGlnThrGlnGlnLysSerAsnLeuGlu 100  
 QY 256 CTGCTCCGATCTCCCTGCTGCTCATCCAGTGTGCTGAGACCCGTCAGTCTCCAGG 315  
 Db 101 LeuLeuArgIleSerLeuLeuLeuIleGlnSerTyrPheGluProValGlnPheLeuArg 120  
 QY 316 AGTGTCTTGCCCAACAGCTGTGTACGGCGCTCTGACAGCAAGCTTATGACCTCTTA 375  
 Db 121 SerValPheAlaAsnSerLeuValTyrGlyAlaSerAspSerAsnValTyrAspLeuLeu 140  
 QY 376 AAGAGCTTAGAGAGAGGATCCAAAGCTGATGGAGGCTGAGAGATGGACCCCGG 435  
 Db 141 LysAspLeuGluGluGlyIleGlnThrLeuMetGlyArgLeuGluAspGlySerProArg 160  
 QY 436 ACTGGGAGATCTTCAAGCAGACCTACAGCAAGTTGACACAACTCAACACAGATGAC 495  
 Db 161 ThrGlyGlnIlePheLysGlnThrTyrSerLysPheAspThrAsnSerHisAsnAspAsp 180  
 QY 496 GCACTACTCAAGAACTACGGGCTGCTCTACTGCTTACAGAAAGACATGAGAGTGCAG 555  
 Db 181 AlaLeuLeuValSerAsnTyrGlyLeuLeuTyrCysAspPheArgLysAspMetAspLysValGlu 200  
 QY 556 ACATTCTCGCATCGTGCAGTGCAGTCCGCTCTGTGAGAGGACAGCTGAGCTTC 606  
 Db 201 ThrPheLeuArgIleValGlnCysArgSerValGluGlySerCysGlyPhe 217

## RESULT 5

AAU11731 standard; protein: 217 AA.

AAU11731:

12-MAR-2002 (first entry)

Growth hormone 1 gene (GH1), S69L mutant.

Growth hormone 1; GH1; osteopathic; gene therapy; protein therapy;  
 diabetes; obesity; infection; acromegaly; gigantism; sodium retention;  
 water retention; metabolic syndrome; mood disorder; sleep disorder;  
 growth hormone dysfunction; familial growth hormone deficiency;  
 short stature; pituitary storage defect; human; mutant; mutant.

Homo sapiens.

Synthetic.

Synthetic.

Synthetic.



FH Key Location/Qualifiers  
 FT Misc-difference 69 /note="Wild type Ser substituted by Leu"  
 FT XX  
 PN MO200185993-A2.  
 XX  
 XX 15-NOV-2001.  
 PD 14-MAY-2001; 2001MO-GB002126.  
 PF  
 XX  
 PR 12-MAY-2000; 2000GB-00011459.  
 PR 14-JUL-2000; 2000EP-00306004.  
 XX  
 PA (UYWA-) UNIV WALES COLLEGE OF MEDICINE.  
 XX  
 PI Cooper DN, Procter AM, Gregory J, Millar DS;  
 DR WPI; 2002-089798/12.  
 XX  
 XX  
 PT Detecting growth hormone variants (GHI), useful in screening patients for  
 PT growth hormone irregularities, comprises comparing the nucleotide  
 PT sequence of a GHI gene from a test sample with that of a standard  
 PT sequence of the human GHI.  
 XX  
 XX  
 PS Claim 18; Page; 95pp; English.  
 XX  
 CC The invention described a method of detecting variation in growth hormone  
 CC 1 (GHI), and therefore GH dysfunction in an individual. The method  
 CC comprises comparing the nucleotide sequence of GHI gene obtained from the  
 CC test sample with a standard human GHI gene sequence, in order to identify  
 CC variation (GHI variant). The method is useful in screening patients for  
 CC growth hormone irregularities or producing variant proteins for treating  
 CC irregularities, and for the early detection and appropriate clinical  
 CC management of familial GH deficiency. The GHI variants are useful in  
 CC therapeutic, diagnostic or detection method, particularly for determining  
 CC binding defects and susceptibility to a disease such as diabetes, obesity  
 CC or infection, for treating acromegaly or gigantism conditions associated  
 CC with lacticogenic, diabetogenic, lipolytic and protein anabolic effects,  
 CC conditions associated with sodium and water retention, metabolic  
 CC syndromes, mood and sleep disorders; diagnosing GH dysfunction and  
 CC determining pituitary storage defects. The GHI variants are especially  
 CC useful in gene therapy or protein therapy. The GHI or GH variant may also  
 CC be used in the preparation of a medicament, diagnostics composition or  
 CC kit, or detection kit. The method has the advantage of: expanding the  
 CC know spectrum of GHI gene mutations; evaluating the role of GHI gene  
 CC mutations in the etiology of short stature; identifying for the mode of  
 CC inheritance of novel lesions; evaluation the effects of GHI mutations on  
 CC the structure and function of the GH molecule and development of rapid  
 CC diagnostic tests for inherited GH deficiency. This sequence is a variant  
 CC of human growth hormone 1 (GHI), one of many variations of the gene  
 CC discussed in the method of the invention. Note: This sequence does not  
 CC appear in the specification but has been created from the GHI wild type  
 CC sequence (AAU11719) given in figure 6  
 XX  
 XX  
 SQ Sequence 217 AA;  
 Alignment Scores:  
 Pred. No.: 5,286-89 Length: 217  
 Score: 1029.50 Matches: 202  
 Percent Similarity: 93.09% Conservative: 0  
 Best Local Similarity: 93.09% Mismatches: 0  
 Query Match: 92.58% Indels: 15  
 DB: 5 Gaps: 1  
 US-09-856-796b-1 (1-609) x AAU11731 (1-217)  
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 DB 1 MetAlaIrnGlySerArgThrSerLeuLeuAlaPheGlyLeuLeuLeuLeuProTyr 20  
 QY 61 CTTCAGAGGAGGAGGCTTCCCAACCATTCCTTATCCAGCTTTTACACGCTACT 120  
 DB 21 LeuGlnGlnGlnGlnSerAlaPheProThrIleProLeuSerArgLeuPheAspAlaSer 40

QY 121 CTCGGGCCCCATGCTGTGACACGAGCTGGCTTTGACACCTACAGAGATT----- 171  
 DB 41 LeuAlaGlnAlaHisArgLeuHisGlnLeuAlaPheAspThrTyrGlnGlnPheGlnGlnAla 60  
 QY 172 -----AACCCCGAGACCTCCCTGCTGTTTC 195  
 DB 61 TyrIleProLeuGlnGlnIleTyrLeuPheLeuGlnAspProGlnThrSerLeuCysPhe 80  
 QY 196 TCAGAGCTTATTCGACACCTTCACACAGAGAGAAACACACAGAAATCCAACTCAGAG 255  
 DB 81 SerGlnSerIleProThrProSerAsnArgGlnGlnThrGlnGlnIleTyrSerAsnLeuGln 100  
 QY 256 CTGCTCCCGCATCTCCCTGCTGCTACATCCAGTGTGGCTGAGACCCGCTGACGTTCTCAGG 315  
 DB 101 LeuLeuAlaGlyIleSerLeuLeuLeuIleGlnIleThrIlePheGlnProValGlnPheLeuArg 120  
 QY 316 AGTGTCTTCGCGCAAGAGCTGTGTACAGGCGGCTCTGACAGCAAGCTTATGACCTCTTA 375  
 DB 121 SerValPheAlaAsnSerLeuValTyrGlyAlaSerAspSerAsnValTyrAspLeuLeu 140  
 QY 376 AAGGACCTTACAGAGAGGATCCAAAGCTGATGGGAGGCTGGAGATGGCGACCCCGCG 435  
 DB 141 LysAspLeuGlnGlnGlnGlyIleGlnThrLeuLeuTyrGlyLeuGlnAspGlySerProArg 160  
 QY 436 ACTGGGCGATCTTTCAGACAGACCTTACAGAGATTGACACAACTCACACAGATGAC 495  
 DB 161 ThrGlyGlnIlePheGlyGlnThrTyrSerIlePheAspThrAsnSerHisAsnAsp 180  
 QY 496 GCATCTACCAAGAACTACGGGCTGCTCTACTGCTTACAGAGAGCATGACAGAGGTGAG 555  
 DB 181 AlaLeuLeuLysAsnTyrGlyLeuLeuTyrCysPheArgLysAspMetAspLysValGln 200  
 QY 556 ACATTCCTGGCGCATCGGCACTGCGGCTGCTGTGAGGGCGACGTGCTTC 606  
 DB 201 ThrPheLeuAlaGlyIleValGlnCysArgSerValGlnGlySerCysGlyPhe 217  
 RESULT 6  
 AAU11719  
 ID AAU11719 standard; protein: 217 AA.  
 AC AAU11719;  
 XX  
 DT 12-MAR-2002 (first entry)  
 XX  
 DE Growth hormone 1 gene (GHI), major isoform.  
 XX  
 KW Growth hormone 1; GHI; osteopathic; gene therapy; protein therapy;  
 KW diabetes; obesity; infection; acromegaly; gigantism; sodium retention;  
 KW water retention; metabolic syndrome; mood disorder; sleep disorder;  
 KW Growth hormone dysfunction; familial growth hormone deficiency;  
 KW short stature; pituitary storage defect; human; chromosome 17q23.  
 XX  
 OS Homo sapiens.  
 OS  
 PN MO200185993-A2.  
 PD 15-NOV-2001.  
 XX  
 PF 14-MAY-2001; 2001MO-GB002126.  
 XX  
 PR 12-MAY-2000; 2000GB-00011459.  
 PR 14-JUL-2000; 2000EP-00306004.  
 XX  
 PA (UYWA-) UNIV WALES COLLEGE OF MEDICINE.  
 XX  
 PI Cooper DN, Procter AM, Gregory J, Millar DS;  
 DR WPI; 2002-089798/12.  
 DR N-PSDB; AAS18887.  
 XX  
 XX  
 PT Detecting growth hormone variants (GHI), useful in screening patients for  
 PT growth hormone irregularities, comprises comparing the nucleotide

```

1 ATGGCTACAGGCTCCCGGAGCTCCCTGCTCTGGCTTTTGGCTGCTCGCTGGCCCTGG
10
1 MetAlaThrGlySerArgInSerLeuLeuLeuAlaPheGlyLeuLeuCysLeuProTrp
20
61 CTTCAAGAGGGGCAAGTGGCTTCCCAACAATTGCCTTATCCAGGCTTTTGAACAACCTAGT
120
21 LeuGlnGlnGlnSerAlaPheProThrIleProLeuSerAlaGlnPheAspAlaSer
40
121 CTCGGGGCCCATGGCTGACACAGCTGAGCTTTGACACCTAACCAAGATT-----
171
41 LeuArgAlaHisArgLeuHisGlnLeuAlaPheAspThrTyrGlnGlnIlePheGlnGlnAla
60
172 -----AACCCGACAGCTCCCTCTGTTTC
195
61 TyrIleProLysGlnGlnIleLysTyrSerPheLeuGlnAlaAsnProGlnIleThrSerLeuCysPhe
80
196 TCAGAGCTTATTCGACACACCTCCACAGGAGGAAACACAAACAGAAATCCAACCTAGAG
255
81 SerGlnSerIleProThrProSerAsnArgGlnGlnIleThrGlnGlnIleLysSerAsnLeuGln
100
256 CTGCTCCGCATCTCTCCCTGCTGCTCAATCCAGTGTGCTGGAGCCCTGCAGTTCCCTCAG
315
101 LeuLeuArgIleSerLeuLeuLeuIleGlnSerTrpLeuGlnIleProValGlnPheLeuArg
120
316 AGTGTCTTTCGCCAACACAGCTGTGTAACGGCGCTCTGACACAGCAACGTTATGACCTCCTA
375
121 SerAlaPheAlaAsnSerLeuValTyrGlnAlaSerAspSerAsnValTyrAspLeuLeu
140
376 AAGGACCTTAGAGGAAGGCAATCCAAACGCTGATGGGGAAGCTGGAAAGATGGCAGCCCCCG
435

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.







QY 556 ACATTCCTGGCATCTGTCAGTGGCTCTGTGGAGGGCAGCTGTGGCTTC 606  
 DB 201 ThrPheLeuArgIleValGlnCysArgSerValGlnGlySerCysGlyPhe 217

## RESULT 11

ID AAU11726 standard; protein; 217 AA.

AC AAU11726;

DT 12-MAR-2002 (first entry)

XX Growth hormone 1 gene (GH1), I30V mutant.

XX Growth hormone 1; GH1, osteopathic; gene therapy; protein therapy;  
 XX diabetes; obesity; infection; acromegaly; gigantism; sodium retention;  
 KW water retention; metabolic syndrome; mood disorder; sleep disorder;  
 KW Growth hormone dysfunction; familial growth hormone deficiency;  
 XX short stature; pituitary storage defect; human; mutant; mutein.  
 XX Homo sapiens.  
 OS Synthetic.

XX Key Location/Qualifiers

XX Misc-difference 30 /note= "Wild type Ile substituted by Val"

XX MO200185993-AZ.

XX 15-NOV-2001.

XX 14-MAY-2001; 2001WO-GB002126.

XX 12-MAY-2000; 2000GB-00011459.

XX 14-JUL-2000; 2000EP-00306004.

XX (UYWA-) UNIV WALES COLLEGE OF MEDICINE.

XX Cooper DN, Procter AM, Gregory J, Millar DS;

XX WPI; 2002-089798/12.

XX Detecting growth hormone variants (GH1), useful in screening patients for  
 XX growth hormone irregularities, comprises comparing the nucleotide  
 XX sequence of a GH1 gene from a test sample with that of a standard  
 XX sequence of the human GH1.

XX Claim 18; Page; 95pp; English.

XX The invention described a method of detecting variation in growth hormone  
 XX (GH1), and therefore GH dysfunction in an individual. The method  
 XX comprises comparing the nucleotide sequence of GH1 gene obtained from the  
 XX test sample with a standard human GH1 gene sequence, in order to identify  
 XX variation (GH1 variant). The method is useful in screening patients for  
 XX growth hormone irregularities or producing variant proteins for treating  
 XX irregularities, and for the early detection and appropriate clinical  
 XX management of familial GH deficiency. The GH1 variants are useful in  
 XX therapeutic, diagnostic or detection method, particularly for determining  
 XX binding defects and susceptibility to a disease such as diabetes, obesity  
 XX or infection; for treating acromegaly or gigantism conditions associated  
 XX with lacticogenic, diabetogenic, lipolytic and protein anabolic effects,  
 XX conditions associated with sodium and water retention, metabolic  
 XX syndromes, mood and sleep disorders; diagnosing GH dysfunction and  
 XX determining pituitary storage defects. The GH1 variants are especially  
 XX useful in gene therapy or protein therapy. The GH1 or GH variant may also  
 XX be used in the preparation of a medicament, diagnostics composition or  
 XX kit, or detection kit. The method has the advantage of: expanding the  
 XX know spectrum of GH1 gene mutations; evaluating the role of GH1 gene  
 XX mutations in the etiology of short stature; identifying of the mode of  
 XX inheritance of novel lesions; evaluation the effects of GH1 mutations on  
 XX the structure and function of the GH molecule and development of rapid  
 XX diagnostic tests for inherited GH deficiency. This sequence is a variant

CC of human growth hormone 1 (GH1), one of many variations of the gene  
 CC discussed in the method of the invention. Note: This sequence does not  
 CC appear in the specification but has been created from the GH1 wild type  
 CC sequence (AAU11719) given in figure 6

XX SQ Sequence 217 AA;

Alignment Scores:  
 Pred. No.: 6,58e-89 Length: 217  
 Score: 1028.50 Matches: 201  
 Percent Similarity: 93.09% Conservative: 1  
 Best Local Similarity: 92.63% Mismatches: 0  
 Query Match: 92.49% Indels: 15  
 DB: Gaps: 1

US-09-856-796b-1 (1-609) x AAU11726 (1-217)

QY 1 ATGAGCTACAGCTCCCGAGACGTCCTGCTCTGCTTTGGCTGCTGCTGCTGCTG 60  
 DB 1 MetAlaThrIleSerArgThrSerLeuLeuAlaPheGlyLeuLeuCysLeuProTyr 20  
 QY 61 CTTCAGAGGGGAGTGGCTTCCCAACCTATCCCTTATCCAGGCTTTTGAACAGCTAGT 120  
 DB 21 LeuGlnGlnGlySerAlaPheProThrValProLeuSerArgLeuPheAspAlaSer 40  
 QY 121 CTCCGCGCCCATGCTCTGCAACGCTGCGCTTGACACTACAGAGATT----- 171  
 DB 41 LeuArgAlaHisArgLeuHisGlnLeuAlaPheAspThrTyrGlnGlnPheGlnGlnAla 60  
 QY 172 -----AACCCCGACCTCCCTGTTTC 195  
 DB 61 TyrIleProLysGlnGlnLysTyrSerPheLeuGlnAsnProGlnThrSerLeuCyPhe 80  
 QY 196 TCAGAGTCTATTCGACACCTCCCAACAGGAGGAGAAACACACAAATCCAACTAGAG 255  
 DB 81 SerGlnSerIleProThrProSerAsnArgGlnGlnThrGlnGlnLysSerAsnLeuGln 100  
 QY 256 CTGCTCCGCATCTCCCTGCTGCTCAATCCAGTCGTCGAGGCCCTGCACTTCTCAGG 315  
 DB 101 LeuLeuArgIleSerLeuLeuLeuGlnSerTrpLeuGlnProValGlnPheLeuArg 120  
 QY 316 AGTGTCTTCGCGCAACAGCTGTCGAGGCGCTCTGACAGCAAGTCTATGACTCTCTA 375  
 DB 121 SerValPheAlaAsnSerLeuValTyrGlnAlaSerAspSerAsnValTyrAspLeuLeu 140  
 QY 376 AAGAGCTTACAGAGGAGGATCCAAAGCTGATGGAGGAGCTGGAAGATGAGACCCCGCG 435  
 DB 141 LysAspLeuGlnGlnGlyIleGlnThrLeuMetGlyArgLeuGlnAspGlySerProArg 160  
 QY 436 ACTGGGAGATCTTCAAGAGACCTTACAGCAAGTTGACACAACTCACACAGATGAC 495  
 DB 161 ThrGlyGlnIlePheIleGlnThrTyrSerLysPheAspThrAsnSerHisAsnAsp 180  
 QY 496 GCACTACTCAGAACTACAGGCGCTGCTCTACCTTACAGAAAGACATGAGAGGTCGAG 555  
 DB 181 AlaLeuLeuLysAsnTyrGlyLeuLeuTyrCysPheArgLysAspMetAspLysValGln 200  
 QY 556 ACATTCCTCGCATCTGTCAGTGGCTCTGTGGAGGGCAGCTGTGGCTTC 606  
 DB 201 ThrPheLeuArgIleValGlnCysArgSerValGlnGlySerCysGlyPhe 217

## RESULT 12

ID AAU11746 standard; protein; 217 AA.

XX AAU11746;

XX 12-MAR-2002 (first entry)

XX Growth hormone 1 gene (GH1), K194R mutant.

XX Growth hormone 1; GH1, osteopathic; gene therapy; protein therapy;  
 KW diabetes; obesity; infection; acromegaly; gigantism; sodium retention;

QY	1	ATGGCTACAGAGGCTCCCGGAGCGTCCCTGCTCTGCGCTTTGGCGCTGCTCTGCGCTGCG	60
Db	1	MetAlaIrmGlySerAlaThrSerLeuLeuLeuAlaPheGlyLeuLeuCysLeuProIrrp	20
QY	61	CTTCAAGAGGGCAGGAGCCTTCCCAACCACTTCCCTTATCCAGAGCTTTTGAACAAGCTAAGT	12
Db	21	LeuGlnGlnGlySerAlaPheProThrIleProLeuSerAlaGluPheAspAsnAlaSer	40
QY	121	CTCGCGCCCATCGTCTGACACAGCTGCGCTTTTGAACACTACAGGAGGTTT-----	177
Db	41	LeuArgAlaIleSarGluLeuHISGlnLeuAlaPheAspThrIlyrGlnGlnPheGlnGlnAla	60
QY	172	-----AACCCCGCAGACTCCCTCTGTTTC	199
Db	61	TyrIleProIlyrGlnGlnIlyrTySerPheLeuGlnIleAsnProGlnIrrrSerLeuCysPhe	80
QY	196	TCAGAGTATATCCGACACCCCTCCAAACAAGGAGGAAACAACAAGAAATCCAATTAGAG	255
Db	81	SerIleuSerIleProIrrrProSerAsnArgGlnGlnIrrrGlnGlnIlyrSerAlaLeuGln	100
QY	256	CTGCTCCGACATCTCCCTGCTGCTCATCATCAGTCCGCGGTGGAGGCCCGCGACGTTCTCAGG	315
Db	101	LeuLeuArgIleSerLeuLeuLeuIleGlnIrrrSerTrpLeuIrrrProValGlnPheLeuArg	120
QY	316	AGTGTCTTCGCCCAACACCGCTGATGATACGGCGCCTCTGACAGCAACGCTATAGACTCCTA	375
Db	121	SerValPheAlaAsnSerLeuValTyrrGlyAlaSerAspSerAsnValTyrrAspLeuLeu	140
QY	376	AAGGACCTTAGAGNAGGATCCAAACGCTGATGGGGAGGCTGGAGAATGGACGCCCGG	435
Db	141	LysAspPheuGlnGlnIlyIleGlnIrrrLeuMetGlyArgLeuGlnIleAspGlySerProArg	160
QY	436	ACGGGCGAGATCTTCAAGACGACCTTACACAGATTGACACAACACTCACACAAGATGAC	495
Db	161	ThrGlyGlnIlePheYsgIrrrThrTyrrSerIlyrPheAspThrAsnSerHISAsnAspAsp	180
QY	496	GCACTACTCAGAACTACCGGGCTGCTCTACTCTCTCAGAGAGACATGACAAAGTCCGAG	555
Db	181	AlaLeuLeuIlyAsnIlyrGlyLeuLeuTyrrCysPheAspArgAspMetAspIlyrValGln	200
QY	556	AACATTCTTCGCGATGTGCAATGTCGCCGCTCTGTGAGAGGCGAGCTGTGCGCTTC	606
Db	201	ThrPheLeuArgIleValGlnCysArgSerValGlnGlySerCysGlyPhe	217
RESULT 13			
ID	AAU11747	Standard, protein; 217 AA.	
AC	AAU11747;		
XX			
DT	12-MAR-2002	(first entry)	
XX			
DE	Growth hormone 1 gene (GH1), K194E mutant.		
XX			
KW	Growth hormone 1; GH1; osteopathic; gene therapy; protein therapy;		
KW	diabetes; obesity; infection; acromegaly; gigantism; sodium retention;		
KW	water retention; metabolic syndrome; mood disorder; sleep disorder;		
KW	Growth hormone dysfunction; familial growth hormone deficiency;		
KW	short stature; pituitary storage defect; human; mutant; mutein.		
OS	Homo sapiens.		









CC know spectrum of GH1 gene mutations; evaluating the role of GH1 gene  
CC mutations in the etiology of short stature; identifying of the mode of  
CC inheritance in novel lesions; evaluation the effects of GH1 mutations on  
CC the structure and function of the GH molecule and development of rapid  
CC diagnostic tests for inherited GH deficiency. This sequence is a variant  
CC of human growth hormone 1 (GH1), one of many variations of the gene  
CC discussed in the method of the invention. Note: This sequence does not  
CC appear in the specification but has been created from the GH1 wild type  
CC sequence (AAU11719) given in figure 6

XX Sequence 217 AA:

Alignment Scores:

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Percent Similarity:	92.63%	Conservative:	0
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Query Match:	92.22%	Indels:	15
DB:	5	Gaps:	1

US-09-856-796B-1 (1-609) x AAU11744 (1-217)

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  |||
DB 1 MetAlaThrGlySerArgThrSerLeuLeuAlaPheGlyLeuLeuCysLeuProTyr 20
OY 61 CTTCAGAGGAGGAGTGCCTTCCCAACCATTCCTTATCCAGGCTTTTGACAAAGCTAGT 120
  |||
DB 21 LeuGlnGlnGlySerAlaPheProThrIleProLeuSerArgLeuPheAspAlaSer 40
OY 121 CTCGCGCGCCCATCGCTGCGACACGAGCTGGGCTTGAACACTACCGAGAGTT----- 171
  |||
DB 41 LeuArgAlaHisArgLeuHisGlnLeuAlaPheAspThrTyrGlnGlnPheGlnGlnAla 60
OY 172 -----AACCCCGAGACTCTCTCTGTTTC 195
  |||
DB 61 TyrIleProLysGlnGlnIleTyrSerPheLeuGlnAsnProGlnThrSerLeuCysPhe 80
OY 196 TCAGAGTCTATTCCGACACCTCTCCAAACAGGAGAGAAACACACAGAAATCCAACTTAGAG 255
  |||
DB 81 SerGlnSerIleProThrProSerAsnArgGlnGlnIleThrGlnGlnIleTyrSerAsnLeuGln 100
OY 256 CTGCTCCGATCTCCCTGCTGCTCATCCAGTCCGTTGAGGCCCGCTGAGTTCTCAGG 315
  |||
DB 101 LeuLeuArgIleSerLeuLeuLeuIleGlnSerTyrLeuGlnProValGlnPheLeuArg 120
OY 316 AGTGTCTTGCCCAACAGCGCTGTGTACGGGAGCTCTGACAGCAACGTCTATGACCTCTTA 375
  |||
DB 121 SerValPheAlaAsnSerLeuValTyrGlyAlaSerAspSerAsnValTyrAspLeuLeu 140
OY 376 AAGGACTTAGAGGAGGATCCAAACGCTGATGAGGAGGCTGGAAGATGGAGCCCGCG 435
  |||
DB 141 LysAspLeuGlnGlnGlnIleGlnThrLeuMetGlyArgLeuGlnAspGlySerProArg 160
OY 436 ACTGGGACAGATCTTCAAGACAGACCTTACAGAGTTTCACACAACTCACACAAAGATGAC 495
  |||
DB 161 ThrGlyGlnIlePheLysGlnThrTyrSerLysPheAspThrAsnSerHisAsnAsp 180
OY 496 GCACTACTCAGAACTACGGGCTGTCTACTGCTTCAAGAGGAGACATGAGCAAGGTCGAG 555
  |||
DB 181 ValLeuLeuLysAsnTyrGlyLeuLeuTyrCysPheArgLysAspMetCysAspValGln 200
OY 556 ACATTCTGGCGCATCGGACATGCGGCTCTGTGAGGAGGAGGCTGTGCTTC 606
  |||
DB 201 ThrPheLeuArgIleValGlnCysArgSerValGlnGlySerCysGlyPhe 217
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Job time: 133.5 secs

GenCore version 5.1.6  
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OM nucleic - protein search, using frame\_plus\_n2p model

Run on: February 6, 2005, 13:14:50 ; Search time 31 Seconds

(without alignments)  
2932.986 Million cell updates/sec

Title: US-09-856-796B-1

Perfect score: 1112

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Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

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4	1024.5	92.1	217	3	US-08-784-582-10
5	1024.5	92.1	217	3	US-08-784-582-10
6	1024.5	92.1	217	3	US-08-785-271-11
7	1024.5	92.1	217	3	US-08-759-628-11
8	1024.5	92.1	217	3	US-09-284-878-1
9	1016.5	91.4	217	4	US-09-929-918-9
10	1016.5	91.4	217	1	US-08-187-756C-4
11	1016.5	91.4	217	2	US-08-710-324A-4
12	999	89.8	198	1	US-08-187-756C-5

13	999	89.8	198	2	US-08-710-324A-5	Sequence 5, Appl
14	999	89.8	198	4	US-09-411-657-5	Sequence 5, Appl
15	926.5	83.3	360	3	US-08-784-582-73	Sequence 73, Appl
16	924.5	83.1	274	3	US-08-784-582-71	Sequence 71, Appl
17	914	82.2	176	3	US-08-791-728-2	Sequence 2, Appl
18	914	82.2	176	3	US-08-990-774-2	Sequence 1, Appl
19	909	81.7	176	3	US-08-791-728-1	Sequence 1, Appl
20	909	81.7	176	3	US-08-791-728-1	Sequence 1, Appl
21	896.5	80.6	191	3	US-08-990-774-1	Sequence 1, Appl
22	891.5	80.2	191	3	US-09-465-461-1	Sequence 1, Appl
23	891.5	80.2	191	3	US-09-284-878-5	Sequence 5, Appl
24	891.5	80.2	191	4	US-09-462-941-1	Sequence 1, Appl
25	891.5	80.2	192	1	US-08-093-383-1	Sequence 1, Appl
26	891.5	80.2	194	2	US-08-383-621-4	Sequence 4, Appl
27	891.5	80.2	241	3	US-08-459-906-4	Sequence 4, Appl
28	891.5	80.2	245	4	US-09-424-620B-25	Sequence 25, Appl
29	891.5	80.2	448	4	US-09-280-030-66	Sequence 66, Appl
30	888.5	79.9	197	4	US-09-916-229A-2	Sequence 2, Appl
31	888.5	79.9	197	4	US-09-949-016-8655	Sequence 8655, Ap
32	888.5	79.9	197	4	US-09-949-016-8655	Sequence 8655, Ap
33	888.5	79.9	197	4	US-09-949-016-8655	Sequence 8657, Ap
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35	884.5	79.5	401	4	US-09-420-819-36	Sequence 36, Appl
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37	880.5	79.2	177	1	US-08-187-756C-6	Sequence 6, Appl
38	880.5	79.2	177	2	US-08-710-324A-6	Sequence 6, Appl
39	880.5	79.2	177	4	US-09-411-657-6	Sequence 6, Appl
40	878.5	79.0	400	4	US-09-420-819-37	Sequence 37, Appl
41	876.5	78.8	191	3	US-08-800-215C-16	Sequence 16, Appl
42	871.5	78.4	191	3	US-09-554-451-3	Sequence 3, Appl
43	867.5	78.0	191	3	US-08-800-215C-18	Sequence 18, Appl
44	867.5	78.0	191	3	US-08-800-215C-20	Sequence 20, Appl
45	800.5	72.0	198	4	US-09-949-016-8650	Sequence 8650, Ap

#### ALIGNMENTS

RESULT 1  
US-08-469-486-51  
Sequence 51, Application US/08469486  
Patent No. 5739281  
GENERAL INFORMATION:  
APPLICANT: Thoegeisen, Hans Christian  
APPLICANT: Holtey, Thor Lae  
APPLICANT: Etzerodt, Michael  
TITLE OF INVENTION: Improved method for the refolding of  
NUMBER OF SEQUENCES: 58  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Fish & Richardson  
STREET: 225 Franklin Street  
CITY: Boston  
STATE: Massachusetts  
COUNTRY: USA  
ZIP: 02110-2804  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/469,486  
FILING DATE:  
CLASSIFICATION: 530  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/192,060  
FILING DATE: February 4, 1994  
ATTORNEY/AGENT INFORMATION:  
NAME: Paul T. Clark  
REGISTRATION NUMBER: 30,162  
REFERENCE/DOCKET NUMBER: 06363/002001  
TELECOMMUNICATION INFORMATION:

256 CIGCICCGACICCCCGCGCCGCAG..CA..C-----





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Db 1 MetAlaThrGlySerArgThrSerLeuLeuAlaPheGlyLeuLeuCySLeuProTrp 20

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Db 21 LeuGlnGluGlySerAlaPheProTrpIleProLeuSerArgLeuPheAspAlaMet 40

Qy 121 CTCGGGCGCCATCGTCTGCACACAGCTGGGCTTTGACACCTACCAAGACTTT----- 170

Db 41 LeuArgAlaHisArgLeuHisGlnLeuAlaPheAspTrpTyrGlnGluPheGlnGluAla 60

Qy 172 -----AACCCGACAGCTCCCTCTGTTTC 195

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Qy 196 TCAGAGTCAATTCGACACACCTTCACACAGAGAGAAACAACAAGAAATCCAACTCAAG 255

Db 81 SerGlnSerIleProThrProSerAsnArgGlnGluThrGlnGlnIleTyrSerAsnLeuGln 100

Qy 256 CTGCTCCGGATCTCCCTGGTGCTCATCAAGTGTGGCTGAGAGCCCGTGACGTTCTCTCAG 315

Db 101 LeuLeuAlaGlyIleSerLeuLeuLeuIleGlnSerTrpLeuGlnProValGlnPheLeuArg 120

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Db 121 SerValPheAlaAsnSerLeuValTyrGlyAlaSerPheSerAsnValTyrAspLeuLeu 140

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Db 141 LysAspLeuGlnGluGlyIleGlnThrLeuMetGlyArgLeuGluAspGlySerProArg 160

Qy 436 ACTGGGAGAGATCTTCAAGCAGACCTTACAGCAAGTTGCACAACAACTGACACAAAGATGAC 495

496 GCACCTACTCAGAGACTGAGGCTGCTCTACTGCTTCCAGAGAGCATGAGCAAGCTGAC 555  
181 Alaleuenuyashantylglyleuenuyrcysphearglysbmetaplysva1glu 200  
556 ACATTCTCGGCATCGTGCAGTGCCTCTGTGGAGGAGCGAGCTGCGCTTC 606  
201 Thrlheleuargilevalgincysargservalgluglysercysglypne 217

RESULT 7  
US-09-284-878-1  
Sequence 1, Application US/09284878  
Patent No. 6342375

GENERAL INFORMATION:  
APPLICANT: Olazaran, Martha Guerrero  
APPLICANT: Saldaña, Hugo Barrera  
APPLICANT: Saldaña, Jose Maria Váder  
TITLE OF INVENTION: Genetically Modified Methylotrophic P. pastoris Yeast for the  
TITLE OF INVENTION: Production and Secretion of the Human Growth Hormone  
FILE REFERENCE: 1829.0010000  
CURRENT APPLICATION NUMBER: US/09/284,878  
CURRENT FILING DATE: 1999-07-21  
PRIOR APPLICATION NUMBER: PCT/MX97/00033  
PRIOR FILING DATE: 1997-10-24  
NUMBER OF SEQ ID NOS: 9  
SOFTWARE: Patent Ver. 2.1  
SEQ ID NO 1  
LENGTH: 217  
TYPE: PRT  
ORGANISM: Homo sapiens  
US-09-284-878-1

Alignment Scores:  
Pred. No.: 1,19e-95 Length: 217  
Score: 1024.50 Matches: 201  
Percent Similarity: 92.63% Conservative: 0  
Best Local Similarity: 92.63% Mismatches: 1  
Query Match: 92.13% Indels: 15  
DB: 3 Gaps: 1

US-09-856-796b-1 (1-609) x US-09-284-878-1 (1-217)

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QY 121 CTCGGGCGCCATCGTGTGACAGAGCTGAGCTTTGACACTTACCAAGAGTTT----- 171  
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556 ACATTCTCGGCATCGTGCAGTGCCTCTGTGGAGGAGCGAGCTGCGCTTC 606  
201 Thrlheleuargilevalgincysargservalgluglysercysglypne 217

RESULT 8  
US-09-929-918-9  
Sequence 9, Application US/09929918  
Patent No. 6773899

GENERAL INFORMATION:  
APPLICANT: Kordyum, Vitaliy A.  
APPLICANT: Chernykh, Svetlana I.  
APPLICANT: Slavchenko, Iryna Yu.  
APPLICANT: Vozianov, Oleksandr  
TITLE OF INVENTION: PHAGE-DEPENDENT SUPER PRODUCTION OF  
TITLE OF INVENTION: BIOLOGICALLY ACTIVE PROTEIN AND PEPTIDES  
FILE REFERENCE: PHAGE.006A  
CURRENT APPLICATION NUMBER: US/09/929,918  
CURRENT FILING DATE: 2001-08-15  
PRIOR APPLICATION NUMBER: 09/318,288  
PRIOR FILING DATE: 1999-05-25  
NUMBER OF SEQ ID NOS: 11  
SOFTWARE: FastSeq for Windows Version 4.0  
SEQ ID NO 9  
LENGTH: 217  
TYPE: PRT  
ORGANISM: Homo sapiens  
US-09-929-918-9

Alignment Scores:  
Pred. No.: 1,19e-95 Length: 217  
Score: 1024.50 Matches: 201  
Percent Similarity: 92.63% Conservative: 0  
Best Local Similarity: 92.63% Mismatches: 1  
Query Match: 92.13% Indels: 15  
DB: 4 Gaps: 1

US-09-856-796b-1 (1-609) x US-09-929-918-9 (1-217)

QY 1 ATGGCTACAGAGCTCCCGACGCTCCCTGCTCTTTGGCTGCTGCTGCTGCTGCTG 60  
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QY 61 CTTCAAGAGGAGGAGGCTTCCCAACCATTCCTTATCCAGGCTTTTGAACAAGCTAGT 120  
DB 21 Leuglmglyseralaphrothrlleproleuserargleupheasphalamet 40  
QY 121 CTCGGGCGCCATCGTGTGACAGAGCTGAGCTTTGACACTTACCAAGAGTTT----- 171  
DB 41 Leuargalashargleuuhsglnleualaphesphrtyrglmglyuphegluglu1a 60  
QY 172 -----AACCCGAGACCTCCCTGCTTTC 195  
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[illegible]

NAME: Brookes, A. Anders

REGISTRATION NUMBER: 36,373



Db 1 MetAlaIaIaIySerIaIgrThrSerLeuLeuAlaPheGlyLeuLeuCySteuSerTrip 20

QY 61 CTTCAAGAGGGCAGTGCCTTCCCAACCATTTCCCTTTATCCAGGCTTTTGGACAACGCTAGT 120

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Db 41 LeuArgAlaIaIaArgLeuIaIaGlnLeuAlaIaPheAspThrTyrGlnIaIaPhe----- 57

QY 181 ACCTCCCTCTGTCTTTCAGAGTCTATTTCCGACACCCCTCCAAACGAGGAGAAACACAAACAG 240

Db 58 ---SerLeuCyAPheSerGlySerIaIaPheProIrrProSerAsnArgGluGluIaIaHrGlnGln 76

QY 241 AATCCAAACCTGAGAGTGCTCGGCACACCCCTGCTGCTCATCCAGTCTGCGCTGAGAGCC 300

1 ATGGCTACAGGCTCCCGGACGTCCCTGCTCTGGCTTTTGGCTGCTCTGCTGCTGCTGG 60

NAME: Brookes, A. Anders  
REGISTRATION NUMBER: 36,373





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GenCore version 5.1.6  
Copyright (c) 1993 - 2005 CompuGen Ltd.

OM nucleic - protein search, using frame\_plus\_n2p model

Run on: February 6, 2005, 13:21:40 ; Search time 115 Seconds

(without alignments)  
3449.614 Million cell updates/sec

Title: US-09-856-796b-1

Perfect score: 1112

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Ygapop 10.0 , Ygapext 0.5  
Fgapop 6.0 , Fgapext 7.0  
Delop 6.0 , Delext 7.0

Searched: 1373511 seqs, 325702437 residues

Total number of hits satisfying chosen parameters: 2747022

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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21: /cgn2\_6/prodata/2/pubppa/US60\_PUBCOMB.pep:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

No.	Score	Match	Length	DB	ID	Description
1	1029.5	92.6	217	9	US-09-853-688-2	Sequence 2, Appli
2	1029.5	92.6	217	9	US-09-853-688-4	Sequence 4, Appli
3	1029.5	92.6	217	10	US-09-969-748C-4	Sequence 4, Appli
4	1029.5	92.6	217	16	US-10-788-318-2	Sequence 2, Appli
5	1029.5	92.6	217	16	US-10-788-318-4	Sequence 2, Appli
6	1024.5	92.1	217	9	US-09-929-918-9	Sequence 9, Appli
7	1017.5	91.5	217	9	US-09-804-409A-16	Sequence 16, Appli
8	1017.5	91.5	217	15	US-10-411-037-48	Sequence 48, Appli
9	1017.5	91.5	217	15	US-10-411-026-48	Sequence 48, Appli
10	1017.5	91.5	217	15	US-10-410-962-48	Sequence 48, Appli
11	1017.5	91.5	217	15	US-10-410-962-48	Sequence 48, Appli
12	1017.5	91.5	217	16	US-10-411-049-48	Sequence 48, Appli
13	1017.5	91.5	217	16	US-10-410-997-48	Sequence 48, Appli
14	1017.5	91.5	217	16	US-10-410-997-48	Sequence 48, Appli
15	1017.5	91.5	217	16	US-10-411-012-48	Sequence 48, Appli
16	1017.5	91.5	217	16	US-10-287-994-48	Sequence 48, Appli
17	1016.5	91.4	217	16	US-10-410-913-48	Sequence 48, Appli
18	1010.5	90.9	232	16	US-10-477-651-2	Sequence 2, Appli
19	898.5	80.8	197	15	US-10-477-651-3	Sequence 3, Appli
20	898.5	80.8	198	15	US-10-621-693-45	Sequence 47, Appli
21	898.5	80.8	198	15	US-10-621-693-45	Sequence 45, Appli
22	898.5	80.8	391	15	US-10-621-693-51	Sequence 51, Appli
23	898.5	80.8	396	15	US-10-621-693-49	Sequence 49, Appli
24	898.5	80.8	412	15	US-10-621-693-74	Sequence 74, Appli
25	898.5	80.8	589	15	US-10-621-693-53	Sequence 53, Appli
26	898.5	80.8	786	15	US-10-621-693-55	Sequence 55, Appli
27	896.5	80.6	313	15	US-10-621-693-76	Sequence 76, Appli
28	896.5	80.6	338	15	US-10-311-473-16	Sequence 16, Appli
29	895.5	80.5	214	14	US-10-153-207-6	Sequence 5, Appli
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31	895.5	80.5	574	15	US-10-621-693-32	Sequence 32, Appli
32	895.5	80.5	576	15	US-10-621-693-32	Sequence 39, Appli
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34	892.5	80.3	192	15	US-10-621-693-66	Sequence 66, Appli
35	892.5	80.3	206	15	US-10-621-693-70	Sequence 70, Appli
36	891.5	80.2	191	14	US-10-153-207-1	Sequence 1, Appli
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42	891.5	80.2	191	15	US-10-621-693-80	Sequence 80, Appli
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#### ALIGNMENTS

RESULT 1  
US-09-853-688-2  
; Sequence 2, Application US/09853688  
; Patent No. US20020081605A1  
GENERAL INFORMATION:  
APPLICANT: COOPER, DAVID N.  
APPLICANT: PROCTER, ANNIE M.  
APPLICANT: GREGORY, JOHN  
APPLICANT: MILLAR, DAVID S.  
TITLE OF INVENTION: METHOD FOR DETECTING GROWTH HORMONE VARIATIONS IN  
FILE REFERENCE: WCM78  
CURRENT APPLICATION NUMBER: US/09/853,688  
CURRENT FILING DATE: 2001-05-14  
NUMBER OF SEQ ID NOS: 66  
SOFTWARE: PatentIn Ver. 2.1  
SEQ ID NO 2  
LENGTH: 217  
TYPE: PRT  
ORGANISM: Homo sapiens  
US-09-853-688-2





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; Sequence 2, Application US/10788318
; Publication No. US20040137510A1
; GENERAL INFORMATION:
; APPLICANT: COOPER, DAVID N.
; APPLICANT: PROCTER, ANNIE M.
; APPLICANT: GREGORY, JOHN
; APPLICANT: MILLAR, DAVID S.
; TITLE OF INVENTION: METHOD FOR DETECTING GROWTH HORMONE VARIATIONS IN
; TITLE OF INVENTION: HUMANS, THE VARIATIONS AND THEIR USES
; FILE REFERENCE: WCM78
; CURRENT APPLICATION NUMBER: US/10/788,318
; NUMBER OF SEQ ID NOS: 66
; SOFTWARE: PatentIn Ver. 2.1.1
; SEQ ID NO 2
; LENGTH: 217
; TYPE: PR1
; ORGANISM: Homo sapiens
US-10-788-318-2

Alignment Scores:
Pred. No.: 5,92e-86 Length: 217
Score: 1029.50 Matches: 202
Percent Similarity: 93.09% Conservative: 0
Best Local Similarity: 93.09% Mismatches: 0
Query Match: 92.58% Indels: 15
DB: 16 Gaps: 1

US-09-856-796B-1 (1-609) x US-10-788-318-2 (1-217)

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QY 172 -----AACCCCGAGACTCCCTCTGTTTC 195
Db 61 TyrIleProLyGlnGlnLysTyrSerPheLeuGlnIleAsnProGlnThrSerLeuCyPhe 80
QY 196 TCGAGATCTATTTCCGACACCTCCGACGGGAGGAAACACAAAGAAATCCACCTTAG 255
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QY 256 CTGCTCCGAGATCCCTGCTGTCTATTCAGTCGTGGCTGGAGCCCGGCGAGTTCCTAGG 315
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Db 201 ThrPheLeuArgIleValGlnCyArgSerValGlnGlySerCyGlnGlyPhe 217

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10

DO NOT INTERFERE WITH THE

1. **Introduction**  
 2. **Background**  
 3. **Methodology**  
 4. **Results**  
 5. **Discussion**  
 6. **Conclusion**  
 7. **References**  
 8. **Appendix**  
 9. **Figure 1**  
 10. **Figure 2**  
 11. **Figure 3**  
 12. **Figure 4**  
 13. **Figure 5**  
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 217. **Figure 209**

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DB 181 AlaleuLeuLysanTyrglyLeuLeuTyCyPheArgLysAspMetAspLysValGlu 200  
QY 556 ACATTCTGCGCATCGTCAGAGTCCGCTGTGTGAGGAGGAGCTGTGCTTC 606  
DB 201 ThrPheLeuArgIleValGlnCysArgSerValGlnIlySerCysglpPhe 217

## RESULT 7

US-09-804-409A-16  
; Sequence 16, Application US/09804409A  
; Patent No. US20020155100A1  
; GENERAL INFORMATION:  
; APPLICANT: KIEFER, TIMOTHY J.  
; APPLICANT: KIEFER, ANTHONY T.  
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR REGULATED PROTEIN  
; FILE REFERENCE: 029996/027 8721  
; CURRENT APPLICATION NUMBER: US/09/804,409A  
; NUMBER OF SEQ ID NOS: 18  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 16  
; LENGTH: 217  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-09-804-409A-16

## Alignment Scores:

Pred. No.: 7.52e-85 Length: 217  
Score: 1017.50 Matches: 200  
Percent Similarity: 92.17% Conservative: 2  
Best Local Similarity: 92.17% Mismatches: 0  
Query Match: 91.50% Indels: 15  
DB: 9 Gaps: 1

US-09-856-796B-1 (1-609) x US-09-804-409A-16 (1-217)

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QY 61 CTTCAAGAGGAGAGTGCCTTCCCAACCATTCCTTATCCAGGCTTTTGAACAAGCTAG 120  
DB 21 LeuGlnGluGlySerAlaPheProThrIleProLeuSerArgProPheAspAlaMet 40  
QY 121 CTCGGCGCCCATGCTGTGACCAAGCTGAGCTTTGACACCTACCAAGAGTTT----- 171  
DB 41 LeuArgAlaHisArgLeuHisGlnLeuAlaPheAspThrTyrglnIlyPheGlnGluAla 60  
QY 172 -----AACCCCAAGACCTCTCTGTTTC 195  
DB 61 TyrIleProLysGlnGlnIlySerPheLeuGlnAsnProGlnThrSerLeuCysPhe 80  
QY 196 TTAGAGTATATCCGACACCTCCCAAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGG 255  
DB 81 SerGlnSerIleProThrProSerAsnArgGlnIlyThrGlnGlnIlySerAsnLeuGln 100  
QY 256 CTGCTCCGATCTCCCTGCTGCTCATCCAGTGTGAGCTGAGCGCCGTGAGTTCCTCAG 315  
DB 101 LeuLeuArgIleSerLeuLeuLeuIleGlnSerIlyPheGlnProValGlnPheLeuArg 120  
QY 316 AGTGTCTTCCCAACAGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 375  
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DB 141 LysAspLeuGlnGlnIlyIleGlnThrLeuMetGlyArgLeuGlnAspIlySerProArg 160  
QY 436 ACTGGGAGATCTTCAAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 495

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QY 496 GCACTACTCAAGACTACGGGCTGCTTACTGCTTCAAGAGCATGACCAAGTCTGAG 555  
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QY 556 ACATTCTGCGCATCGTCAGAGTCCGCTGTGTGAGGAGGAGCTGTGCTTC 606  
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## RESULT 8

US-10-411-037-48  
; Sequence 48, Application US/10411037  
; Publication No. US20040043446A1  
; GENERAL INFORMATION:  
; APPLICANT: Neose Technologies, Inc.  
; APPLICANT: DeFrees, Shawn  
; APPLICANT: Zopf, David  
; APPLICANT: Bayer, Robert  
; APPLICANT: Hakes, David  
; APPLICANT: Chen, Xi  
; APPLICANT: Bove, Caryn  
; TITLE OF INVENTION: ALPHA GALACTOSIDASE A: REMODELING AND GLYCOCONJUGATION OF ALPHA  
; FILE REFERENCE: 040853-01-5082  
; CURRENT APPLICATION NUMBER: US/10/411,037  
; PRIOR FILING DATE: 2003-04-09  
; PRIOR APPLICATION NUMBER: US 60/328,523  
; PRIOR FILING DATE: 2001-10-10  
; PRIOR APPLICATION NUMBER: US 60/344,692  
; PRIOR FILING DATE: 2001-10-19  
; PRIOR APPLICATION NUMBER: US 60/387,292  
; PRIOR FILING DATE: 2002-06-07  
; PRIOR APPLICATION NUMBER: US 60/391,777  
; PRIOR FILING DATE: 2002-06-25  
; PRIOR APPLICATION NUMBER: US 60/396,594  
; PRIOR FILING DATE: 2002-07-17  
; PRIOR APPLICATION NUMBER: US 60/404,249  
; PRIOR FILING DATE: 2002-08-16  
; PRIOR APPLICATION NUMBER: US 60/407,527  
; NUMBER OF SEQ ID NOS: 75  
; SOFTWARE: PatentIn version 3.2  
; SEQ ID NO 48  
; LENGTH: 217  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-10-411-037-48

## Alignment Scores:

Pred. No.: 7.52e-85 Length: 217  
Score: 1017.50 Matches: 200  
Percent Similarity: 92.17% Conservative: 0  
Best Local Similarity: 92.17% Mismatches: 2  
Query Match: 91.50% Indels: 15  
DB: 15 Gaps: 1

US-09-856-796B-1 (1-609) x US-10-411-037-48 (1-217)

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QY 61 CTTCAAGAGGAGAGTGCCTTCCCAACCATTCCTTATCCAGGCTTTTGAACAAGCTAG 120  
DB 21 LeuGlnGlnGlySerAlaPheProThrIleProLeuSerArgProPheAspAlaMet 40  
QY 121 CTCGGCGCCCATGCTGTGACCAAGCTGAGCTTTGACACCTACCAAGAGTTT----- 171  
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QY 172 -----AACCCCAAGACCTCTCTGTTTC 195

Db 61 TyrIleProlysgluInlystySerPheLeuGlnsPnroGlnThrSerLeuCySphe 80  
 QY 196 TCAGAGCTATTTCGACACCCCTCCACAGGAGGAAACACACAGAAATCCAACTAGAG 255  
 Db 81 SerGluSerIleProThrProSerAsnArgGluGlnGlnGlnGlnSerAsnLeuGln 100  
 QY 256 CTGCTCGCATCTCCCTGCTGCTCATCCAGTCTGCTGAGCCCGTGCAGTTCTCTCAGG 315  
 Db 101 LeuLeuArgIleSerLeuLeuLeuIleGlnSerTrpLeuGlnProValGlnPheLeuArg 120  
 QY 316 AGTGTCTTCCCAACAGCCTGTGTACGGCGCTCTGACAGCAAGTCTATGACTCTTA 375  
 Db 121 SerValPheAlaAsnSerLeuValTyrGlyAlaSerAspSerAsnValTyrAspLeuLeu 140  
 QY 376 AAGACCTAAGAGAGGATCCAAACGCTGATGGGAGGCTGGAGAGAGGAGGAGGAGG 435  
 Db 141 LysAspLeuGluGluGlyIleGlnThrLeuMetGlyArgLeuGlnAspGlySerProArg 160  
 QY 436 ACTGGGGAGATCTTCAAGCAGACCTGACAGCAAGTTCGACACAACTCACACAGATGAC 495  
 Db 161 ThrGlyGlnIlePheLeuGlnThrTyrSerIlePheAspThrAsnSerHisAsnAsp 180  
 QY 496 GCACTACTCAAGAACTACGCGGCTGCTCTACTGCTTACAGAAAGACATGACAGTCTGAG 555  
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 QY 556 ACATTCCTGCGCATCTGTCAGTGCCTCTGTGTGAGGGGACGCTGTGGCTTC 606  
 Db 201 ThrPheLeuArgIleValGlnCysArgSerValGluGlySerCysGlyPhe 217

## RESULT 9

US-10-411-026-48  
 ; Sequence 48, Application US/10411026  
 ; Publication No. US20040063911A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Neose Technologies, Inc.  
 ; APPLICANT: Defrees, Shawn  
 ; APPLICANT: Zopf, David  
 ; APPLICANT: Bayer, Robert  
 ; APPLICANT: Hakes, David  
 ; APPLICANT: Chen, Xi  
 ; TITLE OF INVENTION: PROTEIN REMODELING METHODS AND PEPTIDES PRODUCED BY THE  
 ; FILE REFERENCE: 040853-01-5053  
 ; CURRENT APPLICATION NUMBER: US/10/411,026  
 ; CURRENT FILING DATE: 2003-04-09  
 ; PRIOR APPLICATION NUMBER: US 60/328,523  
 ; PRIOR FILING DATE: 2001-10-10  
 ; PRIOR APPLICATION NUMBER: US 60/344,692  
 ; PRIOR FILING DATE: 2001-10-19  
 ; PRIOR APPLICATION NUMBER: US 60/387,292  
 ; PRIOR FILING DATE: 2002-06-07  
 ; PRIOR APPLICATION NUMBER: US 60/391,777  
 ; PRIOR FILING DATE: 2002-06-25  
 ; PRIOR APPLICATION NUMBER: US 60/396,594  
 ; PRIOR FILING DATE: 2002-07-17  
 ; PRIOR APPLICATION NUMBER: US 60/404,249  
 ; PRIOR FILING DATE: 2002-08-16  
 ; PRIOR APPLICATION NUMBER: US 60/407,527  
 ; PRIOR FILING DATE: 2002-08-28  
 ; NUMBER OF SEQ ID NOS: 75  
 ; SOFTWARE: PatentIn version 3.2  
 ; SEQ ID NO 48  
 ; LENGTH: 217  
 ; TYPE: PRT  
 ; ORGANISM: Homo sapiens  
 ; US-10-411-026-48

Alignment Scores:  
 Pred. No.: 7.52e-85 Length: 217  
 Score: 1017.50 Matches: 200  
 Percent Similarity: 92.17% Conservative: 0  
 Best Local Similarity: 92.17% Mismatches: 2

Query Match: 91.50% Indels: 15  
 DB: 15 Gaps: 1

US-09-856-796B-1 (1-609) x US-10-411-026-48 (1-217)

QY 1 AAGGCTACAGGCTCCCGGACGCTCCCTGCTGCTTTGGCCCTGCTGCTGCTGCTG 60  
 Db 1 MetAlaThrGlySerArgThrSerLeuLeuAlaPheGlyLeuLeuLysProTrp 20  
 QY 61 CTTCAGAGAGGAGTGGCTCCCAACATTCCTTATCCAGAGCTTTTGGACCAAGCTAGT 120  
 Db 21 LeuGlnGluGlySerAlaPheProThrIleProLeuSerArgProPheAspAsnAlaMet 40  
 QY 121 CTCCGGCCCATGCTGACACGAGTGGCTTTGACACCTACAGAGATT----- 171  
 Db 41 LeuArgAlaHisArgLeuHisGlnLeuAlaPheAspThrTyrGlnGluPheGluAla 60  
 QY 172 -----AACCCCAAGACTCTCTCTGTTTC 195  
 Db 61 TyrIleProlysgluInlystySerPheLeuGlnsPnroGlnThrSerLeuCySphe 80  
 QY 196 TCAGAGCTATTTCGACACCCCTCCACAGGAGGAAACACACAGAAATCCAACTAGAG 255  
 Db 81 SerGluSerIleProThrProSerAsnArgGluGlnGlnGlnGlnSerAsnLeuGln 100  
 QY 256 CTGCTCGCATCTCCCTGCTGCTCATCCAGTCTGCTGAGCCCGTGCAGTTCTCTCAGG 315  
 Db 101 LeuLeuArgIleSerLeuLeuLeuIleGlnSerTrpLeuGlnProValGlnPheLeuArg 120  
 QY 316 AGTGTCTTCCCAACAGCCTGTGTACGGCGCTCTGACAGCAAGTCTATGACTCTTA 375  
 Db 121 SerValPheAlaAsnSerLeuValTyrGlyAlaSerAspSerAsnValTyrAspLeuLeu 140  
 QY 376 AAGACCTAAGAGAGGATCCAAACGCTGATGGGAGGCTGGAGAGAGGAGGAGGAGG 435  
 Db 141 LysAspLeuGluGluGlyIleGlnThrLeuMetGlyArgLeuGlnAspGlySerProArg 160  
 QY 436 ACTGGGCAATCTTCAAGCAGACCTGACAGCAAGTTCGACACAACTCACACAGATGAC 495  
 Db 161 ThrGlyGlnIlePheLeuGlnThrTyrSerIlePheAspThrAsnSerHisAsnAsp 180  
 QY 496 GCACTACTCAAGAACTACGCGGCTGCTCTACTGCTTACAGAAAGACATGACAGTCTGAG 555  
 Db 181 AlaLeuLeuLysAsnTyrGlyLeuLeuTyrCysPheArgGlyAspMetAspLysValGln 200  
 QY 556 ACATTCCTGCGCATCTGTCAGTGCCTCTGTGTGAGGGGACGCTGTGGCTTC 606  
 Db 201 ThrPheLeuArgIleValGlnCysArgSerValGluGlySerCysGlyPhe 217

RESULT 10  
 US-10-410-962-48  
 ; Sequence 48, Application US/10410962  
 ; Publication No. US20040077836A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Neose Technologies, Inc.  
 ; APPLICANT: Defrees, Shawn  
 ; APPLICANT: Zopf, David  
 ; APPLICANT: Bayer, Robert  
 ; APPLICANT: Hakes, David  
 ; APPLICANT: Chen, Xi  
 ; APPLICANT: Bowe, Caryn  
 ; TITLE OF INVENTION: GRANULOCYTE COLONY STIMULATING FACTOR: REMODELING AND  
 ; FILE REFERENCE: 040853-01-5054  
 ; CURRENT APPLICATION NUMBER: US/10/410,962  
 ; CURRENT FILING DATE: 2003-04-09  
 ; PRIOR APPLICATION NUMBER: US 60/328,523  
 ; PRIOR FILING DATE: 2001-10-10  
 ; PRIOR APPLICATION NUMBER: US 60/344,692  
 ; PRIOR FILING DATE: 2001-10-19  
 ; PRIOR APPLICATION NUMBER: US 60/387,292  
 ; PRIOR FILING DATE: 2002-06-07  
 ; PRIOR APPLICATION NUMBER: US 60/391,777



QY 376 AAGACCTAGAGGAGGATCCAAACGCTGATGAGGAGGCTGAGAGATGAGAGCCCGG 435  
| | | | |  
DB 141 LysAspLeuGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGln 160  
| | | | |  
QY 436 ACTGGGAGATCTTCAAGACGACCTACAGCAAGTTGACAACTACACACAGATGAC 495  
| | | | |  
DB 161 ThrGlyGlnIlePheLeuGlnThrTySerLeuPheAspThrAsnSerHisAsnAspAsp 180  
| | | | |  
QY 496 GCACCTACTCAAGACTACGGGCTGCTTACTGCTTCAAGAGAGACATGAGCAAGTGGAG 555  
| | | | |  
DB 181 AlaLeuLeuLysAsnTyrgIleuLeuTyrcysPheArgLysAspMetAspLysValGln 200  
| | | | |  
QY 556 ACATTCTGCGGATCGTGCAGTGGCGCTCTGTGGAGGAGGCTGAGCTTC 606  
| | | | |  
DB 201 ThrPheLeuArgIleValGlnGlnCysArgSerValGlnGlnGlnGlnGlnGlnGlnGln 217  
| | | | |

## RESULT 12

US-10-410-930-48  
Sequence 48, Application US/10410930  
Publication No. US20040115168A1  
GENERAL INFORMATION:  
APPLICANT: Neose Technologies, Inc.  
APPLICANT: Defrees, Shawn  
APPLICANT: Zopf, David  
APPLICANT: Bayer, Robert  
APPLICANT: Hakes, David  
APPLICANT: Chen, Xi  
APPLICANT: Bove, Caryn  
TITLE OF INVENTION: INTERFERON BETA: REMODELING AND GLYCOCONJUGATION OF INTERFERON  
FILE REFERENCE: 040853-01-5056  
CURRENT APPLICATION NUMBER: US/10/410,930  
CURRENT FILING DATE: 2003-04-09  
PRIOR APPLICATION NUMBER: US 60/328,523  
PRIOR FILING DATE: 2001-10-10  
PRIOR APPLICATION NUMBER: US 60/344,692  
PRIOR FILING DATE: 2001-10-19  
PRIOR APPLICATION NUMBER: US 60/387,292  
PRIOR FILING DATE: 2002-06-07  
PRIOR APPLICATION NUMBER: US 60/391,777  
PRIOR FILING DATE: 2002-06-25  
PRIOR APPLICATION NUMBER: US 60/396,594  
PRIOR FILING DATE: 2002-07-17  
PRIOR APPLICATION NUMBER: US 60/404,249  
PRIOR FILING DATE: 2002-08-16  
PRIOR APPLICATION NUMBER: US 60/407,527  
PRIOR FILING DATE: 2002-08-28  
NUMBER OF SEQ ID NOS: 75  
SOFTWARE: PatentIn version 3.2  
SEQ ID NO 48  
LENGTH: 217  
TYPE: PRT  
ORGANISM: Homo sapiens  
US-10-410-930-48

Alignment Scores:  
Pred. No.: 7.52e-85  
Score: 1017.50  
Percent Similarity: 92.17%  
Best Local Similarity: 92.17%  
Query Match: 91.50%

DB: 16  
Gaps: 1  
Length: 217  
Matches: 200  
Conservative: 2  
Mismatch: 0  
Indels: 15

US-09-856-796b-1 (1-609) x US-10-410-930-48 (1-217)

QY 1 ATGGCTACAGGCTCCGAGACGTCCTGCTGGCTTTGGCTGCTGCTGCTGCTGCTG 60  
| | | | |  
DB 1 MetAlaThrGlySerArgThrSerLeuLeuAlaPheGlyLeuLeuGlnGlnGlnGlnGln 20  
| | | | |  
QY 61 CTTCAGAGGAGGAGGCTTCCCAACCATTCCTTATTCAGAGGCTTTTGTGCAACAGCTAGT 120  
| | | | |  
DB 21 LeuGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGln 40  
| | | | |

QY 121 CTCCGCGCCCATCGCTGACACAGCTGAGCCCTTTGACACCTACAGAGTTT----- 171  
| | | | |  
DB 41 LeuArgIleHisArgLeuHisGlnLeuAlaPheAspThrTyrgIleGlnGlnGlnGlnGln 60  
| | | | |  
QY 172 -----AAGCCCAAGACCTCCCTCTGTTTC 195  
| | | | |  
DB 61 TyrIleProLysGlnGlnLysTyrcysPheLeuGlnAsnProGlnThrSerLeuGlnGln 80  
| | | | |  
QY 196 TCAGAGCTTATTCGACACACCTCCCAACAGGAGAGAAACACAAACAGAAATCCAACTAGAG 255  
| | | | |  
DB 81 SerGlnSerIleProThrProSerAsnArgGlnGlnGlnGlnGlnGlnGlnGlnGlnGln 100  
| | | | |  
QY 256 CTGCTCCGCACTCCCTCTGCTCTCATTCAGTGTGTGGCTGAGAGCCCGTCACTTCTCAG 315  
| | | | |  
DB 101 LeuLeuArgIleSerLeuLeuLeuIleGlnSerTrpLeuGlnProValGlnPheLeuArg 120  
| | | | |  
QY 316 AGTGTCTTGCCCAACAGCTGCTGTGACGGCGCTCTCTGACAGCAAGCTTATGACCTCTA 375  
| | | | |  
DB 121 SerValPheAlaAsnSerLeuValTyrgIleAsnSerAsnValTyrcysPheLeu 140  
| | | | |  
QY 376 AAGACCTAGAGGAGGATCCAAACGCTGATGAGGAGGCTGAGAGATGAGAGCCCGG 435  
| | | | |  
DB 141 LysAspLeuGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGln 160  
| | | | |  
QY 436 ACTGGGAGATCTTCAAGACGACCTACAGCAAGTTGACACAACTACACACAGATGAC 495  
| | | | |  
DB 161 ThrGlyGlnIlePheLeuGlnThrTySerLeuPheAspThrAsnSerHisAsnAspAsp 180  
| | | | |  
QY 496 GCACCTACTCAAGACTACGGGCTGCTTACTGCTTCAAGAGAGACATGAGCAAGTGGAG 555  
| | | | |  
DB 181 AlaLeuLeuLysAsnTyrgIleuLeuTyrcysPheArgLysAspMetAspLysValGln 200  
| | | | |  
QY 556 ACATTCTGCGGATCGTGCAGTGGCGCTCTGTGGAGGAGGCTGAGCTTC 606  
| | | | |  
DB 201 ThrPheLeuArgIleValGlnGlnCysArgSerValGlnGlnGlnGlnGlnGlnGlnGln 217  
| | | | |

## RESULT 13

US-10-410-997-48  
Sequence 48, Application US/10410997  
Publication No. US20040126838A1  
GENERAL INFORMATION:  
APPLICANT: Neose Technologies, Inc.  
APPLICANT: Defrees, Shawn  
APPLICANT: Zopf, David  
APPLICANT: Bayer, Robert  
APPLICANT: Hakes, David  
APPLICANT: Chen, Xi  
APPLICANT: Bove, Caryn  
TITLE OF INVENTION: FOLLICLE STIMULATING HORMONE: REMODELING AND GLYCOCONJUGATION OF  
FILE REFERENCE: 040853-01-5059  
CURRENT APPLICATION NUMBER: US/10/410,997  
CURRENT FILING DATE: 2003-04-09  
PRIOR APPLICATION NUMBER: US 60/328,523  
PRIOR FILING DATE: 2001-10-10  
PRIOR APPLICATION NUMBER: US 60/344,692  
PRIOR FILING DATE: 2001-10-19  
PRIOR APPLICATION NUMBER: US 60/387,292  
PRIOR FILING DATE: 2002-06-07  
PRIOR APPLICATION NUMBER: US 60/391,777  
PRIOR FILING DATE: 2002-06-25  
PRIOR APPLICATION NUMBER: US 60/396,594  
PRIOR FILING DATE: 2002-07-17  
PRIOR APPLICATION NUMBER: US 60/404,249  
PRIOR FILING DATE: 2002-08-16  
PRIOR APPLICATION NUMBER: US 60/407,527  
PRIOR FILING DATE: 2002-08-28  
NUMBER OF SEQ ID NOS: 75  
SOFTWARE: PatentIn version 3.2  
SEQ ID NO 48  
LENGTH: 217  
TYPE: PRT  
ORGANISM: Homo sapiens

RESULT 14  
US-10-411-012-48  
: Sequence 48, Application US/10411012  
: Publication No. US20040132640A1  
: GENERAL INFORMATION:  
: APPLICANT: Neose Technologies, Inc.  
: APPLICANT: Deffres, Shawn  
: APPLICANT: Zopf, David  
: APPLICANT: Bayer, Robert  
: APPLICANT: Hakes, David  
: APPLICANT: Chen, Xi  
: APPLICANT: Bowe, Caryne  
: TITLE OF INVENTION: GLYCOSYLATION METHODS AND PROTEINS/PEPTIDES PRODUCED BY THEM  
: TITLE OF INVENTION: METHODS  
: FILE REFERENCE: 040853-01-5051  
: CURRENT APPLICATION NUMBER: US/10/411,012  
: CURRENT FILING DATE: 2003-04-09

QY	1	ATGGCTTACAGGCTCCCGGACGTCCTGGCTCTGGCTTTTGGCCGCTGCTGCTCCCTGG	60
Db	1	MetAlaThrGlySerIleArgThrIleSerLeuLeuAlaPheMetLeuLeuCysLeuProTrp	20
QY	61	CTTCAAGAGGGCAGTGGCTTTCCCAACATTCCCTTATCCAGGCTTTTGGACACGCTAGT	120
Db	21	LeuGlnGlnGlySerIleAlaPheProThrIleProLeuSerArgProPheAlaAlaMet	40
QY	121	CTCCGGGCCATCGTGTGACACGAGCTGGGCTTTGACACCTACAGAGATT-----	177
Db	41	LeuArgAlaHisArgLeuHisGlnLeuAlaPheAspThrTyrlGlnIlePheGlnGluAla	60
QY	172	-----AACCCCGACGCTCCCTCTGTTTC	195
Db	61	ThrIleProIleGlyGlnGlnIleTyrlSerPheLeuGlnAsnProGlnThrSerLeuCysPhe	80
QY	196	TCAGAGCTATTCCGACACCTTCACAACAGAGAGAAACAACAAGAAATCCAACTAGAG	255
Db	81	SerGlnSerIleProThrProSerAsnArgGlnGlnIleThrGlnGlnIleYsserAsnLeuGln	100
QY	256	CTGGCTCCGCATTCCTCTGCTGCTCATTCACAGTGTGGCTGGAGCCCTGGAGTTCCTCAGG	315
Db	101	LeuLeuArgIleSerLeuLeuLeuIleGlnInsertTrpIleGlnProValGlnPheLeuArg	120

Db 201 ThrPheLeuArgIleValGlnCysArgSerValGlnGlySerCysGlyPhe 217

RESULT 15

US-10-287-994-48  
Sequence 48, Application US/10287994  
Publication No. US20040137557A1  
GENERAL INFORMATION:

APPLICANT: Neose Technologies, Inc.  
APPLICANT: Defrees, Shawn  
APPLICANT: Zopf, David  
APPLICANT: Bayer, Robert  
APPLICANT: Bove, Caryn  
APPLICANT: Hakes, David  
APPLICANT: Chen, Xi  
TITLE OR INVENTION: REMODELING AND GLYCOCOMBINATION OF PEPTIDES  
FILE REFERENCE: 040853-01-5052-00  
CURRENT FILING DATE: 2002-11-05  
PRIOR FILING DATE: 2002-11-05  
PRIOR FILING DATE: 2001-10-10  
PRIOR FILING DATE: 2001-10-10  
PRIOR FILING DATE: 2001-10-19  
PRIOR FILING DATE: 2001-10-19  
PRIOR FILING DATE: 2002-06-07  
PRIOR FILING DATE: 2002-06-07  
PRIOR FILING DATE: 2002-06-25  
PRIOR FILING DATE: 2002-07-17  
PRIOR FILING DATE: 2002-07-17  
PRIOR FILING DATE: 2002-08-16  
PRIOR FILING DATE: 2002-08-16  
PRIOR FILING DATE: 2002-08-28  
PRIOR FILING DATE: 2002-08-28  
NUMBER OF SEQ ID NOS: 62  
SOFTWARE: PatentIn version 3.1  
SEQ ID NO 48  
LENGTH: 217  
TYPE: PRT  
ORGANISM: Homo sapiens  
US-10-287-994-48

Alignment Scores:  
Pred. No.: 7,52e-85 Length: 217  
Score: 1017.50 Matches: 200  
Percent Similarity: 92.17% Conservative: 0  
Best Local Similarity: 92.17% Mismatches: 2  
Query Match: 91.50% Indels: 15  
DB: 16 Gaps: 1

US-09-856-796B-1 (1-609) x US-10-287-994-48 (1-217)

QY 1 ATGGCTACAGGCTCCCGGAGGTCCCTGCTTGGCTTGGCTGCTGCTGCTGCTG 60  
DB 1 MetAlaThrIleSerArgThrSerLeuLeuAlaPheGlyLeuLeuCysLeuProTyr 20  
QY 61 CTCGAGAGGGGAGTGGCTTCCCAACCATTCCTTATCCAGGCTTTTGAACAAGCTAGT 120  
DB 21 LeuGlnIleuGlySerAlaPheProThrIleProLeuSerArgProPheAspAlaMet 40  
QY 121 CTCGCGCCCATCTGCTGACACAGCTGAGCTTTGACACCTTACAGAGATT----- 171  
DB 41 LeuArgIleAlaIleValGlnIleGlnLeuAlaPheAspThrTyrGlnIlePheGlnIleAla 60  
QY 172 -----AACCCCGAGACCTCCCTGTGTTTC 195  
DB 61 TyrIleProIleGlnIleGlnIleTyrSerPheLeuGlnAlaAsnProGlnThrSerLeuCysPhe 80  
QY 196 TCAGAGCTATTCGAGACCCCTCCCAACGAGGAGAAACAACAAGAAATCCAACTAGAG 255  
DB 81 SerIleSerIleProIleProIleProIleProIleProIleProIleProIleProIle 100  
QY 256 CTGCTCGCATCTCCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 315

Db - 101 LeuLeuArgIleSerLeuLeuLeuIleGlnSerTyrPheGlnProValGlnPheLeuArg 120  
QY 316 AGTGTCTTGCCCAACAGCCTGAGTGTACGGCGCCTCTGACAGCAACCTTATGACCTCTTA 375  
DB 121 SerValPheAlaAsnSerLeuValTyrGlyAlaSerAspSerAsnValTyrAspLeuLeu 140  
QY 376 AAGGACCTAGAGGAGGAGCATCCAAAGCTGATGAGGAGGAGGAGGAGGAGGAGGAGGAGG 435  
DB 141 LysAspLeuGlnIleGlnIleGlnIleGlnIleGlnIleGlnIleGlnIleGlnIleGlnIle 160  
QY 436 ACTGGGCAAGTCTTCAAGCAGACCTTACAGCAAGTTCGACACAACTCACACACAGATGAC 495  
DB 161 ThrGlyIlePheIlePheIleGlnIleThrTyrSerIlePheAspThrAsnSerIleAsnAspAsp 180  
QY 496 GCACTACTCAAGAACTACGGGCTGCTCTACTGCTTCAAGGAGGAGGAGGAGGAGGAGGAGG 555  
DB 181 AlaLeuLeuIleValGlnCysArgSerValGlnGlySerCysGlyPhe 200  
QY 556 ACAATCTGCGCATCTGCGAGTGCAGTCCGCTGCTGAGGAGGAGGAGGAGGAGGAGGAGG 606  
DB 201 ThrPheLeuArgIleValGlnCysArgSerValGlnGlySerCysGlyPhe 217

Search completed: February 6, 2005, 13:44:20  
Job time : 119 secs



1 ATGGCTACAGGCTCCCGAAGTCCCTGCTCTTGAGCTTTGAGCTTACTGTGCCTTCAGCCTTCA 60

Db 1 ATGGCTACAGAGCTCCCGAGCTCCCTGCTCTGCTTTTGCCCTGCTCTGCTCCCTG 60  
 QY 61 CTTCAAGAGGAGCTGCTCCCAACCACTTCCCTATCCAGGCTTTTGAACAAGCTAGT 120  
 Db 61 CTTCAAGAGGAGCTGCTCCCAACCACTTCCCTATCCAGGCTTTTGAACAAGCTAGT 120  
 QY 121 CTCGGGGCCCATGCTGCAACAGCTGCTTTGACCTTACAGAGTTTAACTCCCAAG 180  
 Db 121 CTCGGGGCCCATGCTGCAACAGCTGCTTTGACCTTACAGAGTTTAACTCCCAAG 180  
 QY 181 ACCTCCCTGTTTCTGAGAGTATTCGACACCTCTCAACAGGAGGAAACAAACAG 240  
 Db 181 ACCTCCCTGTTTCTGAGAGTATTCGACACCTCTCAACAGGAGGAAACAAACAG 240  
 QY 241 AAATCCAACTAGAGCTGCTCCGATCTCCCTGCTGCTATCCAGTGGCTGAGGCC 300  
 Db 241 AAATCCAACTAGAGCTGCTCCGATCTCCCTGCTGCTATCCAGTGGCTGAGGCC 300  
 QY 301 GTGCAAGTCTCAGAGAGTCTTGCCCAACAGCTGCTGCTATCCAGTGGCTGAGGCC 360  
 Db 301 GTGCAAGTCTCAGAGAGTCTTGCCCAACAGCTGCTGCTATCCAGTGGCTGAGGCC 360  
 QY 361 GTCATGACCTCTTAAGAGAGCTAGAGAGGATCCAAACGCTGATGGGAGGCTGGA 420  
 Db 361 GTCATGACCTCTTAAGAGAGCTAGAGAGGATCCAAACGCTGATGGGAGGCTGGA 420  
 QY 421 GATGCAAGCTCTTAAGAGAGCTAGAGAGGATCCAAACGCTGATGGGAGGCTGGA 480  
 Db 421 GATGCAAGCTCTTAAGAGAGCTAGAGAGGATCCAAACGCTGATGGGAGGCTGGA 480  
 QY 481 TCACACAAGATGAGCACTACTCAAGAACTACGGGCTGCTACTGCTTCAAGAGGAC 540  
 Db 481 TCACACAAGATGAGCACTACTCAAGAACTACGGGCTGCTACTGCTTCAAGAGGAC 540  
 QY 541 ATGCAAGATGAGCACTACTGCGCATGCTGAGTGCAGTGCCTCTGTGAGAGGAGCTGT 600  
 Db 541 ATGCAAGATGAGCACTACTGCGCATGCTGAGTGCAGTGCCTCTGTGAGAGGAGCTGT 600  
 QY 601 GGCCTCTAG 609  
 Db 601 GGCCTCTAG 609

RESULT 2  
 LOCUS AX025440 609 bp DNA linear PAT 16-SEP-2000  
 DEFINITION Sequence 1 from Patent FR2786104.  
 ACCESSION AX025440  
 VERSION AX025440.1 GI:10187116  
 KEYWORDS  
 SOURCE Homo sapiens (human)  
 ORGANISM Homo sapiens  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

REFERENCE 1  
 AUTHORS Haeflner A. and Hirsch F.  
 JOURNAL Patent: FR 2786104-A 1 26-MAY-2000;  
 CENTRE NAT RECH SCIENT (FR)  
 FEATURES  
 source location/Qualifiers  
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 /db\_xref="taxon:9606"  
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 /note="unassigned protein product"  
 /codon\_start=1  
 /protein\_id="CAC09043.1"  
 /db\_xref="GI:10187117"

CDS

translation="WATSKRTSLIAFGILCLPMLQESAPFTIPISLFDNASIRAH  
 RLHSLAPTOYEFNPTSLCFESLPTPSNRETOOKSLVLEIRISLILQSMLEVO  
 FLRSVPANSLVYAGDSNVYDLKDLLEGIOTLMGLIEDGSPRTGIFKQTSKFDIN  
 SHNDALIKNYGLLYCFRKMVKVETFLIIVOCRSVSGSGF"

ORIGIN

Query Match 100.0%; Score 609; DB 6; Length 609;  
 Best Local Similarity 100.0%; Pred. No. 1.5e-132;  
 Matches 609; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATGGCTACAGAGCTCCCGAGCTCCCTGCTCTGCTTTTGCCCTGCTCTGCTCCCTG 60  
 Db 1 ATGGCTACAGAGCTCCCGAGCTCCCTGCTCTGCTTTTGCCCTGCTCTGCTCCCTG 60  
 QY 61 CTTCAAGAGGAGTGGCTTCCCAACCACTTCCCTATCCAGGCTTTTGAACAAGCTAGT 120  
 Db 61 CTTCAAGAGGAGTGGCTTCCCAACCACTTCCCTATCCAGGCTTTTGAACAAGCTAGT 120  
 QY 121 CTCGGGGCCCATGCTGCAACAGCTGCTTTGACCTTACAGAGTTTAACTCCCAAG 180  
 Db 121 CTCGGGGCCCATGCTGCAACAGCTGCTTTGACCTTACAGAGTTTAACTCCCAAG 180  
 QY 181 ACCTCCCTGTTTCTGAGAGTATTCGACACCTCTCAACAGGAGGAAACAAACAG 240  
 Db 181 ACCTCCCTGTTTCTGAGAGTATTCGACACCTCTCAACAGGAGGAAACAAACAG 240  
 QY 241 AAATCCAACTAGAGCTGCTCCGATCTCCCTGCTGCTATCCAGTGGCTGAGGCC 300  
 Db 241 AAATCCAACTAGAGCTGCTCCGATCTCCCTGCTGCTATCCAGTGGCTGAGGCC 300  
 QY 301 GTGCAAGTCTCAGAGAGTCTTGCCCAACAGCTGCTGCTATCCAGTGGCTGAGGCC 360  
 Db 301 GTGCAAGTCTCAGAGAGTCTTGCCCAACAGCTGCTGCTATCCAGTGGCTGAGGCC 360  
 QY 361 GTCATGACCTCTTAAGAGAGCTAGAGAGGATCCAAACGCTGATGGGAGGCTGGA 420  
 Db 361 GTCATGACCTCTTAAGAGAGCTAGAGAGGATCCAAACGCTGATGGGAGGCTGGA 420  
 QY 421 GATGCAAGCTCTTAAGAGAGCTAGAGAGGATCCAAACGCTGATGGGAGGCTGGA 480  
 Db 421 GATGCAAGCTCTTAAGAGAGCTAGAGAGGATCCAAACGCTGATGGGAGGCTGGA 480  
 QY 481 TCACACAAGATGAGCACTACTCAAGAACTACGGGCTGCTACTGCTTCAAGAGGAC 540  
 Db 481 TCACACAAGATGAGCACTACTCAAGAACTACGGGCTGCTACTGCTTCAAGAGGAC 540  
 QY 541 ATGCAAGATGAGCACTACTGCGCATGCTGAGTGCAGTGCCTCTGTGAGAGGAGCTGT 600  
 Db 541 ATGCAAGATGAGCACTACTGCGCATGCTGAGTGCAGTGCCTCTGTGAGAGGAGCTGT 600  
 QY 601 GGCCTCTAG 609  
 Db 601 GGCCTCTAG 609

RESULT 3  
 LOCUS E00974 3387 bp RNA linear PAT 29-SEP-1997  
 DEFINITION cDNA encoding human growth factor 20K.  
 ACCESSION E00974  
 VERSION E00974.1 GI:2169235  
 KEYWORDS UP 1986224988-A/1.  
 SOURCE Homo sapiens (human)  
 ORGANISM Homo sapiens  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

REFERENCE 1 (bases 1 to 3387)  
 AUTHORS Nakajima K. and Nagai J.  
 JOURNAL RECOMBINANT PLASMID OF ESCHERICHIA COLI FOR AMPLIFYING  
 COMPLEMENTARY DNA OF HUMAN GROWTH HORMONE 20K  
 Patent: JP 1986224988-A 1 06-OCT-1986;  
 NAKAJIMA KUNIO

COMMENT OS Human  
 PN JP 1986224988-A/1  
 PD 06-OCT-1986  
 PE 29-MAR-1985 JP 1985066208  
 PI NAKAJIMA KUNIO, NAGAI JUN  
 PC C12N15/00//C12P21/02, (C12N15/00, C12R1:19);



QY	1	ATGCTTAAGAGTCTCCCGAGCTCCTGCTCTCGAGGTTTGTGGCTGCTGCTGCGCCCTGG	60
Db	13	ATGGCTGAAGGCTCTCCCGACGCTCCTGCTCTCGAGGTTTGTGGCTGCTGCTGCTGCTG	72
QY	61	CTTCAAGAGGGGAGGCGCTTCCCAACCATTCCTCATCAGGCTTTTGTACAACGCTAGT	120
Db	73	CTTCAAGAGGGGAGGCGCTTCCCAACCATTCCTCATCAGGCTTTTGTACAACGCTAG	132
QY	121	CTCCGCGCCCATCTGTCTGCAACGAGTGGCTTGTGACCTACAGAGATTAAACCCCGAG	180
Db	133	CTCCGCGCCCGTGTGCTGTACAGGCTGGCATATGACCTTACAGGAGTTTAAACCCCGAG	192
QY	181	ACCTCCCTCTGTTTCTCAGAGTCTATTCGACACCTCCAAACAGGAGGAAACACAAACAG	240
Db	193	ACCTCCCTCTGCTTCTCAAGTCTATTCMAACCTTCCAAACAGGAGTGAACAGCAGCAG	252
QY	241	AAATCCAACTTAGAGCTGTGCTCCGCAATCTCCGCTCATCAGTCTGATGGCTGAGAGCC	300
Db	253	AAATCTAACCTTAGAGTGTGCTCCGCAATCTCCGCTCATCAGTCTGATGGCTGAGAGCC	312
QY	301	GTCGAGTTCCTGAGAGTGTCTTCGCAACAGGCTGTGTACGAGCGCCTCTGACAGCAAC	360
Db	313	GTCGAGTTCCTGAGAGGCTCTTCGCAACAGGCTGTGTATGGCGCCTCTGACAGCAAC	372
QY	361	GTCCTATGACCTCCTTAAGGACCTTAGAGGAAGGATCCAAACGCTGATGGGAGGCTGGAA	420
Db	373	GTCCTATGCGACCTGAAGGACCTTAGAGGAAGGATCCAAACGCTGATGGGAGGCTGGAA	432
QY	421	GATGGAGGCCCCCGGACTGGGCGAATCTTACACACACCTACAGCAGAGTTGACACAAAC	480
Db	433	GATGGAGGCCCCCGGACTGGGCGAATCTTACACACACCTACAGCAGAGTTTGTACAAAAA	492
QY	481	TGACACACGATGACGACTACTACAGAACTAGGGCTGCTTAAGCTTACAGAAAGAC	540
Db	493	TGCGACACGATATCGACTGCTCAAGAACTACGGGCTGCTTAAGCTTACAGAAAGAC	552

QY 541 ATGCAAGAGTGCAGATCTTCTGCGCATGTCAGTGGCGGCTGTGTGAGGAGGAGCTGT 600  
DB 553 ATGCAAGAGTGCAGATCTTCTGCGCATGTCAGTGGCGGCTGTGTGAGGAGGAGCTGT 612  
QY 601 GGCTTCTAG 609  
DB 613 GGCTTCTAG 621

RESULT 6  
AX300799 654 bp DNA linear PAT 30-NOV-2001  
LOCUS Sequence 1 from Patent WO0185993.  
DEFINITION AX300799  
ACCESSION AX300799  
VERSION AX300799.1 GI:17382080  
KEYWORDS  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.  
REFERENCE 1  
AUTHORS Cooper,D.N., Procter,A.M., Gregory,J.D. and Millar,D.S.  
TITLE Method for detecting growth hormone variations in humans, the  
JOURNAL variations and their uses  
Patent: WO 0185993-A 1 15-NOV-2001;  
University of Wales College of Medicine (GB)  
FEATURES  
source 1..654  
/organism="Homo sapiens"  
/mol\_type="unassigned DNA"  
/db\_xref="taxon:9606"

ORIGIN  
Query Match 91.0%; Score 554; DB 6; Length 654;  
Best Local Similarity 93.1%; Pred. No. 1.3e-119;  
Matches 609; Conservative 0; Mismatches 0; Indels 45; Gaps 1;

QY 1 ATGGCTACAGGCTCCCGAGCGTCCCTGCTCTGCTGCTTTGGGCTGCTGCTGCTGCTGCTG 60  
DB 1 ATGGCTACAGGCTCCCGAGCGTCCCTGCTCTGCTGCTTTGGGCTGCTGCTGCTGCTGCTG 60  
QY 61 CTTCAGAGGGGAGGAGGCTTCCCAACATTCCTTATCCAGGCTTTTGAACAGCTAGT 120  
DB 61 CTTCAGAGGGGAGGAGGCTTCCCAACATTCCTTATCCAGGCTTTTGAACAGCTAGT 120  
QY 121 CTCCGGCGCCATCGTCTGCAACAGCTGGCTTTGACACCTACAGAGTTT----- 171  
DB 121 CTCCGGCGCCATCGTCTGCAACAGCTGGCTTTGACACCTACAGAGTTTGGGAGAGCC 180  
QY 172 -----AACCCCGACAGCTCTCTGTTTC 195  
DB 181 TATATCCCAAGAAAGAGATATTCTCTGAGAAACCCCGACAGCTCTCTGTTTC 240  
QY 196 TCAGAGTATATTCGACACCTCCCAAGAGGAGAAACAGAAATCCAACTAGAG 255  
DB 241 TCAGAGTATATTCGACACCTCCCAAGAGGAGAAACAGAAATCCAACTAGAG 300  
QY 256 CTGCTCCGATCTCCCTGCTGCTCATTCAGTGTGTGAGGCGCGGTCAGTTCCTCAGG 315  
DB 301 CTGCTCCGATCTCCCTGCTGCTCATTCAGTGTGTGAGGCGCGGTCAGTTCCTCAGG 360  
QY 316 AGTGTCTTCCGCAACAGCTGTGTGAGGCGCTTGAACAGCAAGTCTATGACTCTTA 375  
DB 361 AGTGTCTTCCGCAACAGCTGTGTGAGGCGCTTGAACAGCAAGTCTATGACTCTTA 420  
QY 376 AAGGACTTGAAGAGGAGGATCCAAACGCTGATGGGAGAGCTGGAATGAGAGCCCGGG 435  
DB 421 AAGGACTTGAAGAGGAGGATCCAAACGCTGATGGGAGAGCTGGAATGAGAGCCCGGG 480  
QY 436 ACTGGGAGATCTTCAAGCAGACCTACAGAGTTCGACAAATCTCACACAGATGAC 495  
DB 481 ACTGGGAGATCTTCAAGCAGACCTACAGAGTTCGACAAATCTCACACAGATGAC 540

QY 496 GCACACTCAAGAACTACAGGAGGCTGCTTACAGTCTTACAGGAGACATGAGAGCTGAG 555  
DB 541 GCACACTCAAGAACTACAGGAGGCTGCTTACAGTCTTACAGGAGACATGAGAGCTGAG 600  
QY 556 ACATTCCTGCGCATGTCAGTGCAGTCCGCTCTGAGAGGAGGAGCTTGGCTTCTAG 609  
DB 601 ACATTCCTGCGCATGTCAGTGCAGTCCGCTCTGAGAGGAGGAGCTTGGCTTCTAG 654

RESULT 7  
AX149376 807 bp DNA linear PAT 08-JUN-2001  
LOCUS AX149376  
DEFINITION Sequence 25 from Patent WO0136635.  
ACCESSION AX149376  
VERSION AX149376.1 GI:14347892  
KEYWORDS  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.  
REFERENCE 1  
AUTHORS Majumder,K., Prayaga,S.K. and Burgess,C.  
TITLE Neurite outgrowth-promoting factor homologue and nucleic acids  
JOURNAL encoding same  
Patent: WO 0136635-A 25 25-MAY-2001;  
Curagen Corporation (US)  
FEATURES  
source 1..807  
/organism="Homo sapiens"  
/mol\_type="unassigned DNA"  
/db\_xref="taxon:9606"

ORIGIN  
Query Match 91.0%; Score 554; DB 6; Length 807;  
Best Local Similarity 93.1%; Pred. No. 1.3e-119;  
Matches 609; Conservative 0; Mismatches 0; Indels 45; Gaps 1;

QY 1 ATGGCTACAGGCTCCCGAGCGTCCCTGCTCTGCTGCTTTGGGCTGCTGCTGCTGCTGCTG 60  
DB 51 ATGGCTACAGGCTCCCGAGCGTCCCTGCTCTGCTGCTTTGGGCTGCTGCTGCTGCTGCTG 110  
QY 61 CTTCAGAGGGGAGGAGGCTTCCCAACATTCCTTATCCAGGCTTTTGAACAGCTAGT 120  
DB 111 CTTCAGAGGGGAGGAGGCTTCCCAACATTCCTTATCCAGGCTTTTGAACAGCTAGT 170  
QY 121 CTCCGGCGCCATCGTCTGCAACAGCTGGCTTTGACACCTACAGAGTTT----- 171  
DB 171 CTCCGGCGCCATCGTCTGCAACAGCTGGCTTTGACACCTACAGAGTTTGAAGAGCC 230  
QY 172 -----AACCCCGACAGCTCTCTGTTTC 195  
DB 231 TATATCCCAAGAAAGAGATATTCTCTGAGAAACCCCGACAGCTCTCTGTTTC 290  
QY 196 TCAGAGTATATTCGACACCTCCCAAGAGGAGAAACAGAAATCCAACTAGAG 255  
DB 291 TCAGAGTATATTCGACACCTCCCAAGAGGAGAAACAGAAATCCAACTAGAG 350  
QY 256 CTGCTCCGATCTCCCTGCTGCTCATTCAGTGTGTGAGGCGCGGTCAGTTCCTCAGG 315  
DB 351 CTGCTCCGATCTCCCTGCTGCTCATTCAGTGTGTGAGGCGCGGTCAGTTCCTCAGG 410  
QY 316 AGTGTCTTCCGCAACAGCTGTGTGAGGCGCTTGAACAGCAAGTCTATGACTCTTA 375  
DB 411 AGTGTCTTCCGCAACAGCTGTGTGAGGCGCTTGAACAGCAAGTCTATGACTCTTA 470  
QY 376 AAGGACTTGAAGAGGAGGATCCAAACGCTGATGGGAGAGCTGGAATGAGAGCCCGGG 435  
DB 471 AAGGACTTGAAGAGGAGGATCCAAACGCTGATGGGAGAGCTGGAATGAGAGCCCGGG 530  
QY 436 ACTGGGAGATCTTCAAGCAGACCTACAGAGTTCGACAAATCTCACACAGATGAC 495  
DB 531 ACTGGGAGATCTTCAAGCAGACCTACAGAGTTCGACAAATCTCACACAGATGAC 590

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QY      496 GCACTACTCAAGAACTACGGGGCTGCTCTACTGCTTCAGAGAGACATGAGCAAGGTGAG 555
DB      591 GCACTACTCAAGAACTACGGGGCTGCTCTACTGCTTCAGAGAGACATGAGCAAGGTGAG 650
QY      556 ACATTCTCGGCATCGTGCAGTGCCTCTCTGAGAGGGAGCTGTGGCTTTCTAG 609
DB      651 ACATTCTCGGCATCGTGCAGTGCCTCTCTGAGAGGGAGCTGTGGCTTTCTAG 704

RESULT 8
LOCUS    AXI49381                807 bp    DNA        linear    PAT 08-JUN-2001
DEFINITION
Sequence 30 from Patent WO0136635.
ACCESSION AXI49381
VERSION    AXI49381.1  GI:14347893
KEYWORDS
SOURCE     Homo sapiens (human)
ORGANISM   Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

REFERENCE
1
AUTHORS   Majumder, K., Prayaga, S. K. and Burgess, C.
TITLE      Neurite outgrowth-promoting factor homologue and nucleic acids
            encoding same
JOURNAL    Patent: WO 0136635-A 30 25-MAY-2001;
            Curagen Corporation (US)
FEATURES
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                        /mol_type="unassigned DNA"
                        /db_xref="taxon:9606"

ORIGIN
Query Match      91.0%; Score 554; DB 6; Length 807;
Best Local Similarity 93.1%; Pred. No. 1,3e-119;
Matches 609; Conservative 0; Mismatches 0; Indels 45; Gaps 1;

QY      1  ATGGCTACAGAGCTCCCGAGCTCCCTGCTCTGCTGCTTTGGCTGCTGCTGCTGCTG 60
DB      51  ATGGCTACAGAGCTCCCGAGCTCCCTGCTCTGCTGCTTTGGCTGCTGCTGCTGCTG 110
QY      61  CTTCAAGAGGGCAGTGCCTTCCCAACCATTCCTTATCCAGGCTTTTGAACAAGCTAGT 120
DB      111 CTTCAAGAGGGCAGTGCCTTCCCAACCATTCCTTATCCAGGCTTTTGAACAAGCTAGT 170
QY      121 CTGGGCGCCATCGTCTGCAACGAGCTGCGCTTTGACACCTACGAGATT----- 171
DB      171 CTGGGCGCCATCGTCTGCAACGAGCTGCGCTTTGACACCTACGAGATTGGAAGAGCC 230
QY      172 -----AACCCGAGACCTCCCTCTGTTTC 195
DB      231 TATATCCCAAGAAAGAAAGATTCATTCTCGCAGAACCCCGAGACTCTCTGTTTC 290
QY      196 TCAGAGCTATATTCGAGACCTCTCAACAGAGAGAAACAACAAGAAATCCAACTAGAG 255
DB      291 TCAGAGCTATATTCGAGACCTCTCAACAGAGAGAAACAACAAGAAATCCAACTAGAG 350
QY      256 CTGCTCCGCATCTCCCTGCTGCTCATCGTGTGCTGGAGCCCGTGCAGTTCTCAGG 315
DB      351 CTGCTCCGCATCTCCCTGCTGCTCATCGTGTGCTGGAGCCCGTGCAGTTCTCAGG 410
QY      316 AGTGTCTTGCCCAACAGCTGTGTGAGGGGCTCTGACAGCAAGCTCTATGAACTCTTA 375
DB      411 AGTGTCTTGCCCAACAGCTGTGTGAGGGGCTCTGACAGCAAGCTCTATGAACTCTTA 470
QY      376 AAGAACCTNAGAGAGAGCTCAAAAGCTGATGGAGAGGTGGAAGATGGCAACCCCGG 435
DB      471 AAGAACCTNAGAGAGAGCTCAAAAGCTGATGGAGAGGTGGAAGATGGCAACCCCGG 530
QY      436 ACTGGGAGATCTTCAAGAGAGCTTACAGCAAGTTGAGCAACAACCTACAGCAAGATGAC 495
DB      531 ACTGGGAGATCTTCAAGAGAGCTTACAGCAAGTTGAGCAACAACCTACAGCAAGATGAC 590

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QY      496 GCACTACTCAAGAACTACGGGGCTGCTCTACTGCTTCAGAGAGACATGAGCAAGGTGAG 555
DB      591 GCACTACTCAAGAACTACGGGGCTGCTCTACTGCTTCAGAGAGACATGAGCAAGGTGAG 650
QY      556 ACATTCTCGGCATCGTGCAGTGCCTCTCTGAGAGGGAGCTGTGGCTTTCTAG 609
DB      651 ACATTCTCGGCATCGTGCAGTGCCTCTCTGAGAGGGAGCTGTGGCTTTCTAG 704

RESULT 9
LOCUS    E00952                3477 bp    DNA        linear    PAT 29-SEP-1997
DEFINITION
Plasmid DNA for amplifying human growth factor gene in E.coli.
ACCESSION E00952
VERSION    E00952.1  GI:2169213
KEYWORDS   JP 1986202689-A/1.
SOURCE     Synthetic construct
ORGANISM   Synthetic construct
            other sequences: artificial sequences.
            1 (bases 1 to 3477)
REFERENCE
1
AUTHORS   Nakajima, K. and Nagai, J.
TITLE      RECOMBINANT PLASMID OF ESCHERICHIA COLI FOR AMPLIFICATION OF HUMAN
            GROWTH HORMONE COMPLEMENTARY STRAND DNA
JOURNAL    Patent: JP 1986202689-A 1 08-SEP-1986;
            NAKAJIMA KUNIO
FEATURES
            COMMENT        OS Artificial gene
                        OC Artificial sequence; Genes.
                        PN JP 1986202689-A/1
                        PD 08-SEP-1986
                        PP 04-MAR-1985  JP 1985042404
                        PT NAKAJIMA KUNIO, NAGAI JUN
                        PC C12N15/00//C12P21/02;
                        CC strandedness: Double;
                        CC topology: Linear;
                        CC hypothetical: No;
                        CC anti-sense: No;
                        FH Key
                        FH Location/Qualifiers
                        misc_feature      280
                        FT /note="G=(G)n"
                        FT misc_feature      1107
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                        FT Location/Qualifiers
                        1..3477
                        /organism="synthetic construct"
                        /mol_type="genomic DNA"
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ORIGIN
Query Match      91.0%; Score 554; DB 6; Length 3477;
Best Local Similarity 93.1%; Pred. No. 1,1e-119;
Matches 609; Conservative 0; Mismatches 0; Indels 45; Gaps 1;

QY      1  ATGGCTACAGAGCTCCCGAGCTCCCTGCTCTGCTGCTTTGGCTGCTGCTGCTGCTG 60
DB      354 ATGGCTACAGAGCTCCCGAGCTCCCTGCTCTGCTGCTTTGGCTGCTGCTGCTGCTG 413
QY      61  CTTCAAGAGGGCAGTGCCTTCCCAACCATTCCTTATCCAGGCTTTTGAACAAGCTAGT 120
DB      414 CTTCAAGAGGGCAGTGCCTTCCCAACCATTCCTTATCCAGGCTTTTGAACAAGCTAGT 473
QY      414 CTTCAAGAGGGCAGTGCCTTCCCAACCATTCCTTATCCAGGCTTTTGAACAAGCTAGT 473
DB      474 CTTCAAGAGGGCAGTGCCTTCCCAACCATTCCTTATCCAGGCTTTTGAACAAGCTAGT 533
QY      121 CTGGGCGCCATCGTCTGCAACGAGCTGCGCTTTGACACCTACGAGATT----- 171
DB      474 CTTGGGCGCCATCGTCTGCAACGAGCTGCGCTTTGACACCTACGAGATTGGAAGAGCC 533
QY      172 -----AACCCGAGACCTCCCTCTGTTTC 195
DB      534 TATATCCCAAGAAAGAAAGATTCATTCTCGCAGAACCCCGAGACTCTCTGTTTC 593
QY      196 TCAGAGCTATATTCGAGACCTCTCAACAGAGAGAAACAACAAGAAATCCAACTAGAG 255
DB      594 TCAGAGCTATATTCGAGACCTCTCAACAGAGAGAAACAACAAGAAATCCAACTAGAG 653

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QY 256 CTGCTCCGATCTCCCTGCTGCTCATCGTGTGCTGAGCCCTGCGATTCTCTCAG 315  
DB 654 CTGCTCCGATCTCCCTGCTGCTCATCGTGTGCTGAGCCCTGCGATTCTCTCAG 713  
QY 316 AGTGTCTTCCGCAAGCAGCTGTGTGTAAGGCGCTCTGACAGCAAGCTATGACCTCTCA 375  
DB 714 AGTGTCTTCCGCAAGCAGCTGTGTGTAAGGCGCTCTGACAGCAAGCTATGACCTCTCA 773  
QY 376 AAGGACCTTAGAGGAGGATCTCAAAAGCTGATGAGGAGGCTGGAAGATGCGAGCCCGG 435  
DB 774 AAGGACCTTAGAGGAGGATCTCAAAAGCTGATGAGGAGGCTGGAAGATGCGAGCCCGG 833  
QY 436 ACTGGGCGAGATCTTCAAGCAGACCTTAGAGGAGGATCTGACAGCAAGCTATGACAGTAC 495  
DB 834 ACTGGGCGAGATCTTCAAGCAGACCTTAGAGGAGGATCTGACAGCAAGCTATGACAGTAC 893  
QY 496 GCACTACTCAAGAACTAGAGGCTGCTCTACTGCTTCAAGGAGGAGATGACAGTCTGAG 555  
DB 894 GCACTACTCAAGAACTAGAGGCTGCTCTACTGCTTCAAGGAGGAGATGACAGTCTGAG 953  
QY 556 ACATTCTCTGCGCATCTGTCAGTGTGCTGTGTGAGGAGGAGCTGTGCTCTAG 609  
DB 954 ACATTCTCTGCGCATCTGTCAGTGTGCTGTGTGAGGAGGAGCTGTGCTCTAG 1007

## RESULT 10

LOCUS CQ827137 600 bp DNA linear PAT 29-JUN-2004  
DEFINITION Sequence 7 from Patent WO2004050703.  
ACCESSION CQ827137  
VERSION CQ827137.1 GI:49455716  
KEYWORDS  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens

## REFERENCE

1 Fagan, R. J., Phelps, C. B., Rodrigues, T. M., York, M. and de Triani, M.  
TITLE Splice variant of the human pituitary growth hormone  
JOURNAL Patent: WO 2004050703-A 7 17-JUN-2004;  
ARBS TRADING S.A. (CH)  
FEATURES  
source 1..600  
Location/Qualifiers  
/organism="Homo sapiens"  
/mol\_type="unassigned DNA"  
/db\_xref="taxon:9606"

## ORIGIN

Query Match 90.9%; Score 553.8; DB 6; Length 600;  
Best Local Similarity 95.7%; Pred. No. 1,4e-119;  
Matches 583; Conservative 0; Mismatches 17; Indels 9; Gaps 1;

QY 1 ATGGCTACAGGCTCCCGAGAGTCCCTGCTCTGCTTTGGCTTGGCTGCTGCTGCTGCTG 60  
DB 1 ATGGCTACAGGCTCCCGAGAGTCCCTGCTCTGCTTTGGCTTGGCTGCTGCTGCTGCTG 60  
QY 61 CTTCAAGAGGAGGAGTGTCTTCCCAACCATTCCTTATCCAGGCTTTTGAACAAGCTAGT 120  
DB 61 CTTCAAGAGGAGGAGTGTCTTCCCAACCATTCCTTATCCAGGCTTTTGAACAAGCTAGT 120  
QY 121 CTCGGGCGCCATCTGTCAGACAGTGTGCTTGTGACACCTTACAGAGATTAAACCCCGAG 180  
DB 121 CTCGGGCGCCATCTGTCAGACAGTGTGCTTGTGACACCTTACAGAGATTAAACCCCGAG 180  
QY 181 ACCTCCCTCTGTTTCTAGAGTCTATTCGAGACACCTTCAACAGGAGAAACACACAG 240  
DB 181 ACCTCCCTCTGTTTCTAGAGTCTATTCGAGACACCTTCAACAGGAGAAACACACAG 240  
QY 241 AAATCAACCTTAGAGCTGCTCGCATCTCCCTGCTGCTATCAGTGTGCTGAGAGCC 300  
DB 241 AAATCAACCTTAGAGCTGCTCGCATCTCCCTGCTGCTATCAGTGTGCTGAGAGCC 300  
QY 291 AAATCAACCTTAGAGCTGCTCGCATCTCCCTGCTGCTATCAGTGTGCTGAGAGCC 291

QY 301 GTGAGATTCTCAGAGAGTGTCTTCCCAACAGCCTGTGTATAGGAGCCCTCTGACAGCAAC 360  
DB 292 GTGAGATTCTCAGAGAGTGTCTTCCCAACAGCCTGTGTATAGGAGCCCTCTGACAGCAAC 360  
QY 361 GTCTATGACCTTCTTAAAGGAGCTTAAAGGAGGAGGATCTCAACAGCTATGAGGAGGCTGAA 420  
DB 362 GTCTATGACCTTCTTAAAGGAGCTTAAAGGAGGAGGATCTCAACAGCTATGAGGAGGCTGAA 420  
QY 421 GATGGACACCCCGGACCTGGGAGATCTTCAAGCAGACCTTACAGAGATTGACACAAAC 480  
DB 422 GATGGACACCCCGGACCTGGGAGATCTTCAAGCAGACCTTACAGAGATTGACACAAAC 480  
QY 481 TCACACAGATGAGAGGAGCTTCTCAAGAACTACAGGAGGAGCTTCTTCTGCTTCAAGAGAG 540  
DB 472 TCACACAGATGAGAGGAGCTTCTCAAGAACTACAGGAGGAGCTTCTTCTGCTTCAAGAGAG 531  
QY 541 ATGACAGAGTCTGAGACATTCCTGCGCATCTGTCAGTGTGAGTGTGAGGAGGAGCTGT 600  
DB 532 ATGACAGAGTCTGAGACATTCCTGCGCATCTGTCAGTGTGAGTGTGAGGAGGAGCTGT 591  
QY 601 GCTTCTTCTG 609  
DB 592 GCTTCTTCTG 600

## RESULT 11

LOCUS AX659150 609 bp DNA linear PAT 22-MAR-2003  
DEFINITION Sequence 5 from Patent WO02101002.  
ACCESSION AX659150  
VERSION AX659150.1 GI:29161385  
KEYWORDS  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens

## REFERENCE

1 Becary, J. L.  
TITLE New polynucleotides and polypeptides of the HGH-V gene  
JOURNAL Patent: WO 02101002-A 5 19-DEC-2002;  
Genodysee (FR)  
FEATURES  
source 1..609  
Location/Qualifiers  
/organism="Homo sapiens"  
/mol\_type="unassigned DNA"  
/db\_xref="taxon:9606"

## ORIGIN

Query Match 90.8%; Score 553; DB 6; Length 609;  
Best Local Similarity 94.3%; Pred. No. 2.2e-119;  
Matches 574; Conservative 0; Mismatches 35; Indels 0; Gaps 0;

QY 1 ATGGCTACAGGCTCCCGAGAGTCCCTGCTCTGCTTTGGCTTGGCTGCTGCTGCTGCTG 60  
DB 1 ATGGCTACAGGCTCCCGAGAGTCCCTGCTCTGCTTTGGCTTGGCTGCTGCTGCTGCTG 60  
QY 61 CTTCAAGAGGAGGAGTGTCTTCCCAACCATTCCTTATCCAGGCTTTTGAACAAGCTAGT 120  
DB 61 CTTCAAGAGGAGGAGTGTCTTCCCAACCATTCCTTATCCAGGCTTTTGAACAAGCTAGT 120  
QY 121 CTCGGGCGCCATCTGTCAGACAGTGTGCTTGTGACACCTTACAGAGATTAAACCCCGAG 180  
DB 121 CTCGGGCGCCATCTGTCAGACAGTGTGCTTGTGACACCTTACAGAGATTAAACCCCGAG 180  
QY 181 ACCTCCCTCTGTTTCTAGAGTCTATTCGAGACACCTTCAACAGGAGAAACACACAG 240  
DB 181 ACCTCCCTCTGTTTCTAGAGTCTATTCGAGACACCTTCAACAGGAGAAACACACAG 240  
QY 241 AAATCAACCTTAGAGCTGCTCGCATCTCCCTGCTGCTATCAGTGTGCTGAGAGCC 300  
DB 241 AAATCAACCTTAGAGCTGCTCGCATCTCCCTGCTGCTATCAGTGTGCTGAGAGCC 300  
QY 301 GTGAGATTCTCAGAGAGTGTCTTCCCAACAGCCTGTGTATAGGAGCCCTCTGACAGCAAC 360



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Db      301 GTGAGGCTCTCAGAGCGTCTTCGCAACAGCCTGATGTATGGCCCTTCGACACACAC 360
OY      361 GTCTATGACCTCTCTAAAGAGCCTTAGAGAGAGGATCCAAAGCTGATGGGGAGGCTGAA 420
Db      361 GTCTATGACCTCTCTAAAGAGCCTTAGAGAGAGGATCCAAAGCTGATGGGGAGGCTGAA 420
OY      421 GATGGCAGCCCCGGAGCTGGGAGATCTTCAAGCAGACCTTAGAGAGTTCAGACAAAC 480
Db      421 GATGGCAGCCCCGGAGCTGGGAGATCTTCAAGCAGACCTTAGAGAGTTCAGACAAAC 480
OY      481 TCACACAGATGACGACACTACTCAGAACTACGAGGCTGCTCTACTGCTTCAGAGAGAC 540
Db      481 TCACACAGATGACGACACTACTCAGAACTACGAGGCTGCTCTACTGCTTCAGAGAGAC 540
OY      541 ATGACAAGGTGAGAGACATTCCTGCGCATGTCGACAGTCCGCTCTGTGAGGGGAGCTGT 600
Db      541 ATGACAAGGTGAGAGACATTCCTGCGCATGTCGACAGTCCGCTCTGTGAGGGGAGCTGT 600
OY      601 GGCCTTCTAG 609
Db      601 GGCCTTCTAG 609

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RESULT 12
AX719124 609 bp DNA linear PAT 15-APR-2003
LOCUS Sequence 5 from Patent EP1295938.
DEFINITION AX719124
ACCESSION AX719124
VERSION AX719124.1 GI:29891612
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE
1 Bescary, J.L.
AUTHORS Corrected sequence of the hgh-v gene and an allelic variant
TITLE Patent: EP 1295938-A 5 26-MAR-2003;
JOURNAL Genodyssee (FR)

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/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"
Location/Qualifiers

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ORIGIN
Query Match 90.8%; Score 553; DB 6; Length 609;
Best Local Similarity 94.3%; Pred. No. 2.2e-119;
Matches 574; Conservative 0; Mismatches 35; Indels 0; Gaps 0;

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OY      1 ATGGCTACAGGCTCCCGAGCGTCTGCTCTGCTGCTTTGGCGCTGCTGCTGCTGCTG 60
Db      1 ATGGCTACAGGCTCCCGAGCGTCTGCTCTGCTGCTTTGGCGCTGCTGCTGCTGCTG 60
OY      61 CTTCACAGGAGGAGCTGCTCCCAACCAATTCCTTATCCAGGCTTTTACAAAGCTAGT 120
Db      61 CTTCACAGGAGGAGCTGCTCCCAACCAATTCCTTATCCAGGCTTTTACAAAGCTAGT 120
OY      121 CTCGGCGCCCATGCTGTCACAGCTGGGCTTTGACACTTACAGAGATTAAACCCCAAG 180
Db      121 CTCGGCGCCCATGCTGTCACAGCTGGGCTTTGACACTTACAGAGATTAAACCCCAAG 180
OY      181 ACCTCCCTCTGTTTCTCAGAGTCTATTCGACACCTTCCAAAGGAGGAAACACACAG 240
Db      181 ACCTCCCTCTGTTTCTCAGAGTCTATTCGACACCTTCCAAAGGAGGAGGAAACACAG 240
OY      241 AAATCCAACTTAGAGCTGCTGCGCATCTCCCTGCTGCTCATTCAGTCGCTGAGGCC 300
Db      241 AAATCCAACTTAGAGCTGCTGCGCATCTCCCTGCTGCTCATTCAGTCGCTGAGGCC 300
OY      301 GTGCAATTCTCAGAGAGTCTTTCGCAACAGCTGATGAGGCGCTCTGACAGCAAC 360

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Db      301 GTGAGGCTCTCAGAGCGTCTTCGCAACAGCCTGATGTATGGCCCTTCGACACACAC 360
OY      361 GTCTATGACCTCTCTAAAGAGCCTTAGAGAGAGGATCCAAAGCTGATGGGGAGGCTGAA 420
Db      361 GTCTATGACCTCTCTAAAGAGCCTTAGAGAGAGGATCCAAAGCTGATGGGGAGGCTGAA 420
OY      421 GATGGCAGCCCCGGAGCTGGGAGATCTTCAAGCAGACCTTAGAGAGTTCAGACAAAC 480
Db      421 GATGGCAGCCCCGGAGCTGGGAGATCTTCAAGCAGACCTTAGAGAGTTCAGACAAAC 480
OY      481 TCACACAGATGACGACACTACTCAGAACTACGAGGCTGCTCTACTGCTTCAGAGAGAC 540
Db      481 TCACACAGATGACGACACTACTCAGAACTACGAGGCTGCTCTACTGCTTCAGAGAGAC 540
OY      541 ATGACAAGGTGAGAGACATTCCTGCGCATGTCGACAGTCCGCTCTGTGAGGGGAGCTGT 600
Db      541 ATGACAAGGTGAGAGACATTCCTGCGCATGTCGACAGTCCGCTCTGTGAGGGGAGCTGT 600
OY      601 GGCCTTCTAG 609
Db      601 GGCCTTCTAG 609

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RESULT 13
CO827155 677 bp DNA linear PAT 29-JUN-2004
LOCUS Sequence 25 from Patent WO2004050703.
DEFINITION CO827155
ACCESSION CO827155
VERSION CO827155.1 GI:49455732
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE
1 Fagan, R.J., Phelps, C.B., Rodriguez, T.M., Yorke, M. and de Tiani, M.
AUTHORS Splice variant of the human pituitary growth hormone
TITLE Patent: WO 2004050703-A 25 17-JUN-2004;
JOURNAL ARRS TRADING S.A. (CH)

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FEATURES
source 1..677
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"
Location/Qualifiers

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ORIGIN
Query Match 90.5%; Score 551.2; DB 6; Length 677;
Best Local Similarity 95.6%; Pred. No. 5.8e-119;
Matches 581; Conservative 0; Mismatches 18; Indels 9; Gaps 1;

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OY      1 ATGGCTACAGGCTCCCGAGCGTCTGCTCTGCTGCTTTGGCGCTGCTGCTGCTGCTG 60
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OY      34 ATGGCTACAGGCTCCCGAGCGTCTGCTCTGCTGCTTTGGCGCTGCTGCTGCTGCTG 93
Db      34 ATGGCTACAGGCTCCCGAGCGTCTGCTCTGCTGCTTTGGCGCTGCTGCTGCTGCTG 93
OY      61 CTTCACAGGAGGAGCTGCTCCCAACCAATTCCTTATCCAGGCTTTTACAAAGCTAGT 120
Db      61 CTTCACAGGAGGAGCTGCTCCCAACCAATTCCTTATCCAGGCTTTTACAAAGCTAGT 120
OY      94 CTTCACAGGAGGAGCTGCTCCCAACCAATTCCTTATCCAGGCTTTTACAAAGCTAGT 153
Db      94 CTTCACAGGAGGAGCTGCTCCCAACCAATTCCTTATCCAGGCTTTTACAAAGCTAGT 153
OY      121 CTCGGCGCCCATGCTGTCACAGCTGGGCTTTGACACTTACAGAGATTAAACCCCAAG 180
Db      121 CTCGGCGCCCATGCTGTCACAGCTGGGCTTTGACACTTACAGAGATTAAACCCCAAG 180
OY      154 CTCGGCGCCCATGCTGTCACAGCTGGGCTTTGACACTTACAGAGATTAAACCCCAAG 204
Db      154 CTCGGCGCCCATGCTGTCACAGCTGGGCTTTGACACTTACAGAGATTAAACCCCAAG 204
OY      181 ACCTCCCTCTGTTTCTCAGAGTCTATTCGACACCTTCCAAAGGAGGAAACACACAG 240
Db      181 ACCTCCCTCTGTTTCTCAGAGTCTATTCGACACCTTCCAAAGGAGGAAACACACAG 240
OY      205 GTAAGCTCTTGGGAAATGAGTCTATTCGACACCTTCCAAAGGAGGAAACACACAG 264
Db      205 GTAAGCTCTTGGGAAATGAGTCTATTCGACACCTTCCAAAGGAGGAAACACACAG 264
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OY      301 GTGCAATTCTCAGAGAGTCTTTCGCAACAGCTGATGAGGCGCTCTGACAGCAAC 360
Db      301 GTGCAATTCTCAGAGAGTCTTTCGCAACAGCTGATGAGGCGCTCTGACAGCAAC 360
OY      325 GTGCAATTCTCAGAGAGTCTTTCGCAACAGCTGATGAGGCGCTCTGACAGCAAC 384

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QY 361 GTCATATGACCTCTCTTAAGAGCCTAGAGAGGAGCATCAACGCTGATGAGGAGGCTGAA 420  
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QY 421 GATGAGAGCCCGGAGCTGGGAGATCTTCAAGCAGACCTACAGCAAGTTTCACACAAAC 480  
Db 445 GATGAGAGCCCGGAGCTGGGAGATCTTCAAGCAGACCTACAGCAAGTTTCACACAAAC 504  
QY 481 TCACCAAGAGTACGACCTACTACTCAAGAACTACAGGCTCTCTACTCTTCAAGAGAGAC 540  
Db 505 TCACCAAGAGTACGACCTACTACTCAAGAACTACAGGCTCTCTACTCTTCAAGAGAGAC 564  
QY 541 ATGACAAAGTACGAGCATTCTCGGAGATGAGCAGTGGCTCTCTCTTCAAGAGAGAG 600  
Db 565 ATGACAAAGTACGAGCATTCTCGGAGATGAGCAGTGGCTCTCTCTTCAAGAGAGAG 624  
QY 601 GGCTTCTA 608  
Db 625 GGCTTCCA 632

## RESULT 14

AX481369 654 bp DNA linear PAT 16-AUG-2002  
LOCUS AX481369  
DEFINITION Sequence 3 from Patent WO0205532.  
ACCESSION AX481369  
VERSION AX481369.1 GI:22316286  
KEYWORDS  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens

REFERENCE 1  
AUTHORS Andersen, K.V., Drustrup, J. and Christiansen, J.  
TITLE Improved growth hormone molecules  
JOURNAL Patent: WO 0205532-A 3 18-JUL-2002;  
Maxygen Aps (DK); Maxygen Holdings Ltd. (KY)  
FEATURES  
source 1. .654  
/organism="Homo sapiens"  
/mol\_type="unassigned DNA"  
/db\_xref="taxon:9606"

## ORIGIN

Query Match 90.4%; Score 550.8; DB 6; Length 654;  
Best Local Similarity 92.8%; Pred. No. 7.3e-119;  
Matches 607; Conservative 0; Mismatches 2; Indels 45; Gaps 1;

QY 1 ATGGCTACAGGCTCCCGAGAGCTCCCTGCTCTGCTTTTGGCCCTGCTGCTGCTGCTG 60  
Db 1 ATGGCTACAGGCTCCCGAGAGCTCCCTGCTCTGCTTTTGGCCCTGCTGCTGCTGCTG 60  
QY 61 CTTCAGAGAGGAGAGTGGCTTCCCAACCATTCCTTATCCAGAGCTTTTGAACAAGCTAGT 120  
Db 61 CTTCAGAGAGGAGAGTGGCTTCCCAACCATTCCTTATCCAGAGCTTTTGAACAAGCTAGT 120  
QY 121 CTCGGGGCCCATGCTGTGACACAGCTGGCTTTTGAACCTACAGAGAGTTT----- 171  
Db 121 CTCGGGGCCCATGCTGTGACACAGCTGGCTTTTGAACCTACAGAGAGTTTGAAGAAGCC 180  
QY 172 -----AACCCCAAGCTTCCCTCTGTTTC 195  
Db 181 TATATCCCAAGAGAGAGATTTATTCCTGCAAAACCCCAAGCTTCCCTCTGTTTC 240  
QY 196 TCAGAGTCTATTTCCGACACCTTCCACAGAGAGAGAAACAACAAGAAATCCAACTAGAG 255  
Db 241 TCAGAGTCTATTTCCGACACCTTCCACAGAGAGAGAAACAACAAGAAATCCAACTAGAG 300  
QY 256 CTGCTCCGATCTCCCTGCTGCTCATCAAGTGTGCTGAGAGCCGTGCAAGTTCTCTCAG 315  
Db 301 CTGCTCCGATCTCCCTGCTGCTCATCAAGTGTGCTGAGAGCCGTGCAAGTTCTCTCAG 360

QY 316 AGTCTTTGCCCAACAGCTGGTGTACGGCGCTTGTGACAGCAACCTTATGACTCTTA 375  
Db 361 AGTCTTTGCCCAACAGCTGGTGTACGGCGCTTGTGACAGCAACCTTATGACTCTTA 420  
QY 376 AAGGACCTTGAAGAGAGGATCCAAAGCTGATGAGGAGGCTGGAAGATGAGAGCCCGG 435  
Db 421 AAGGACCTTGAAGAGAGGATCCAAAGCTGATGAGGAGGCTGGAAGATGAGAGCCCGG 480  
QY 436 ACTGGGAGATCTTCAAGAGAGCTTACAGCAAGTTTCACAACTCACAAACAGTAGAC 495  
Db 481 ACTGGGAGATCTTCAAGAGAGCTTACAGCAAGTTTCACAACTCACAAACAGTAGAC 540  
QY 496 GCACTACTCAAGAACTACAGGAGCTGCTTACTGCTTCAAGAGAGAGATGAGAGCTGAG 555  
Db 541 GCACTACTCAAGAACTACAGGAGCTGCTTACTGCTTCAAGAGAGAGATGAGAGCTGAG 600  
QY 556 ACATTCCTGCGCATGTCAGTGGCTGCTCTGCTGAGAGGAGAGCTGCTGCTTCTAG 609  
Db 601 ACATTCCTGCGCATGTCAGTGGCTGCTCTGCTGAGAGGAGAGCTGCTGCTTCTAG 654

## RESULT 15

AX766683 654 bp DNA linear PAT 25-JUN-2003  
LOCUS AX766683  
DEFINITION Sequence 1 from Patent WO03042408.  
ACCESSION AX766683  
VERSION AX766683.1 GI:32260452  
KEYWORDS  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens

REFERENCE 1  
AUTHORS Cooper, D.N., Procter, A.M., Gregory, J. and Millar, D.S.  
TITLE Sequence variants of the human growth hormone gene and methods for  
JOURNAL detection  
University of Wales College of Medicine (GB)  
FEATURES  
source 1. .654  
/organism="Homo sapiens"  
/mol\_type="unassigned DNA"  
/db\_xref="taxon:9606"

## ORIGIN

Query Match 90.4%; Score 550.8; DB 6; Length 654;  
Best Local Similarity 92.8%; Pred. No. 7.3e-119;  
Matches 607; Conservative 0; Mismatches 2; Indels 45; Gaps 1;

QY 1 ATGGCTACAGGCTCCCGAGAGCTCCCTGCTCTGCTTTTGGCCCTGCTGCTGCTGCTG 60  
Db 1 ATGGCTACAGGCTCCCGAGAGCTCCCTGCTCTGCTTTTGGCCCTGCTGCTGCTGCTG 60  
QY 61 CTTCAGAGAGGAGAGTGGCTTCCCAACCATTCCTTATCCAGAGCTTTTGAACAAGCTAGT 120  
Db 61 CTTCAGAGAGGAGAGTGGCTTCCCAACCATTCCTTATCCAGAGCTTTTGAACAAGCTAGT 120  
QY 121 CTCGGGGCCCATGCTGTGACACAGCTGGCTTTTGAACCTACAGAGAGTTT----- 171  
Db 121 CTCGGGGCCCATGCTGTGACACAGCTGGCTTTTGAACCTACAGAGAGTTTGAAGAAGCC 180  
QY 172 -----AACCCCAAGCTTCCCTCTGTTTC 195  
Db 181 TATATCCCAAGAGAGAGATTTATTCCTGCAAAACCCCAAGCTTCCCTCTGTTTC 240  
QY 196 TCAGAGTCTATTTCCGACACCTTCCACAGAGAGAGAAACAACAAGAAATCCAACTAGAG 255  
Db 241 TCAGAGTCTATTTCCGACACCTTCCACAGAGAGAGAAACAACAAGAAATCCAACTAGAG 300  
QY 256 CTGCTCCGATCTCCCTGCTGCTCATCAAGTGTGCTGAGAGCCGTGCAAGTTCTCTCAG 315  
Db 301 CTGCTCCGATCTCCCTGCTGCTCATCAAGTGTGCTGAGAGCCGTGCAAGTTCTCTCAG 360

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QY 316 AGTGTCTTGGCCAAACAGCCTGGTGTACGGCGCCTTGACAGCAAGCTTATGACCTTCTTA 375
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    |||||
QY 376 AAGGACTAGAGGAGGATCCAAACGCTGATGGGAGGCTGGAAGATGGCAGCCCCCG 435
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Db 421 AAGGACTAGAGGAGGATCCAAACGCTGATGGGAGGCTGGAAGATGGCAGCCCCCG 480
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QY 436 ACTGGGAGATCTTCAAGCAGACCTACAGCAAGTTCACAAACTCACAAGATGAC 495
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Db 481 ACTGGGAGATCTTCAAGCAGACCTACAGCAAGTTCACAAACTCACAAGATGAC 540
    |||||
QY 496 GCATCTACTCAAGAACTACGGGCTGCTCTACTGCTTCAAGAAAGACATGAAACAGTCGAG 555
    |||||
Db 541 GCATCTACTCAAGAACTACGGGCTGCTCTACTGCTTCAAGAAAGACATGAAACAGTCGAG 600
    |||||
QY 556 ACATTCTGCGCATCGTGCAGTGCCTCTGTGGAAGGGCAGCTGTGGCTTCTAG 609
    |||||
Db 601 ACATTCTGCGCATCGTGCAGTGCCTCTGTGGAAGGGCAGCTGTGGCTTCTAG 654
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Job time : 3093 secs

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OM nucleic - nucleic search, using sw model

Run on: February 7, 2005, 07:20:19 ; Search time 479 Seconds

(without alignment)  
7526.352 Million cell updates/sec

Title: US-09-856-796B-1

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Scoring table: IDENTITY\_NUC  
Gapop 10.0 , Gapext 1.0

Searched: 4390206 seqs, 2959870667 residues

Total number of hits satisfying chosen parameters: 8780412

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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2: geneseq1990s.\*  
3: geneseq2000s.\*  
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5: geneseq2001bs.\*  
6: geneseq2002as.\*  
7: geneseq2002bs.\*  
8: geneseq2003as.\*  
9: geneseq2003bs.\*  
10: geneseq2003cs.\*  
11: geneseq2003ds.\*  
12: geneseq2004as.\*  
13: geneseq2004bs.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	609	100.0	609	3	AAA46696
2	599.8	98.5	1354	13	ADQ38456 Human SNP
3	599.8	98.5	1452	13	ADQ38467 Human SNP
4	554	91.0	654	6	AA818887
5	554	91.0	654	6	AA818888
6	554	91.0	654	6	AA818888
7	553.8	90.9	600	12	ADP43293
8	553	90.8	609	8	AA51435
9	552.6	90.7	855	13	ADQ38488
10	552.4	90.7	3557	1	AA60801
11	551.2	90.5	677	12	ADP43297
12	550.8	90.4	654	6	ABK90830
13	550.8	90.4	654	10	ADQ61349
14	550.8	90.4	654	10	ACC58425
15	550.8	90.4	654	10	ADU93049
16	550.8	90.4	654	12	ADP19728
17	550.8	90.4	769	4	AA146249
18	550.8	90.4	5594	2	AAV33629
19	550.8	90.4	7080	2	AAV33621
20	549.8	90.3	700	1	AA60678

21	549.2	90.2	654	12	ADM32918
22	549.2	90.2	769	4	AA146250
23	549.2	90.2	799	4	AA17490
24	549.2	90.2	799	4	AA86395
25	549.2	90.2	799	10	ACC78890
26	549.2	90.2	799	12	ADN49719
27	549.2	90.2	814	2	AAQ04700
28	547.2	89.9	821	9	AA160072
29	546.2	89.7	651	10	ABX14644
30	544.8	89.5	1497	13	ADQ38457
31	544.6	89.4	651	1	AAV71239
32	541.8	89.0	821	9	AA159998
33	539.2	88.5	1443	13	ADQ38475
34	538.2	88.4	651	1	AA81286
35	538.2	88.4	1043	13	ADQ38479
36	536.4	88.1	663	2	AAV60639
37	530.8	87.2	1495	13	ADQ38455
38	526.8	86.5	812	4	AA83835
39	525	86.2	681	10	ADG17919
40	525	86.2	699	10	ADG17918
41	523.2	85.9	528	1	AA82235
42	514.6	84.5	597	12	ADP71337
43	508.8	83.5	808	4	AA83836
44	505.8	83.1	600	12	ADP71312
45	503.8	82.7	965	13	ADQ38453

## ALIGNMENTS

RESULT 1	
AAA46696	ADQ38456 standard; DNA; 609 BP.
ID	AAA46696
AC	AAA46696;
DT	25-SEP-2000 (first entry)
XX	
DE	DNA encoding a human growth hormone (hGH).
XX	
KW	Human, growth hormone; hGH; inhibitor; nuclear factor-kappaB; NF-kappaB;
KW	multi-drug resistance gene; malignant hemopathy; solid tumour;
KW	malignant blood disease; leukaemia; lymphoma; solid cancer; ds.
OS	Homo sapiens.
XX	
PH	Key
FT	Location/Qualifiers
FT	1..609
FT	/*tag= a
FT	/product= "growth hormone"
XX	
PN	WO200030587-A2.
XX	
PD	02-JUN-2000.
XX	
PF	24-NOV-1999; 99WO-FR002897.
XX	
PR	25-NOV-1998; 98FR-00014858.
XX	
PA	(CNRS ) CENT NAT RECH SCI.
XX	
PI	Hirsch F, Haeflner A;
XX	
DR	WPI, 2000-399901/34.
XX	
DR	P-PSDB; AAV93637.
XX	
PT	Treatment of hematological or solid tumors using an inhibitor of the
PT	activation of nuclear factor-kappaB, particularly to prevent development
PT	of resistance to chemotherapeutics.
XX	
PS	Claim 4; Page 26-27; 30pp; French.
XX	
CC	The present sequence encodes a human growth hormone (hGH). The human

XX  
cardiant; gene therapy; human; gene; ds.  
KM  
KM  
KM  
KM  
XX

237 CTTCCGCGCCATGGTCTGCACAGCATGGCATTTCAGCAAGG

Seq	Sequence	1354 BP	284 A	396 C	344 G	309 T	0 U	21 Other
Qy	Query Match	98.5%	Score 599.8	DB 13	Length 1354			
	Best Local Similarity	97.4%	Pred. No. 1.5e-137					
	Matches 593	Conservative 14	Mismatches 2	Indels 0	Gaps 0			
Qy	1	ATGGCTACAGAGCTCCCGAGACTCCCTCTCTCTGCTTTTGGCTCTGCTCTGCTCTGCTCTG	60					
Db	117	ATGGCTACAGAGCTCCCGAGACTCCCTCTCTCTGCTTTTGGCTCTGCTCTGCTCTGCTCTG	176					
Qy	61	CTTCAAGAGGAGCTGCTTTCCCAACATTCCTTATCCAGAGCTTTTGGACACGCTAGT	120					
Db	177	CTTCAAGAGGAGAGCTGCTTCCMAACATTTCTTATCCAGAGCTTTTGGACACGCTATG	236					
Qy	121	CTCCGCGCCCATGCTGTCTGACACAGCTGGCTTTGACACTACAGAGTTTAACTCCCCAG	188					
Db	237	CTCCGCGCCCATGCTGTCTGACACAGCTGGCTTTGACACTACAGAGTTTAACTCCCCAG	296					
Qy	161	ACTCTCTCTGTTTCTCAGACTTATTTCCGACACCCCTCCAAACAGAGGAGAAACACAAACAG	240					

Db 297 ACCCTCCTCTGTTCTCAGAGTCTATTCCAGACCCCTCAACGGGAGGAAACAAACAG 356  
QY 241 AATTCACCTAGAGTGTCCGATCTCCCTGTGTATTCAGTGTGGCTGGAGCC 300  
Db 357 AATTCACCTAGAGTGTCTGTGATCTCTCTGTCTATTCAGTGTGGCTGGAGCC 416  
QY 301 GTGACGTTCTCAGAGTGTCTGTGCAACAGCGCTGTGAGCGGCTGTGACAGAAC 360  
Db 417 GTGACGTTCTCAGAGTGTCTGTGCAACAGCGCTGTGAGCGGCTGTGACAGAAC 476  
QY 361 GTCTATGACCTCTTAAAGACCTAGAGAGGATCCAAACGCTGATGGGAGGCTGAA 420  
Db 477 DTCATGACCTCTTAAAGACCTAGAGAGGATCCAAACGCTGATGGGAGGCTGAA 536  
QY 421 GATGGAGCCCCCGGAGCTGGGAGATCTTCAAGCAAGCCTTACAGCAAGTTGACACAAAC 480  
Db 537 GATGGAGCCCCCGGAGCTGGGAGATCTTCAAGCAAGCCTTACAGCAAGTTGACACAAAM 596  
QY 481 TCACACAGATGAGGACCTACCTACAGAACTAGCGGCTGTCTACTGTCTTCAAGAGAC 540  
Db 597 TCCACACAGATGAGGACCTACCTACAGAACTAGCGGCTGTCTACTGTCTTCAAGAGAC 656  
QY 541 ATGACCAAGTGCAGACATTTCTGCGCATCTGTCAGTGCAGTGCCTGTGAGAGGACCTGT 600  
Db 657 ATGACCAAGTGCAGACATTTCTGCGCATCTGTCAGTGCAGTGCCTGTGAGAGGACCTGT 716  
QY 601 GGCTTCTAG 609  
Db 717 GGCTTCTAG 725

RESULT 3  
ADQ38467  
ID ADQ38467 standard; DNA; 1452 BP.  
AC ADQ38467;  
XX  
DT 18-NOV-2004 (first entry)  
XX  
DE Human SNP containing myocardial infarction-associated gene, SEQ ID 130.  
XX  
KW Myocardial infarction; detection; single nucleotide polymorphism; SNP;  
KW cardiac; gene therapy; human; gene; ds.  
XX  
OS Homo sapiens.  
XX  
PN WO2004058052-A2.  
XX  
PD 15-JUL-2004.  
XX  
PF 22-DEC-2003; 2003WO-US040978.  
XX  
PR 20-DEC-2002; 2002US-0434778P.  
PR 10-MAR-2003; 2003US-045133P.  
PR 30-APR-2003; 2003US-046412P.  
PR 23-SEP-2003; 2003US-0504955P.  
XX  
PA (APPL-) APPLERA CORP.  
XX  
PI Cargill M, Devlin J, Iakubova O;  
XX  
DR WPI; 2004-533949/51.  
DR P-Psds; ADQ39295.  
XX  
PT Identifying an individual who has an altered risk for developing  
PT myocardial infarction by detecting a single nucleotide polymorphism in  
XX the individual's nucleic acids.  
XX  
PS Claim 7; SEQ ID NO 130; 145bp; English.  
XX  
CC The invention relates to a novel method for identifying an individual who  
CC has an altered risk for developing myocardial infarction. The method

CC comprises detecting a single nucleotide polymorphism (SNP) in any one of  
CC the nucleotide sequences given in the specification in the individual's  
CC nucleic acids, where the presence of the SNP is correlated with an  
CC altered risk for myocardial infarction in the individual. The invention  
CC further comprises: an isolated nucleic acid molecule comprising at least  
CC 8 contiguous nucleotides where one of the nucleotides is an SNP given in  
CC the specification or its complement and encoding any one of the amino  
CC acid sequences given in the specification; an isolated polypeptide  
CC comprising an amino acid sequence given in the specification; an antibody  
CC that specifically binds to the polypeptide or its antigen-binding  
CC fragment; an amplified polynucleotide containing an SNP given in the  
CC specification and which is between about 16 and 1000 nucleotides in  
CC length; a kit for detecting an SNP in a nucleic acid, comprising the  
CC polynucleotide, a buffer and an enzyme; a method of detecting an SNP in a  
CC nucleic acid molecule; a method of detecting a variant polypeptide; and a  
CC method for identifying an agent useful in treating or preventing  
CC myocardial infarction. The novel detection method has cardiac activity.  
CC The nucleic acids of the invention may be used in gene therapy. The  
CC method is useful in identifying an individual who has an increased or  
CC decreased risk for developing myocardial infarction and for preparing a  
CC composition for treating or preventing myocardial infarction. This  
CC polynucleotide sequence represents a human myocardial infarction-  
CC associated gene containing one or more SNP's of the invention. Note: This  
CC sequence was not shown in the specification. The sequence has come from  
CC an electronic sequence listing downloaded from the WIPO website.  
SQ Sequence 1452 BP; 312 A; 418 C; 369 G; 328 T; 0 U; 25 Other;  
Query Match 98.5%; Score 599.8; DB 13; Length 1452;  
Best Local Similarity 97.4%; Pred. No. 1.6e-137;  
Matches 593; Conservative 14; Mismatches 2; Indels 0; Gaps 0;  
QY 1 ATGGCTCAGAGGCTCCCGAGCCCTGCTCTGCTTTGGCTGTCTGCTCCCTGG 60  
Db 215 ATGGCTCAGAGGCTCCCGAGCCCTGCTCTGCTTTGGCTGTCTGCTCCCTGG 274  
QY 61 CTTCAAGAGGAGGAGGCTTCCCAACATTCCTTATCCAGGCTTTTGACAAAGCTACT 120  
Db 275 CTTCAAGAGGAGGAGGCTTCCCAACATTCCTTATCCAGGCTTTTGACAAAGCTACT 334  
QY 121 CTCGCGGCCATCTGTCACACAGCTGCTTTGACACCTACAGAGTTTAACCCCGAG 180  
Db 335 CTCGCGGCCATCTGTCACACAGCTGCTTTGACACCTACAGAGTTTAACCCCGAG 394  
QY 181 ACCTCCCTCTGTTTTCAGAGTCTATTCGACACCTTCCAAAGGAGGAAACACACAG 240  
Db 395 ACCTCCCTCTGTTTTCAGAGTCTATTCGACACCTTCCAAAGGAGGAAACACACAG 454  
QY 241 AATTCACCTAGAGTGTCTCCGATCTCCCTGTCTCATTCAGTGTGTGAGGCC 300  
Db 455 AATTCACCTAGAGTGTCTCCGATCTCCCTGTCTCATTCAGTGTGTGAGGCC 514  
QY 301 GTGACGTTCTCAGAGTGTCTTGGCAACAGCGCTGTGAGCGGCTGTGACAGAAC 360  
Db 515 GTGACGTTCTCAGAGTGTCTTGGCAACAGCGCTGTGAGCGGCTGTGACAGAAC 574  
QY 361 GTCTATGACCTCTTAAAGACCTAGAGAGGATCCAAACGCTGATGGGAGGCTGAA 420  
Db 575 DTCATGACCTCTTAAAGACCTAGAGAGGATCCAAACGCTGATGGGAGGCTGAA 634  
QY 421 GATGGAGCCCCCGGAGCTGGGAGATCTTCAAGCAAGCCTTACAGCAAGTTGACACAAAC 480  
Db 635 GATGGAGCCCCCGGAGCTGGGAGATCTTCAAGCAAGCCTTACAGCAAGTTGACACAAAM 694  
QY 481 TCACACAGATGAGGACCTACCTACAGAACTAGCGGCTGTCTACTGTCTTCAAGAGAC 540  
Db 695 TCCACACAGATGAGGACCTACCTACAGAACTAGCGGCTGTCTACTGTCTTCAAGAGAC 754  
QY 541 ATGACCAAGTGCAGACATTTCTGCGCATCTGTCAGTGCAGTGCCTGTGAGAGGACCTGT 600  
Db 755 ATGACCAAGTGCAGACATTTCTGCGCATCTGTCAGTGCAGTGCCTGTGAGAGGACCTGT 814  
QY 601 GGCTTCTAG 609





QY	1	ATGGCTACAGGCTCCCGGACGTCCCGTCTCTGAGCTTTGGACCTTGCTCTGAGCTGACCTGAG	60
Db	62	ATGGCTACAGGCTCCCGGAGCTCCCTGCTCTGAGCTTTGGACCTTGCTCTGAGCTGACCTGAG	121
QY	61	CTTCAAGAGGGGAGTGCCTTCCCAACCATTCCTTATCAGAGCTTTTGAACAAGCTAGT	120
Db	122	CTTCAAGAGGGGAGTGCCTTCCCAACCATTCCTTATCAGAGCTTTTGAACAAGCTAGT	181
QY	121	CTGCGGCGCCATGCTGTGCAACCAAGTGGCTTTTGACACTTACAGAGATT-----	171
Db	182	CTCCGCGCCCATGCTGTGCAACCAAGTGGCTTTTGACACTTACAGAGATTGAAGAGCC	241
QY	172	-----AACCCGCAACCTCCCTCTGTTTC	195
Db	242	TATATCCCAAGGAACAAGATATTCACTCTGCAAGAACCCCAAGACCTCCCTGTTTC	301
QY	196	TCAGAGTCTATTCCGACACCCCTCCAAAGGAGGAAACAACAAGAAATCCAACTTAGAG	255
Db	302	TCAGAGTCTATTCCGACACCCCTCCAAAGGAGGAAACAACAAGAAATCCAACTTAGAG	361
QY	256	CTGCTCCGCAATCTTCCTGCTGCTCATCCAGTCTGTGGACCGGTGAGTCTCTCAGG	315
Db	362	CTGCTCCGCAATCTTCCTGCTGCTCATCCAGTCTGTGGACCGGTGAGTCTCTCAGG	421
QY	316	AGGTCTTGCSCAACAGACCTGTGTGACGAGCGCTCTGCACGAAACGTATGACTTCTTA	375
Db	422	AGGTCTTGCSCAACAGACCTGTGTGACGAGCGCTCTGCACGAAACGTATGACTTCTTA	481
QY	376	AAGGACCTTAGAGGAAGGATCCAAACGCTGATGAGGAGGCTGGAAGATGGCAACCCCGG	435
Db	482	AAGGACCTTAGAGGAAGGATCCAAACGCTGATGAGGAGGCTGGAAGATGGCAACCCCGG	541
QY	436	ACTGGGCGATCTTTCAGACACCTTACAGCAAGTTGACACAAATTCACCAACGATGAC	495
Db	542	ACTGGGCGATCTTTCAGACACCTTACAGCAAGTTGACACAAATTCACCAACGATGAC	601
QY	496	GCACTACTCAAGAACTACGGGCTGCTTACTGCTTTCAGGAAGACATGACAAAGTGGAG	555
Db	602	GCACTACTCAAGAACTACGGGCTGCTTACTGCTTTCAGGAAGACATGACAAAGTGGAG	661
QY	556	ACATTCCTGGCGATGTCGATGCGGCTCTGTGGAAGGCAAGCTGTGGCTTCTAG	609

Db 662 ACATTCCGCGCATCGTGCA GTGCCGCTCTGTGGAGGGCAGCTGTGGCTTCTAG /A-

RESULT 7  
ADP43293  
ID ADP43293 standard; DNA; 600 BP

AC ADP43293

DT 09-SEP-2004 (first entry)

Human pituitary growth hormone variant INSP101 gene

AA ds; gene; gynecological; cytostatic; anti-HIV; osteopathic; endocrine; antiangiogenic; immunosuppressive; antiinflammatory; cardiovascular; neuroprotective; analgesic; antidiabetic; anorectic; immunomodulator; nephrotropic; virucide; fungicide; antibacterial; antiparasitic; noctropic; vaccine; INSP101; reproductive disorder; pregnancy disorder; gestational trophoblastic disease; developmental disorder; Silver-Russell syndrome; growth disorder; growth hormone deficiency; Cushing's disease; endocrine disorder; cell proliferative disorder; neoplasm; carcinoma; pituitary tumor; ovary tumor; melanoma; placental site trophoblastic tumor; adenocarcinoma; choriocarcinoma; osteosarcoma; angiogenesis; myeloproliferative disorder; autoimmune disorder; inflammatory disorder; cardiovascular disorder; neurological disorder; pain; metabolic disorder; diabetes mellitus; osteoporosis; obesity; cachexia; AIDS; renal disease; lung injury; aging.

Key	Location/Qualifiers
FM	1..600
FT	/tag= a
CDS	/product= "pituitary growth hormone variant INSP101"
FT	
FM	

PN WO2004030703-A1  
XX  
PD 17-JUN-2004.

PF 05-DEC-2003; 2003WO-GB005295.

05-DEC-2002; 2002GB-00028441.

PA (ARES-) ARES TRADING SA.

Fagan RJ, Phelps CB, Rodrigues TM, Yorke M, De Tiani M;

WPI; 2004-450722/42.

XX  
DN  
X

XX  
DN  
X

PT bacterial and parasitic infections.

PS Claim 9; SEQ ID NO 7; 83pp; English.

AA The invention relates to a polypeptide (I) comprising a fully defined  
CC INSP101 sequence of 199 or 173 amino acids (SI), its fragment functioning  
CC as a growth hormone, or having an antigenic determinant in common with  
CC (I) having (SI), or the functional equivalent of (SI) or its fragment.  
CC (I) is useful for diagnosing a disease in a patient, which involves  
CC assessing the level of expression of a natural gene encoding (I), or  
CC assessing the activity of (I), in tissue from the patient and comparing  
CC the level of expression or activity to a control level, where a level  
CC that is different to the control level is indicative of disease, where  
CC the method is carried out in vitro. The disease includes, but is not  
CC limited to reproductive disorders, pregnancy disorder, such as  
CC gestational trophoblastic disease, developmental disorders such as Silver  
CC-Russell syndrome, growth disorders, growth hormone deficiency, Cushing's  
CC disease, endocrine disorders, cell proliferative disorders, including  
CC neoplasia, carcinoma, pituitary tumor, ovary tumor, melanoma, lung,  
CC colorectal, breast, pancreas, head and neck, placental site trophoblastic





CC disease e.g. foetal abnormalities such as foetal aneuploidy. The  
CC invention is also useful in gene therapy. The present sequence is hGH-V  
CC isoform DNA. hGH-V gene codes for placental growth hormone (PGH)  
XX  
SQ Sequence 609 BP; 131 A; 192 C; 154 G; 132 T; 0 U; 0 Other;





Oy 556 ACATTCTGGCGCATCTGTCAGTCCGCTCTGTGAGGGGACGCTGTGGCTTCTAG 609  
 .. |||||  
 Db 601 ACATTCTGGCGCATCTGTCAGTCCGCTCTGTGAGGGGACGCTGTGGCTTCTAG 654  
 .. |||||

RESULT 13  
ADC61349  
ID ADC61349 standard; DNA; 654 BP.

ID	ADC61349 standard; DNA; 654 BP.
XX	
AC	ADC61349;

DT	18-DEC-2003	(first entry)
XX		
DE	Human Growth Hormone 1, GH1, coding sequence.	
XX		
KM	Growth Hormone; GH1; human; gene; chromosome 17q23; ds.	
XX		
OS	Homo sapiens.	
XX		
FH	Key	Location/Qualifiers
FT	CDS	1..654
FT		/+tag= a
FT		/product= "Human growth hormone, GH1"
PN	WO2003042408-A2.	
XX		
PD	22-MAY-2003.	
XX		

PD 22-MAY-2003,  
17

PF 12-NOV-2002; 2002WO-GB005103.

AA  
PR 12-NOV-2001: 2001GB-00027213

XX (117242-1) INTV WATER COLLECTOR ON VESSEL

XX  
XX  
XX

COLLEGE OF MEDICINE.

XX  
C00621 UN, Procter AM, Gregory J, Millar DS;

DR WPI; 2003-449578/42.  
DR P-PSDB: ADG61299

**Notations :**

as an indicator of growth hormone (GH) dysfunction compares favorably with a variation in pituitary-expressed growth hormone (GH1), u

the human GHI gene.

Table 1: FSC 6.0, 7.0nm, Peak 1-4

1971 12 21 10 11 AM

pituitary-expressed Growth Hormone (GH) affective to act as an indi-

of Growth Hormone (GH) dysfunction in an individual. The method comparing the sequence obtained from the test individual with the

sequence of the human GH1 gene. The present sequence is the coding sequence, flanked by 5' and 3' noncoding regions.

The detection comprises PCR amplification of the GH1 gene of the

individual using a GH1 gene-specific fragment that is unique to the gene whose sequence is not found in the four narX loci (see Fig. 1).

in the GH cluster, and one or more GH1-gene specific primers that bind to the homologous flanking regions.

GH1) genes in the GH cluster (ADC61308-). The gene encoding GH1 is

located on chromosome 1/q23 within a cluster of five related genes.

Sequence 654 BP; 150 A; 207 C; 160 G; 137 T; 0 U; 0 Other;

Query Match	90.4%;	Score 550.8;	DB 10;	Length 654;
-------------	--------	--------------	--------	-------------

Matches 607; Conservative 0; Mismatches 2; Indels 45; Gaps 222; Local similarity 92.8%; Pred. No. 1.5e-125;

[illegible][illegible][illegible]

01 C1CAGAGGGCAGTGGCTTCCCAACCAATTCCCTTATCCAGGCTTTTGACCAACGCTAGT

.....

Db	61	CTTCAGAGGGCAGTGCCTCTCCCAACATCCCTTATCCAGGCTTTTGACAAAGCTA	120
OY	121	CTCGGCGCCATCCGTGTGACACGAGCTGGGCTTTGACACTACCAAGATT	171
Db	121	CTCGGCGCCATCGTGTGACCAAGCTGGGCTTTGACACTACCAAGATTGAAGAGCC	180
OY	172	-----MACCCCAAGCTCCCTCTGTTTC	195
Db	181	TATATCCCAAGGAACAGAAATTCATTCTCGAGAACCCCAAGCTCCCTCTGTTTC	240
OY	196	TCAGAGTCTATTCGACACCTCTCAAAGAGGAGAAACAAACAGAAATCCAACTTAG	255
Db	241	TCAGAGTCTATTCGACACCTCTCAAAGAGGAGAAACAAACAGAAATCCAACTTAG	300
OY	256	CTGCTCCGCAATCCCTGCTGCTCATCCAGTGTGCTGAGCGCCGTGCAATTCCTCA	315
Db	301	CTGCTCCGCAATCCCTGCTGCTCATCCAGTGTGAGCGCCGTGCAATTCCTCA	360
OY	316	AGTGTCTTCGCCAACAGCTGTGTATCGAGGCTCTTGACAGCAACGTATATGACTCTTA	375
Db	361	AGTGTCTTCGCCAACAGCTGTGTATCGAGGCTCTTGACAGCAACGTATATGACTCTTA	420
OY	376	AAGBACCTTGAGGAAGGCATCCAAAGCTGATGGGGAGCTGGAAATGSCACCCCG	435
Db	421	AAGBACCTTGAGGAAGGCATCCAAAGCTGATGGGGAGCTGGAAATGSCACCCCG	480
OY	436	ACTGGGCAATCTTCAAGCAGACCTACAGCAAGTTCACAAACTCACAAAGATGAC	495
Db	481	ACTGGGCAATCTTCAAGCAGACCTACAGCAAGTTCACAAACTCACAAAGATGAC	540
OY	496	GCACTACTCAAGAACTACGGGCTGCTCTACTGTTTCAGAAAGCATGACAAAGTGCAG	555
Db	541	GCACTACTCAAGAACTACGGGCTGCTCTACTGTTTCAGAAAGCATGACAAAGTGCAG	600
OY	556	ACATTCCTGCGCATCTGCAAGTGCCTCTCTGAGAGGCGAAGCTGTGCTTTAG	609
Db	601	ACATTCCTGCGCATCTGCAAGTGCCTCTCTGAGAGGCGAAGCTGTGCTTTAG	654

RESULT 14  
ACC58425  
ID ACC58425 standard; cDNA; 654 BP.

XX	AC	ACC58425;
XX	DT	26-AUG-2003 (first entry)
XX	DE	Human growth hormone GHI gene coding sequence.
XX	KM	Growth hormone; GHI gene; human; cytosolic; antidiabetic; anorectic;
XX	KW	antimicrobial; cardiact; gene therapy; chromosome 17q;
XX	OS	single nucleotide polymorphism; gene; ss.
XX	FT	Homo sapiens.
XX	FT	Key
XX	FT	CDS
XX	FT	Location/Qualifiers
XX	FT	1..654
XX	FT	/*tag= a
XX	FT	/product= "Human growth hormone"
XX	FT	1..78
XX	FT	/*tag= b
XX	FT	79..651
XX	FT	/*tag= c
XX	FT	/product= "Human growth hormone"
XX	FN	WO2003042245-A2.
XX	PD	22-MAY-2003.
XX	PF	12-NOV-2002; 2002WO-GB005112.
XX	PR	12-NOV-2001; 2001GB-00027214.
XX	PR	14-NOV-2001; 2001GB-00027328.

XX	PA	(UWMA -) UNIV WALES COLLEGE OF MEDICINE.
XX	PI	Cooper DN, Procter AM, Gregory J, Millar DS, Lewis M, Ullied A;
XX	DR	WPI; 2003-449559/42.
XX	DR	P-PSDBJ; ABRA42662.
XX	PT	New polynucleotide comprising a variant of the human growth hormone
XX	PT	nucleic acid sequence, GH1, useful for diagnosing or treating obesity,
XX	PT	diabetes, infection, cancer or cardiac conditions.
XX	PS	Disclosure; Fig 5; 62pp; English.
CC	CC	The present sequence is the coding sequence of the human growth hormone
CC	CC	GH1 gene. The invention relates to naturally-occurring mutations (see
CC	CC	ACC58424) that have been detected in a cohort of patients with short
CC	CC	stature. Methods are provided for detection of these variants, for screening
CC	CC	patients for growth hormone irregularities, and for producing variant
CC	CC	proteins for use in therapeutic diagnostic or detection methods, e.g.
CC	CC	for determination of susceptibility of an individual to diabetes,
CC	CC	obesity, infection, cancer or a cardiac condition, and in gene therapy
XX	SQ	Sequence 654 BP; 150 A; 207 C; 160 G; 137 T; 0 U; 0 Other;
QY	Query Match	90.4%; Score 550.8; DB 10; Length 654;
Db	Best Local Similarity	92.8%; Pred. No. 1.5e-125; Indels 45; Gaps 1
Db	Matches 607; Conservative	0; Mismatches 2;
QY	1	AAGGCTACAGGGCTCCCGAGCGTCCCGTCCTGCGCTTTTGAGCAACGCTACT 60
Db	1	AAGGCTACAGGGCTCCCGAGCGTCCCGTCCTGCGCTTTTGAGCAACGCTACT 60
QY	61	CTTCAAGAGGGGAGTGCCTCTCCCAACCATTCCTTAATCAGGCTTTTGACAACGCTACT 120
Db	61	CTTCAAGAGGGGAGTGCCTCTCCCAACCATTCCTTAATCAGGCTTTTGACAACGCTACT 120
QY	121	CTCCGGGCCCATGTGTGCAACGAGTGGCTTTTGACACTCACGAGAATT----- 171
Db	121	CTCCGGGCCCATGTGTGCAACGAGTGGCTTTTGACACTCACGAGAATT----- 180
QY	172	-----AACCCCCAGACCTCCCTGCTTTC 195
Db	181	TATATCCAAAGGAACAGAGTAGTATTCATTCCTGACAGAACCCCAGACTCCCTGCTTTC 240
QY	196	TCAGAGTCTATTTCGACACCCCTCCACAGGAGGAGAAACACAGAAATCCAACCTAGAG 255
Db	241	TCAGAGTCTATTTCGACACCCCTCCACAGGAGGAGAAACACAGAAATCCAACCTAGAG 300
QY	256	CTGTCCGGCAATCCCGTGCCTCATCGATCGTGAGTGGAGCCCGTGACGTTCTCAGG 315
Db	301	CTGTCCGGCAATCCCGTGCCTCATCGATCGTGAGTGGAGCCCGTGACGTTCTCAGG 360
QY	316	AGTGTCTTCGGCAACAGCCTGTGTGTAGCGGCGCTTGACAGCAAAGCTGTATGACTCTCTA 375
Db	361	AGTGTCTTCGGCAACAGCCTGTGTGTAGCGGCGCTTGACAGCAAAGCTGTATGACTCTCTA 420
QY	376	AAGACCTTAGAGGAAGGATCAACAGCTGATGGGAGGCTGGAAGATGTGCAAGCCCCGG 433
Db	421	AAGACCTTAGAGGAAGGATCAACAGCTGATGGGAGGCTGGAAGATGTGCAAGCCCCGG 480
QY	436	ACTGGGCGATCTTCAGACAGACTTACAGCAAGTTGCAACAACTCACACACAGATGAC 493
Db	481	ACTGGGCGATCTTCAGACAGACTTACAGCAAGTTGCAACAACTCACACACAGATGAC 544
QY	496	GCACTACTCAGAACTAAGGGCTGCTCAATGCTTACAGGAAGACATGACAAAGTGCAG 555
Db	541	GCACTACTCAGAACTAAGGGCTGCTCAATGCTTACAGGAAGACATGACAAAGTGCAG 600
QY	556	ACATTCCTGGCGATGTGACAGTGCAGCTCTGTGAGGCGACCTGTGCTTCTAG 609
Db	601	ACATTCCTGGCGATGTGACAGTGCAGCTCTGTGAGGCGACCTGTGCTTCTAG 654



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1 ATGGCTACAGGCTCCCGACGTCCCTGCTCCTGGCTTTGGCCCTGCTCTGCGCCCTGG 60

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Db 2270 ATGGCTACAGGCTCCGAGCGTCCGCTGCTGGCTTTGGCTGCTGCTGCTGCTGCTG 2229
QY 61 CTTCAAGAGGAGGAGGCTCTCCCAACCATTCCTTTTCAAGGCTTTTGAACAAGCTAGT 120
Db 2330 CTTCAAGAGGAGGAGGCTCTCCCAACCATTCCTTTTCAAGGCTTTTGAACAAGCTAGT 2389
QY 121 CTCGGCGCCCATGCTGTCAGCAGCTGGGCTTTGACACCTTACAGAGATT----- 171
Db 2390 CTCGGCGCCCATGCTGTCAGCAGCTGGGCTTTGACACCTTACAGAGATTGAAAGACC 2449
QY 172 -----AACCCTGAGCTTCCCTCTGTTTC 195
Db 2450 TATATCCCAAGAGAAAGAGATTTATTCCTGACAGAACCCCGACAGACTCTCTGTTTC 2509
QY 196 TCAGAGCTATTTCCGACACCCCTCCAAAGAGAGAAACAAACAGAAATCCAACTAGAG 255
Db 2510 TCAGAGCTATTTCCGACACCCCTCCAAAGAGAGAAACAAACAGAAATCCAACTAGAG 2569
QY 256 CTCGCTCCGCAATCTCCCTGCTGCTCATTCAGTGGCTGGAGCCCGTGCAGTTCTCAGG 315
Db 2570 CTCGCTCCGCAATCTCCCTGCTGCTCATTCAGTGGCTGGAGCCCGTGCAGTTCTCAGG 2629
QY 316 AGTGTCTTCCGCAAGAGCTGCTGTATCGGCGCTCTGACAGCAACGCTTATGACTCTTA 375
Db 2630 AGTGTCTTCCGCAAGAGCTGCTGTATCGGCGCTCTGACAGCAACGCTTATGACTCTTA 2689
QY 376 AAGGACCTAGAGAGAGGATCCAAAGCTGATGGAGAGGCTGGAAGATGGACACCCCGG 435
Db 2690 AAGGACCTAGAGAGAGGATCCAAAGCTGATGGAGAGGCTGGAAGATGGACACCCCGG 2749
QY 436 ACTGGGCGAGATCTTCAAGAGAGCTTACAGAGATTGACACAACTCACAGAGATGAC 495
Db 2750 ACTGGGCGAGATCTTCAAGAGAGCTTACAGAGATTGACACAACTCACAGAGATGAC 2809
QY 496 GCACTACTCAAGAACTACGAGGCTGCTCTACTGCTTTCAGAGAGGACATGACAAAGTTCAG 555
Db 2810 GCACTACTCAAGAACTACGAGGCTGCTCTACTGCTTTCAGAGAGGACATGACAAAGTTCAG 2869
QY 556 ACATTCTCGCGCATGTCGATGCGGCTGCTGTGAGAGGCGAGCTGTGGCTTTTGA 609
Db 2870 ACATTCTCGCGCATGTCGATGCGGCTGCTGTGAGAGGCGAGCTGTGGCTTTTGA 2923

```

RESULT 2  
US-09-380-190A-21  
Sequence 21, Application US/09380190A  
Patent No. 6410220

## GENERAL INFORMATION:

APPLICANT: NATURE TECHNOLOGY CORPORATION, ET AL.  
TITLE OF INVENTION: SELF-ASSEMBLING GENES, VECTORS AND USES THEREOF  
NUMBER OF SEQUENCES: 74  
CORRESPONDENCE ADDRESS:

ADDRESSEE: MUEITING, RAASCH & GERHARDT, P.A.  
STREET: 119 NORTH FOURTH STREET, SUITE 203  
CITY: MINNEAPOLIS  
STATE: MINNESOTA  
COUNTRY: USA

ZIP: 55401

## COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/380,190A

FILING DATE: 26-Aug-1999

CLASSIFICATION: &lt;Unknown&gt;

## PRIOR APPLICATION DATA:

APPLICATION NUMBER: PCT/US98/03918

FILING DATE: 28-FEB-98

ATTORNEY/AGENT INFORMATION:

NAME: MUEITING, ANN M.  
REGISTRATION NUMBER: 33,977  
REFERENCE/DOCKET NUMBER: 228..00010201  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 612-305-1217  
TELEFAX: 612-305-1228  
INFORMATION FOR SEQ ID NO: 21:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 7080 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: DNA (genomic)  
SEQUENCE DESCRIPTION: SEQ ID NO: 21:  
US-09-380-190A-21

Query Match 90.4%; Score 550.8; DB 3; Length 7080;  
Best Local Similarly 92.8%; Pred. No. 3,8e-153;  
Matches 607; Conservative 0; Mismatches 2; Indels 45; Gaps 1;

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QY 1 ATGGCTACAGGCTCCGAGCGTCCGCTGCTGGCTTTGGCTGCTGCTGCTGCTGCTG 60
Db 2848 ATGGCTACAGGCTCCGAGCGTCCGCTGCTGGCTTTGGCTGCTGCTGCTGCTGCTG 2907
QY 61 CTTCAAGAGGAGGAGGCTCTCCCAACCATTCCTTTTCAAGGCTTTTGAACAAGCTAGT 120
Db 2908 CTTCAAGAGGAGGAGGCTCTCCCAACCATTCCTTTTCAAGGCTTTTGAACAAGCTAGT 2967
QY 121 CTCGGCGCCCATGCTGTCAGCAGCTGGGCTTTGACACCTTACAGAGATT----- 171
Db 2968 CTCGGCGCCCATGCTGTCAGCAGCTGGGCTTTGACACCTTACAGAGATTGAAAGACC 3027
QY 172 -----AACCCTGAGCTTCCCTCTGTTTC 195
Db 3028 TATATCCCAAGAGAAAGAGATTTATTCCTGACAGAACCCCGACAGACTCTCTGTTTC 3087
QY 196 TCAGAGCTATTTCCGACACCCCTCCAAAGAGAGAAACAAACAGAAATCCAACTAGAG 255
Db 3088 TCAGAGCTATTTCCGACACCCCTCCAAAGAGAGAAACAAACAGAAATCCAACTAGAG 3147
QY 256 CTCGCTCCGCAATCTCCCTGCTGCTCATTCAGTGGCTGGAGCCCGTGCAGTTCTCAGG 315
Db 3148 CTCGCTCCGCAATCTCCCTGCTGCTCATTCAGTGGCTGGAGCCCGTGCAGTTCTCAGG 3207
QY 316 AGTGTCTTCCGCAAGAGCTGCTGTATCGGCGCTCTGACAGCAACGCTTATGACTCTTA 375
Db 3208 AGTGTCTTCCGCAAGAGCTGCTGTATCGGCGCTCTGACAGCAACGCTTATGACTCTTA 3267
QY 376 AAGGACCTAGAGAGAGGATCCAAAGCTGATGGAGAGGCTGGAAGATGGACACCCCGG 435
Db 3268 AAGGACCTAGAGAGAGGATCCAAAGCTGATGGAGAGGCTGGAAGATGGACACCCCGG 3327
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Db 3328 ACTGGGCGAGATCTTCAAGAGAGCTTACAGAGATTGACACAACTCACAGAGATGAC 3387
QY 496 GCACTACTCAAGAACTACGAGGCTGCTCTACTGCTTTCAGAGAGGACATGACAAAGTTCAG 555
Db 3388 GCACTACTCAAGAACTACGAGGCTGCTCTACTGCTTTCAGAGAGGACATGACAAAGTTCAG 3447
QY 556 ACATTCTCGCGCATGTCGATGCGGCTGCTGTGAGAGGCGAGCTGTGGCTTTTGA 609
Db 3448 ACATTCTCGCGCATGTCGATGCGGCTGCTGTGAGAGGCGAGCTGTGGCTTTTGA 3501

```

RESULT 3

US-09-284-878-2

Sequence 2, Application US/09284878

Patent No. 6342375

## GENERAL INFORMATION:

APPLICANT: Olazaran, Martha Guerrero

APPLICANT: Saldana, Hugo Barrera

APPLICANT: Salgado, Jose Maria Viader

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1 GENERAL INFORMATION:
2 APPLICANT: VENTER, J. Craig et al.
3 TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
4 TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
5 FILE REFERENCE: CL001307
6 CURRENT APPLICATION NUMBER: US/09/949, 016
7 PRIORITY FILING DATE: 2000-04-14
8 PRIOR APPLICATION NUMBER: 60/241,755
9 PRIOR FILING DATE: 2000-10-20
10 PRIOR APPLICATION NUMBER: 60/237,768
11 PRIOR FILING DATE: 2000-10-03
12 PRIOR APPLICATION NUMBER: 60/231,498
13 PRIOR FILING DATE: 2000-09-08
14 NUMBER OF SEQ ID NOS: 207012
15 SOFTWARE: FastSeq for Windows Version 4.0
16 SEQ ID NO 2779
17 LENGTH: 821
18 TYPE: DNA
19 ORGANISM: Human

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Query Match	88.1%	Score 536.8;	DB 4;	Length 821;
Best Local Similarity	92.5%	Pred. No. 1.9e+149;		
Matches 605, Conservative	0;	Mismatches 2;	Indels 47;	Gaps 2

QY	1	ATGGCTACAGGCTCCCGAAGCTCCGTGCTCTGGCTTTTGGCTGCTGCTGCGCCCTGAG	60
Db	63	ATGGCTACAGGCTCCCGAAGCTCCGTGCTCTGGCTTTTGGCTGCTGCTGCGCCCTGAG	122
QY	61	CTTCAGAGGGCAGTGCCTTCCCAACATTCCTTATCCAGGCTTTTGGACACGCTAGT	120
Db	123	CTTCAGAGGGCAGTGCCTTCCCAACATTCCTTATCCAGGCTTTTGGACACGCTAGT	182
QY	121	CTCGGCCCATGCTCTGGACACAGCTGGCTTTTGAACCTTCCAGAGTTT-----	171
Db	183	CTCGGCCCATGCTCTGGACACAGCTGGCTTTTGAACCTTCCAGAGCTTTGAAGAGCC	242
QY	172	-----AACCCGACGCTCCCTCTGTTTC	195
Db	243	TATATCCCAAGAAACAGAGTATTCAATTCCTGGAGAACCCCGACCTCCCTCTGTTTC	302
QY	196	TCAGAGTCTATTCGCAACCTCTCCACAAGGAGGAAACACAAGAAATCCAACTTAGG	255
Db	303	TCAGAGTCTATTCGCAACCTCTCCACAAGGAGGAAACACAAGAAATCCAACTTAGG	362
QY	256	CTGCTCCGCAATTCCTCCGTGCTATCCAGTCGAGGCGTGGAGCCCGTGCAGTTCCTCAGG	315
Db	363	CTGCTCCGCAATTCCTCCGTGCTATCCAGTCGAGGCGCCGTCGCAAGTTCCTCAGG	422
QY	316	AGTGTCTTCGCAACAGCTGATGTAAGGCGCTCTGACACAGCAACGTATAGACTCTCTA	375
Db	423	AGTGTCTTCGCAACAGCTGATGTAAGGCGCTCTGACACAGCAACGTATAGACTCTCTA	482
QY	376	AAGGACTTAGAGGAGGCATCCAAACGTGATGAGGAGGCTGAAAGATGCGAGCCCTGG	435
Db	483	AAGGACTTAGAGGAGGCATCCAAACCTGATGAGG--GGCTGGAAGATGGAGCCCTGG	540
QY	436	ACTGGGAGAGTCTTCAAGCAGACCTAAGCAGAGTTGCACAAACTCACACAGATGAC	495
Db	541	ACTGGGAGAGTCTTCAAGCAGACCTAAGCAGAGTTGCAACAACTCACACAGATGAC	600
QY	496	GCACTACTCAAGACTACGGGCTGCTCTAATGCTTACAGAAAGCATGACAAAGTTCGAG	555
Db	601	GCACTACTCAAGACTACGGGCTGCTCTAATGCTTACAGAAAGCATGACAAAGTTCGAG	660
QY	556	ACATTTCTGGGCATCTGTCAGTGCCTCTGTGTGAGGGCAGCTGTGCTTTTAG	609
Db	661	ACATTTCTGGGCATCTGTCAGTGCCTCTGTGTGAGGGCAGCTGTGCTTTTAG	714

RESULT 5  
US-09-949-016-2780  
Sequence 2780, Application US/09949016

QY	1	ATGGCTACAGAGCTCCCGGACGCTCCGTGCTCCGTGGCTTTTGGCTGTCCTGACCTGGC	60
Db	63	ATGGCTACAGAGCTCCCGGACGCTCCGTGCTCCGTGGCTTTTGGCTGTCCTGCTGCTGGC	122
QY	61	CTTCAGAGGGGAGTGCTCTCCCAACCATTCCTTATCCAGGCTTTTGGACAAGCTAGT	120
Db	123	CTTCAGAGGGGAGTGCTCTCCCAACCATTCCTTATCCAGGCTTTTGGACAACGCTATG	182
QY	121	CTCGGCGGCATCGCTGTGACACAGCTGGCGCTTGGACCTACACAGAGTT-----	171
Db	183	CTCGGCGGCATCGCTGTGACACAGCTGGCGCTTGGACCTACACAGAGTTTGAAGAGCC	242
QY	172	-----AACCCGACAGCTCCCTCTGTTTC	195
Db	243	TATATCCCAAGAGACAGATGATTGATTCTGTGAGAAACCCGACAGCTCCCTCTGTTTC	302
QY	196	TCAGAGTCTATTTCGACACACCTCCAAACGGAGGAAACAAACAGAAATCCAACCTAAG	255
Db	303	TCAGAGTCTATTTCGACACACCTCCAAACGGAGGAAACAAACAGAAATCCAACCTAAG	362
QY	256	CTGCTCCGCAATCTCCCTGTGCTACACAGTGTGGCTGGAGCCGCTGAGTTCCCTACG	315
Db	363	CTGCTCCGCAATCTCCCTGTGCTACACAGTGTGGCTGGAGCCGCTGAGTTCCCTACG	422
QY	316	AGTGTCTTCGCAACAGCGCTGTGTATACGGCGGCTCTGACAGCAAGTCTATGACCTCTA	375
Db	423	AGTGTCTTCGCAACAGCGCTGTGTATACGGCGGCTCTGACAGCAAGTCTATGACCTCTA	482
QY	376	AAGGACCTTAGAGGAAGGATCCAAACGCTGATGGGAGGCTGGAAAGATGGCAGCCCGG	435
Db	483	AAGGACCTTAGAGGAAGGATCCAAACGCTGATGGG--GGCTGGAAGATGGCAGCCCGG	540
QY	436	ACTGGGCGAGATCTTCAAGGACGACTACAGCAGATTGACACAAATCAACAAAGATGAC	495
Db	541	ACTGGGCGAGATCTTCAAGGACGACTACAGCAGATTGACACAAATCAACAAAGATGAC	600
QY	496	GCACTACTCAAGAACTACGGGCTGTCTTACTGCTTCAAGAAAGACATGGACAAAGTCCAG	555
Db	601	GCACTACTCAAGAACTACGGGCTGTCTTACTGCTTCAAGAAAGACATGGACAAAGTCCAG	660
QY	556	ACATTCCCGCGCATGTGACAGGCGGCTCTGTGAGGGGACAGTGTGGCTTTCAG	609
Db	661	ACATTCCCGCGCATGTGACAGGCGGCTCTGTGAGGGGACAGTGTGGCTTTCAG	714

QY	1	ATGGGTAAAGGCTCCCGGAAGTCCCTGGCTCCGAGCTTTTGGCTGTCTCGCCGCTGG	60
Db	63	ATGGGTAAAGGCTCCCGGAAGTCCCTGGCTCCGAGCTTTTGGCTGTCTCGCCGCTGG	122
QY	61	CTTCAAGAGGCAAGTGCCTTCCCAACATTCCTTATTCAGGCTTTTGAACAAGCTAGT	120
Db	123	CTTCAAGAGGCAAGTGCCTTCCCAACATTCCTTATTCAGGCTTTTGAACAAGCTAGT	182
QY	121	CTCCGGCGCCATCGTCTGACCAAGTGGCCTTTGACACTTACCAGAGCTT-----	171
Db	183	CTCCGGCGCCATCGTCTGACCAAGTGGCCTTTGACACTTACCAGAGAGTTAAGAAGCC	242
QY	172	-----AACCCGACACCTCCCTGTGTTT	195
Db	243	TATATCCAAAGAACAGAGATTTCATTCTCGAGAAACCCCAAGCTCCTCTGTTC	302
QY	196	TCAGAGTCTATTCGACACCTCCAAACAGGAGAAACAAACAGAAATCCAACTTAG	255
Db	303	TCAGAGTCTATTCGACACCTCCAAACAGGAGAAACAAACAGAAATCCAACTTAG	362
QY	256	CTGCTCCGCAATCCCTCTGTCTATTCAGTGTGGCTGGACCCGTGAGTTCTCTAAG	315
Db	363	CTGCTCCGCAATCCCTCTGTCTATTCAGTGTGGCTGGACCCGTGAGTTCTCTAAG	422
QY	316	AGTGTCTTCGCCAACAGGCTGGTGTACGGCGCCTCTGACAGCAAGTCTATGACCTCTA	375
Db	423	AGTGTCTTCGCCAACAGGCTGGTGTACGGCGCCTCTGACAGCAAGTCTATGACCTCTA	482
QY	376	AAGGACTTAGAAGAAAGCATCCAAACGCTGATGGGAGGCTGGAAGATGGACGCCCG	435
Db	483	AAGGACTTAGAAGAAAGCATCCAAACGCTGATGGG--GGCTGGAAGATGGACGCCCG	540
QY	436	ACTGGGCGAGATCTTCAAGCAGACCTACAGCAAGTTGCAACAAATCACAACAAGTAG	495
Db	541	ACTGGGCGAGATCTTCAAGCAGACCTACAGCAAGTTGCAACAAATCACAACAAGTAG	600
QY	496	GCACCTACTCAAGAACTACGGGCTGTCTTACTGCTTCAGGAAGACATGACAAAGTTCAG	555
Db	601	GCACCTACTCAAGAACTACGGGCTGTCTTACTGCTTCAGGAAGACATGACAAAGTTCAG	660
QY	556	ACATTCTCGGCGCATGTGACAGTCCGCTCTGTGGAGGGCAGCTGTGGCTTCTAG	609
Db	661	ACATTCTCGGCGCATGTGACAGTCCGCTCTGTGGAGGGCAGCTGTGGCTTCTAG	714

## RESULT





DB 61 CTTCAAGAGGAGGAGGCTTCCCAACCAATCCCTATCCAGGCTTTTGACACCTATG 120  
QY 121 CTCGGGCGCCATGCTGTGACAGAGCTGGCTTTGACCTACAGAGTTTAAACCCGAG 180  
DB 121 CTCGGGCGCCGCTGCTGTACAGAGCTGGCTTTGACCTATCAGAGTTT----- 171  
QY 181 ACCCTCTCTGTTTCTCAGAGCTATTCGCAACCCCTCCAAAGAGGAGAACACAAAC 240  
DB 172 ---TCCCTCTGCTTCTCAGAGCTATTCGCAACCCCTCCAAAGAGGAGGAGGAGGAG 228  
QY 241 AATCAACCACTAGAGCTGCTCCGCAATCTCCCTGCTGCTATCCAGTGTGAGAGGCC 300  
DB 229 AATCACTACAGAGCTGCTCCGCAATCTCCCTGCTGCTATCCAGTGTGAGAGGCC 288  
QY 301 GTGCAATCTCTCAGAGCTGCTCCGCAACAGCTGTGTGAGAGGCCCTCTGACAGCAAC 360  
DB 289 GTGCAAGCTCTCAGAGAGGCTTCTCCGCAACAGCTGTGTATGAGGAGGCCCTCGAGAGCAAC 348  
QY 361 GTCTATGACCTCTTAAAGAGCTTACAGAGAGGAGCTCAAAAGCTGATGAGGAGGCTGAA 420  
DB 349 GTCTATGACCTCTTAAAGAGCTTACAGAGAGGAGCTCAAAAGCTGATGAGGAGGCTGAA 408  
QY 421 GATGCAAGCCCTCCGCAATCTTCCAGAGAGAGCTTACAGAGAGTTTGAACAAAC 480  
DB 409 GATGCAAGCCCTCCGCAATCTTCCAGAGAGAGCTTACAGAGAGTTTGAACAAAC 468  
QY 481 TCACACAGAGAGAGCTTACAGAGAGAGCTTACAGAGAGAGCTTACAGAGAGAG 540  
DB 469 TCACACAGAGAGAGAGCTTACAGAGAGAGCTTACAGAGAGAGCTTACAGAGAGAG 528  
QY 541 ATGCAAGAGAGAGAGCTTACAGAGAGAGCTTACAGAGAGAGCTTACAGAGAGAG 600  
DB 529 ATGCAAGAGAGAGAGCTTACAGAGAGAGCTTACAGAGAGAGCTTACAGAGAGAG 588  
QY 601 GGCTTCTAG 609  
DB 589 GGCTTCTAG 597

## RESULT 11

US-09-411-657-2  
Sequence 2, Application US/09411657  
Patent No. 6566328  
GENERAL INFORMATION:  
APPLICANT: Rosen, et al.  
TITLE OF INVENTION: Human Growth Factor  
NUMBER OF SEQUENCES: 7  
CORRESPONDENCE ADDRESS:  
ADDRESSER: Human Genome Sciences, Inc.  
STREET: 9410 Key West Avenue  
CITY: Rockville  
STATE: MD  
COUNTRY: USA  
ZIP: 20850  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patentin Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/09/411,657  
FILING DATE:  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/710,324  
FILING DATE:  
ATTORNEY/AGENT INFORMATION:  
NAME: Brookes, A. Anders  
REGISTRATION NUMBER: 36,373  
REFERENCE/DOCKET NUMBER: PF104DL.SKB  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 301-309-8504

TELEFAX: 301-309-8439  
INFORMATION FOR SEQ ID NO: 2:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 597 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: DNA (genomic)  
US-09-411-657-2

Query Match 82.6%; Score 503; DB 4; Length 597;  
Best Local Similarity 90.6%; Pred. No. 1.8e-139;  
Matches 552; Conservative 0; Mismatches 45; Indels 12; Gaps 1;

QY 1 ATGGCTACAGAGCTCCCGAGAGCTCCCTGCTGCTTTGGCTGCTGCTGCTGCTG 60  
DB 1 ATGGCTACAGAGCTCCCGAGAGCTCCCTGCTGCTGCTGCTGCTGCTGCTGCTG 60  
QY 61 CTTCAAGAGGAGGAGGCTTCCCAACCAATCCCTATCCAGGCTTTTGAACAAGCTAGT 120  
DB 61 CTTCAAGAGGAGGAGGCTTCCCAACCAATCCCTATCCAGGCTTTTGAACAAGCTAG 120  
QY 121 CTCGGGCGCCATGCTGTGACAGAGCTGGCTTTGACCTTACAGAGAGTTTAAACCCGAG 180  
DB 121 CTCGGGCGCCGCTGCTGTACAGAGCTGGCTTTGACCTTACAGAGAGTTTAAACCCGAG 180  
QY 181 ACCCTCTCTGTTTCTCAGAGCTATTCGCAACCCCTCCAAAGAGGAGAACACAAAC 240  
DB 172 ---TCCCTCTGCTTCTCAGAGCTATTCGCAACCCCTCCAAAGAGGAGGAGGAGGAG 228  
QY 241 AATCAACCACTAGAGCTGCTCCGCAATCTCCCTGCTGCTATCCAGTGTGAGAGGCC 300  
DB 229 AATCACTACAGAGCTGCTCCGCAATCTCCCTGCTGCTATCCAGTGTGAGAGGCC 288  
QY 301 GTGCAATCTCTCAGAGCTGCTCCGCAACAGCTGTGTGAGAGGCCCTCTGACAGCAAC 360  
DB 289 GTGCAAGCTCTCAGAGAGGCTTCTCCGCAACAGCTGTGTATGAGGAGGCCCTCGAGAGCAAC 348  
QY 361 GTCTATGACCTCTTAAAGAGCTTACAGAGAGGAGCTCAAAAGCTGATGAGGAGGCTGAA 420  
DB 349 GTCTATGACCTCTTAAAGAGCTTACAGAGAGGAGCTCAAAAGCTGATGAGGAGGCTGAA 408  
QY 421 GATGCAAGCCCTCCGCAATCTTCCAGAGAGAGCTTACAGAGAGTTTGAACAAAC 480  
DB 409 GATGCAAGCCCTCCGCAATCTTCCAGAGAGAGCTTACAGAGAGTTTGAACAAAC 468  
QY 481 TCACACAGAGAGAGCTTACAGAGAGAGCTTACAGAGAGAGCTTACAGAGAGAG 540  
DB 469 TCACACAGAGAGAGAGCTTACAGAGAGAGCTTACAGAGAGAGCTTACAGAGAGAG 528  
QY 541 ATGCAAGAGAGAGAGCTTACAGAGAGAGCTTACAGAGAGAGCTTACAGAGAGAG 600  
DB 529 ATGCAAGAGAGAGAGCTTACAGAGAGAGCTTACAGAGAGAGCTTACAGAGAGAG 588  
QY 601 GGCTTCTAG 609  
DB 589 GGCTTCTAG 597

## RESULT 12

US-08-117-809A-1  
Sequence 1, Application US/08117809A  
Patent No. 5436713  
GENERAL INFORMATION:  
APPLICANT: HONJO, Masaru  
APPLICANT: YOSHINO, Setuo  
APPLICANT: NAKAYAMA, Akira  
APPLICANT: NAITO, Naokazu  
TITLE OF INVENTION: PROCESS FOR PRODUCTION OF HUMAN GROWTH  
NUMBER OF SEQUENCES: 2  
CORRESPONDENCE ADDRESS:  
ADDRESSER: Burns, Doane, Swecker & Mathis

STREET: George Mason Bldg., Washington & Prince Sts.  
CITY: Alexandria  
STATE: Virginia  
COUNTRY: United States  
ZIP: 22313-1404  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent In Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/117,809A  
FILING DATE: 09-SEP-1993  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: JP 240936/1992  
FILING DATE: 09-SEP-1992  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: JP 009911/1993  
FILING DATE: 25-JAN-1993  
ATTORNEY/AGENT INFORMATION:  
NAME: Crane-Feury, Sharon E.  
REGISTRATION NUMBER: 36,113  
REFERENCE/DOCKET NUMBER: 029430-163  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (703) 836-6620  
TELEFAX: (703) 836-2021  
INFORMATION FOR SEQ ID NO: 1:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 859 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: double  
TOPOLOGY: linear  
MOLECULE TYPE: DNA (genomic)  
ORGANISM: Bacillus amyloliquefaciens  
STRAIN: MT-272  
FEATURE:  
NAME/KEY: CDS  
LOCATION: 251..859  
FEATURE:  
NAME/KEY: misc feature  
LOCATION: 179..208  
OTHER INFORMATION: /note= "Nucleotides 179-208 are S  
OTHER INFORMATION: promoter."  
FEATURE:  
NAME/KEY: sig\_peptide  
LOCATION: 251..331  
FEATURE:  
NAME/KEY: RBS  
LOCATION: 236..242  
FEATURE:  
NAME/KEY: mat\_peptide  
LOCATION: 332..859  
US-08-117-809A-1

Query Match 82.2%; Score 500.6; DB 1; Length 859;  
Best local Similarity 96.4%; Pred. No. 1.1e-138;  
Matches 512; Conservative 0; Mismatches 19; Indels 0; Gaps 0;

76 GCCTTCCCAACATTCCTTATCCAGAGCTTTTGAACAAGCTAGCTCCGCCCATCGT 135  
329 GCCTTCCCAATACACACTTTGGGCTATTCGATTAAGCAAGCTACGTCTACCGA 388  
136 CTGCACCAAGCTGGCTTTGACACCTACCAAGAGTTTAAACCCCAAGACCTCCTGTTT 195  
389 CTACATCAGCTGGGCTTTGACACCTACCAAGAGTTTAAACCCCAAGACCTCCTGTTT 448  
196 TCAGAGCTATTCCGACACCTCCACAGGAGGAGAAACAACAAGAAATCCAACTAGAG 255  
449 TCAGAGCTATTCCGACACCTCCACAGGAGGAGAAACAACAAGAAATCCAACTAGAG 508  
256 CTGCTCCGATCTCCCTGCTGCTATTCAGTGTGCTGAGAGCCGCTGACAGTTCTCAG 315

509 CTGCTCCGATCTCCCTGCTGCTCATTCAGTCGAGTGGAGCCCGTGACGTTCTCAG 568  
316 AGTCTCTCCGCAACACCTGGTGTATAGGGGCTCTTACAGCAAGCTCTTATGACTCTTA 375  
569 AGTGTCTTCGCCACACACCTGGTGTATAGGGGCTCTTACAGCAAGCTCTTATGACTCTTA 628  
376 AAGACCTAGAGGAAGGATCCAAAGCTGATGGGGAGGCTGGAAAGTGGACGCCCGG 435  
629 AAGACCTAGAGGAAGGATCCAAAGCTGATGGGGAGGCTGGAAAGTGGACGCCCGG 688  
436 ACTGGGAGATCTTCAAGACACCTACAGCAAGTTGACACAACTCAGCAAGATGAC 495  
689 ACTGGGAGATCTTCAAGACACCTACAGCAAGTTGACACAACTCAGCAAGATGAC 748  
496 GCACTACTCAAGAACTACGCGGCTGCTTACTGCTTCAAGAAAGATGACAAAGTGCAG 555  
749 GCACTACTCAAGAACTACGCGGCTGCTTACTGCTTCAAGAAAGATGACAAAGTGCAG 808  
556 ACATTCCTGGCATTCGTGCGATGCGGCTGCTGTGAGAGGCGACGTTGGCTTC 606  
809 ACATTCCTGGCATTCGTGCGATGCGGCTGCTGTGAGAGGCGACGTTGGCTTC 859

RESULT 13  
US-08-117-809A-2  
Sequence 2, Application US/08117809A  
Patent No. 5496713  
GENERAL INFORMATION:  
APPLICANT: HONJO, Masaru  
APPLICANT: YOSHINO, Setuo  
APPLICANT: NAKAYAMA, Akira  
TITLE OF INVENTION: PROCESS FOR PRODUCTION OF HUMAN GROWTH  
TITLE OF INVENTION: HORMONE  
NUMBER OF SEQUENCES: 2  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Burns, Doane, Swecker & Mathis  
STREET: George Mason Bldg., Washington & Prince Sts.  
CITY: Alexandria  
STATE: Virginia  
COUNTRY: United States  
ZIP: 22313-1404  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent In Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/117,809A  
FILING DATE: 09-SEP-1993  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: JP 240936/1992  
FILING DATE: 09-SEP-1992  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: JP 009911/1993  
FILING DATE: 25-JAN-1993  
ATTORNEY/AGENT INFORMATION:  
NAME: Crane-Feury, Sharon E.  
REGISTRATION NUMBER: 36,113  
REFERENCE/DOCKET NUMBER: 029430-163  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (703) 836-6620  
TELEFAX: (703) 836-2021  
INFORMATION FOR SEQ ID NO: 2:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 859 base pairs  
TYPE: nucleic acid  
STRANDEDNESS: double  
TOPOLOGY: linear  
MOLECULE TYPE: DNA (genomic)  
ORIGINAL SOURCE:



ORGANISM: *Bacillus amyloliquefaciens*  
STRAIN: MT-272  
FEATURE:  
NAME/KEY: misc feature  
LOCATION: 179..208  
OTHER INFORMATION: /note= "Nucleotides 179-208 are S  
OTHER INFORMATION: promoter."  
FEATURE:  
NAME/KEY: CDS  
LOCATION: 251..859  
FEATURE:  
NAME/KEY: RBS  
LOCATION: 236..242  
FEATURE:  
NAME/KEY: sig\_peptide  
LOCATION: 251..331  
FEATURE:  
NAME/KEY: mat\_peptide  
LOCATION: 332..859  
US-08-117-809A-2

Query Match 81.7%; Score 497.4; DB 1; Length 859;  
Best Local Similarity 96.0%; Pred. No. 9.8e-138;  
Matches 510; Conservative 0; Mismatches 21; Indels 0; Gaps 0;  
QY 76 GCCTTCCCAACATTCCTTATCCAGGCTTTTGAACAGCTAGTCTCGGCCCATGT 135  
DB 329 GCCTTCCCACTATACACTTTCGGCTATTATGATAGCAAGTCTACGTCTACCGA 388  
QY 136 CTGACACAGCTGGCTTTGACACTTACAGAGTTTAAACCCCAAGCTCTCTGTTTC 195  
DB 389 CTACATAGCTGGCTTTGACACTTACAGAGTTTAAACCCCAAGCTCTCTGTTTC 448  
QY 196 TCAGAGCTTATTCGACACCTTCCACAGAGAGAGAAACACACAGAAATCCACTAG 255  
DB 449 TCAGAGCTTATTCGACACCTTCCACAGAGAGAGAAACACACAGAAATCCACTAG 508  
QY 256 CTGCTCCGATCTCCCTGCTGCTCATCATCGTGGCTGGAGGCCCGGCACTTCTAG 315  
DB 509 CTGCTCCGATCTCCCTGCTGCTCATCATCGTGGCTGGAGGCCCGGCACTTCTAG 568  
QY 316 AGTGTCTTGGCCAAACAGCTGTGTATAGGCGCTCTGACAGCAACGCTTATGACCTTA 375  
DB 569 AGTGTCTTGGCCAAACAGCTGTGTATAGGCGCTCTGACAGCAACGCTTATGACCTTA 628  
QY 376 AAGGACTTAAAGAGGAGCATCCAAAGCTGATGGGAGGCTGGAAGATGACGCCCGG 435  
DB 629 AAGGACTTAAAGAGGAGCATCCAAAGCTGATGGGAGGCTGGAAGATGACGCCCGG 688  
QY 436 ACTGGGAGATCTTCAAGCAGACTTACAGCAAGTTTGACACAAATCTACACAGATGAC 495  
DB 689 ACTGGGAGATCTTCAAGCAGACTTACAGCAAGTTTGACACAAATCTACACAGATGAC 748  
QY 496 GCACTTCTCAAGAACTACGGGGCTGTCTACTGCTTCAAGAAAGACATGACAGTGGAG 555  
DB 749 GCACTTCTCAAGAACTACGGGGCTGTCTACTGCTTCAAGAAAGACATGACAGTGGAG 808  
QY 556 ACAATTCCTGCGCATCTGACAGTCCGCTCTGTGAGAGGAGGAGCTGTGGCTTC 606  
DB 809 ACAATTCCTGCGCATCTGACAGTCCGCTCTGTGAGAGGAGGAGCTGTGGCTTC 859

RESULT 14  
US-08-187-756C-1  
Sequence 1, Application US/08187756C  
Patent No. 5597709  
GENERAL INFORMATION:  
APPLICANT: ROSEN, ET AL.  
TITLE OF INVENTION: Human Growth Hormone  
NUMBER OF SEQUENCES: 7  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: CARELLA, BYRNE, BAIN, GILFILLAN,  
ADDRESSER: CECCHI, STEWART & OLSTEIN

STREET: 6 BECKER FARM ROAD  
CITY: ROSELAND  
STATE: NEW JERSEY  
COUNTRY: USA  
ZIP: 07068  
COMPUTER READABLE FORM:  
MEDIUM TYPE: 3.5 INCH DISKETTE  
COMPUTER: IBM PS/2  
OPERATING SYSTEM: MS-DOS  
SOFTWARE: WORD PERFECT 5.1  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/187,756C  
FILING DATE: January 27, 1994  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER:  
FILING DATE:  
ATTORNEY/AGENT INFORMATION:  
NAME: FERRARO, GREGORY D.  
REGISTRATION NUMBER: 36,134  
REFERENCE/DOCKET NUMBER: 325800-55  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 201-994-1700  
TELEFAX: 201-994-1744  
INFORMATION FOR SEQ ID NO: 1:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 654 BASE PAIRS  
TYPE: NUCLEIC ACID  
STRANDEDNESS: SINGLE  
TOPOLOGY: LINEAR  
MOLECULE TYPE: cDNA  
US-08-187-756C-1

Query Match 81.0%; Score 493.2; DB 1; Length 654;  
Best Local Similarity 87.3%; Pred. No. 1.5e-136;  
Matches 571; Conservative 0; Mismatches 38; Indels 45; Gaps 1;  
QY 1 ATGGCTACAGGCTCCGAGAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 60  
DB 1 ATGGCTACAGGCTCCGAGAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 60  
QY 61 CTTCAAGAGGAGAGGCTGCTTCCCAACATTCCTTATCCAGGCTTTTGAACAGCTAGT 120  
DB 61 CTTCAAGAGGAGAGGCTGCTTCCCAACATTCCTTATCCAGGCTTTTGAACAGCTAGT 120  
QY 121 CTCCGGGCCCATGTGTGACACAGCTGGCTTTGAACCTTACAGGAGTTTGAAGAGCC 171  
DB 121 CTCCGGGCCCATGTGTGACACAGCTGGCTTTGAACCTTATCAGGAGTTTGAAGAGCC 180  
QY 172 -----AACCCCAAGCTCTCTGTTTC 195  
DB 181 TATATCTTAAGAGAGAGATTCATTCTGCAAGACCCCAAGCTCTCTCTGTTTC 240  
QY 196 TCAAGTCTATTCGACACCTTCCAAAGAGAGAGAAACACAGAAATCCAACTTAGAG 255  
DB 241 TCAAGTCTATTCGACACCTTCCAAAGAGAGAGAAACACAGAAATCCAACTTAGAG 300  
QY 256 CTGCTCCGATCTCCCTGCTGCTCATTCAGTGTGCTGAGAGCCCGTGAAGTTCTCAGG 315  
DB 301 CTGCTCCGATCTCCCTGCTGCTCATTCAGTGTGCTGAGAGCCCGTGAAGTTCTCAGG 360  
QY 316 AGTGTCTTGGCCAAACAGCTGTGTATAGGCGCTTGAACAGCAAGCTTATGACCTCTTA 375  
DB 361 AGTGTCTTGGCCAAACAGCTGTGTATAGGCGCTTGAACAGCAAGCTTATGACCTCTTA 420  
QY 376 AAGGACTTAAAGAGGAGCATCCAAAGCTGATGGGAGGCTGGAAGATGACGCCCGCG 435  
DB 421 AAGGACTTAAAGAGGAGCATCCAAAGCTGATGGGAGGCTGGAAGATGACGCCCGCG 480  
QY 436 ACTGGGAGATCTTCAAGCAGACTTACAGCAAGTTTGACACAAATCTACACAGATGAC 495  
DB 481 ACTGGGAGATCTTCAAGCAGACTTACAGCAAGTTTGACACAAATCTACACAGATGAC 540

QY 496 GCACCTACTCAAGAACTACGGGCTGCTCTACTGCTTCAGAGAGACATGACAGAGTCGAG 555  
DB 541 GCACCTGCTCAAGAACTACGGGCTGCTCTACTGCTTCAGAGAGACATGACAGAGTCGAG 600  
QY 556 ACATTCTCGGCGATGTCGAGTCGCCCTCTGTGAGAGGCGAGCTGTGCTTAG 609  
DB 601 ACATTCTCGGCGATGTCGAGTCGCCCTCTGTGAGAGGCGAGCTGTGCTTAG 654

## RESULT 15

US-08-710-324A-1  
Sequence 1, Application US/08710324A

Patent No. 5962411

GENERAL INFORMATION:

APPLICANT: Rosen, et al.

TITLE OF INVENTION: Human Growth Factor

NUMBER OF SEQUENCES: 7

CORRESPONDENCE ADDRESS:

ADDRESSEE: Human Genome Sciences, Inc.

STREET: 9410 Key West Avenue

CITY: Rockville

STATE: MD

COUNTRY: USA

ZIP: 20850

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/710,324A

FILING DATE: 16-SEP-1996

CLASSIFICATION: 435

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/187,756

FILING DATE: 27-JAN-1994

ATTORNEY/AGENT INFORMATION:

NAME: Brookes, A. Anders

REGISTRATION NUMBER: 36,373

REFERENCE/DOCKET NUMBER: PF104D1.SKB

TELECOMMUNICATION INFORMATION:

TELEPHONE: 301-309-8504

TELEFAX: 301-309-8439

INFORMATION FOR SEQ ID NO: 1:

SEQUENCE CHARACTERISTICS:

LENGTH: 654 base pairs

TYPE: nucleic acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: DNA (genomic)

US-08-710-324A-1

Query Match 81.0%; Score 493.2; DB 2; Length 654;

Best Local Similarity 87.3%; Pred. No. 1.5e-136;

Matches 571; Conservative 0; Mismatches 38; Indels 45; Gaps 1;

QY 1 ATGGCTACAGGCTCCCGAGCGTCCCTGCTCTGCTGCTTTGGCGCTGCTGCTGCTGCTG 60  
DB 1 ATGGCTACAGGCTCCCGAGCGTCCCTGCTCTGCTGCTTTGGCGCTGCTGCTGCTGCTG 60  
QY 61 CTTCAAGAGGAGCAGTGCCTTCCCAACATTCCTTATCCAGGCTTTTGAACAAGCTAGT 120  
DB 61 CTTCAAGAGGAGCAGTGCCTTCCCAACATTCCTTATCCAGGCTTTTGAACAAGCTATG 120  
QY 121 CTCGCGCCCATCTGCTGACCAAGCTGCGCTTTGACACTTACCAAGAGTTT----- 171  
DB 121 CTCGCGCGCCCATCTGCTGACCAAGCTGCGCTTTGACACTTACCAAGAGTTTGAAGAGCC 180  
QY 172 -----AACCCCAAGACTCCCTCTGTTTC 195  
DB 181 TATATCCGGAAGAGCAGAGTATTCATTCCTGACAGAACCCCAAGACTCCCTCTGTTTC 240  
QY 196 TCAGAGTCTATTCGACACCCCTCAACAGAGGAGAAACACAAAGAAATCAACTAGAG 255

DB 241 TCAGAGTCTATTCGACACCCCTCAACAGAGGAGTGAAGAAACGACAGAGAAATCAACTAGAG 300  
QY 256 CTGCTCCGCAATCTTCCTGCTGCTCTCATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 315  
DB 301 CTGCTCCGCAATCTTCCTGCTGCTCTCATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 360  
QY 316 AGTGTCTTCGCAACAGCTGTGTGTACGCGGCTCTGTACAGCAACGTCTATGACCTCTA 375  
DB 361 AGCGTCTTCGCAACAGCTGTGTGTATGTGGCGCTCTGAGAGACAGTCTATTCGCACTG 420  
QY 376 AAGACCTAGAGAGAGCATTCNAACGCTGTATGTGGAGAGCTGTGAAGATGTGACGCCCCG 435  
DB 421 AAGACCTAGAGAGAGCATTCNAACGCTGTATGTGGAGAGCTGTGAAGATGTGACGCCCCG 480  
QY 436 ACTGGGAGATCTTCAAGCAGACCTTACAGCAAGTTTCAACAACTACACAAAGATGAC 495  
DB 481 ACTGGGAGATCTTCAATCAGTCTTACAGCAAGTTTGAACAAATGCAACAAAGATGAC 540  
QY 496 GCACCTACTCAAGAACTACGGGCTGCTCTACTGCTTTCAGGAAGGACATGACAAAGTCGAG 555  
DB 541 GCACCTGCTCAAGAACTACGGGCTGCTCTACTGCTTTCAGGAAGGACATGACAAAGTCGAG 600  
QY 556 ACATTCTCGGCGATGTCGAGTCGCCCTGTGTGAGAGGCGAGCTGTGCTTAG 609  
DB 601 ACATTCTCGGCGATGTCGAGTCGCCCTGTGTGAGAGGCGAGCTGTGCTTAG 654

Search completed: February 7, 2005, 12:30:44

Job time : 166 secs

GenCore version 5.1.6  
Copyright (c) 1993 - 2005 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: February 7, 2005, 11:40:04 ; Search time 477 Seconds  
(without alignments)  
7348.526 Million cell updates/sec

Title: US-09-856-796B-1

Perfect score: 609  
Sequence: 1 atggtacagcgtcccgac.....aggagcagctgtgctctag 609

Scoring table: IDENTITY NUC  
Gapop 10.0, Gapext 1.0

Searched: 431806 seqs, 2877871033 residues

Total number of hits satisfying chosen parameters: 8627612

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%

Listing first 45 summaries

Database:

Published Applications NA:\*

- 1: /cgn2\_6/ptodata/1/pubpna/US07\_PUBCOMB.seq:\*
- 2: /cgn2\_6/ptodata/1/pubpna/PCT\_NEW\_PUB.seq:\*
- 3: /cgn2\_6/ptodata/1/pubpna/US06\_NEW\_PUB.seq:\*
- 4: /cgn2\_6/ptodata/1/pubpna/US06\_PUBCOMB.seq:\*
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- 6: /cgn2\_6/ptodata/1/pubpna/PCTUS\_PUBCOMB.seq:\*
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- 12: /cgn2\_6/ptodata/1/pubpna/US09C\_PUBCOMB.seq:\*
- 13: /cgn2\_6/ptodata/1/pubpna/US10\_PUBCOMB.seq:\*
- 14: /cgn2\_6/ptodata/1/pubpna/US10\_PUBCOMB.seq:\*
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- 17: /cgn2\_6/ptodata/1/pubpna/US10C\_PUBCOMB.seq:\*
- 18: /cgn2\_6/ptodata/1/pubpna/US10C\_PUBCOMB.seq:\*
- 19: /cgn2\_6/ptodata/1/pubpna/US10C\_PUBCOMB.seq:\*
- 20: /cgn2\_6/ptodata/1/pubpna/US11\_NEW\_PUB.seq:\*
- 21: /cgn2\_6/ptodata/1/pubpna/US11\_NEW\_PUB.seq:\*
- 22: /cgn2\_6/ptodata/1/pubpna/US60\_PUBCOMB.seq:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	554	91.0	654	9	US-09-853-688-1
2	554	91.0	654	9	US-09-853-688-3
3	554	91.0	654	18	US-10-788-318-1
4	554	91.0	654	18	US-10-788-318-3
5	550.8	90.4	821	10	US-09-969-748C-3
6	549.2	90.2	799	9	US-09-804-409A-17
7	549.2	90.2	799	17	US-10-411-037-47
8	549.2	90.2	799	17	US-10-411-026-47
9	549.2	90.2	799	17	US-10-410-962-47
10	549.2	90.2	799	17	US-10-411-049-47
11	549.2	90.2	799	18	US-10-410-930-47

12	549.2	90.2	799	18	US-10-410-997-47	Sequence 47, Appli
13	549.2	90.2	799	18	US-10-411-012-47	Sequence 47, Appli
14	549.2	90.2	799	18	US-10-287-994-47	Sequence 47, Appli
15	549.2	90.2	799	18	US-10-410-913-47	Sequence 47, Appli
16	546.2	89.7	651	18	US-10-477-651-1	Sequence 1, Appli
17	541.8	89.0	821	16	US-10-289-845-1	Sequence 1, Appli
18	477.2	78.4	4723	9	US-09-733-967-3	Sequence 3, Appli
19	477.2	78.4	4723	18	US-10-821-273-73	Sequence 73, Appli
20	475.4	78.1	2445	17	US-10-621-693-75	Sequence 81, Appli
21	474.2	77.9	587	17	US-10-621-693-81	Sequence 85, Appli
22	473.8	77.8	2307	17	US-10-621-693-85	Sequence 85, Appli
23	473.8	77.7	600	17	US-10-621-693-67	Sequence 67, Appli
24	472.8	77.6	579	10	US-09-819-094-19	Sequence 19, Appli
25	472.8	77.6	579	17	US-10-714-067-19	Sequence 19, Appli
26	472.8	77.6	588	17	US-10-621-693-7	Sequence 7, Appli
27	472.8	77.6	603	17	US-10-621-693-46	Sequence 46, Appli
28	472.8	77.6	2370	17	US-10-621-693-54	Sequence 54, Appli
29	472.4	77.6	789	9	US-09-876-478-1	Sequence 1, Appli
30	472.4	77.6	1248	17	US-10-621-693-73	Sequence 73, Appli
31	472.2	77.5	1165	17	US-10-621-693-83	Sequence 83, Appli
32	471.6	77.4	592	17	US-10-621-693-79	Sequence 79, Appli
33	471.2	77.4	576	10	US-09-884-010-22	Sequence 22, Appli
34	470.8	77.3	591	17	US-10-621-693-41	Sequence 41, Appli
35	470.8	77.3	606	17	US-10-621-693-44	Sequence 44, Appli
36	470.8	77.3	1185	17	US-10-621-693-50	Sequence 50, Appli
37	470.8	77.3	1200	17	US-10-621-693-48	Sequence 48, Appli
38	470.8	77.3	1779	17	US-10-621-693-52	Sequence 52, Appli
39	470.6	77.3	602	17	US-10-621-693-65	Sequence 65, Appli
40	470.2	77.2	593	17	US-10-621-693-77	Sequence 77, Appli
41	470.2	77.2	639	17	US-10-621-693-69	Sequence 69, Appli
42	470.2	77.2	945	17	US-10-311-473-15	Sequence 15, Appli
43	469.8	77.1	573	17	US-10-621-693-1	Sequence 1, Appli
44	469.8	77.1	588	17	US-10-311-473-1	Sequence 1, Appli
45	469.8	77.1	630	17	US-10-621-693-71	Sequence 71, Appli

#### ALIGNMENTS

RESULT 1  
US-09-853-688-1  
Sequence 1, Application US/09853688  
Patent No. US20020081605A1  
GENERAL INFORMATION:  
APPLICANT: COOPER, DAVID N.  
APPLICANT: PROCTER, ANNIE M.  
APPLICANT: GREGORY, JOHN  
APPLICANT: MILLAR, DAVID S.  
TITLE OF INVENTION: METHOD FOR DETECTING GROWTH HORMONE VARIATIONS IN  
FILE REFERENCE: WCM78  
CURRENT APPLICATION NUMBER: US/09/853,688  
CURRENT FILING DATE: 2001-05-14  
NUMBER OF SEQ IDS: 66  
SOFTWARE: PatentIn Ver. 2.1  
SEQ ID NO 1  
LENGTH: 654  
TYPE: DNA  
ORGANISM: Homo sapiens  
FEATURE:  
NAME/KEY: CDS  
LOCATION: (1)...(651)  
US-09-853-688-1  
Query Match 91.0%; Score 554; DB 9; Length 654;  
Best local similarity 93.1%; Pred. No. 2.6e-14;  
Matches 609; Conservative 0; Mismatches 0; Indels 45; Gaps 1;  
Oy 1 ATGGCTACAGGCTCCCGAGGCTCCCTGCTTTGGCCCTGCTGCTCCCTG 60  
Db 1 ATGGCTACAGGCTCCCGAGGCTCCCTGCTTTGGCCCTGCTGCTCCCTG 60  
Oy 61 CTTCAAGAGGAGCTGCTTCCCAACATTCCTTATCCAGGCTTTTGACAGCTAGT 120

Db	61	CTTCAAGAGGSGAGTGGCTTTCCACCAATTCCTTATCCAGGCTTTTGTACAAAGCTAAGT	120
Qy	121	CTCCGCGCCATCGTCTGCAACGACTGGCTTTGACACCTACCAAGAGTTT-----	171
Db	121	CTCCGCGCCCATGCTGTGCAACGACTGGCTTTGACACCTACCAAGAGTTTGAAGAAGCC	180
Qy	172	-----AACCCCAAGCTTCCCTCTGTATTC	195
Db	181	TATATCCCAAGAAACAGAGTATTATTCCTGTCAGAAACCCCAAGACTTCCCTGTATTC	240
Qy	196	TCAGAGTCTATTCCGACACCCCTTCCACAGGAGAGAAACACAAAGAAATCCAACTTAGAG	255
Db	241	TCAGAGTCTATTCCGACACCCCTTCCACAGGAGAGAAACACAAAGAAATCCAACTTAGAG	300
Qy	256	CTGCTCCGCACTCCCTGCTGCTCATCCAGTGGCTGGAGCCGTGGACGTTCTCTCAGG	315
Db	301	CTGCTCCGCACTCCCTGCTGCTCATCCAGTGGCTGGAGCCGTGGACGTTCTCTCAGG	360
Qy	316	AGTGTCTTTCGCAACAGCTGTGGTATCGGCGCTCTGACAGCAACGTCATATGACTTCTTA	375
Db	361	AGTGTCTTTCGCAACAGCTGTGGTATCGGCGCTCTGACAGCAACGTCATATGACTTCTTA	420
Qy	376	AAGGACTTAGAGAAAGGCAATCCAAACGCTGATGGGAGGCTGGAAAGTGGCAAGCCCCGG	435
Db	421	AAGGACTTAGAGAAAGGCAATCCAAACGCTGATGGGAGGCTGGAAAGTGGCAAGCCCCGG	480
Qy	436	ACTGGGCGAGATCTTCAAGCAGACCTTACAGCAAGTTGACACAAATCTCACAAACGATGAC	495
Db	481	ACTGGGCGAGATCTTCAAGCAGACCTTACAGCAAGTTGACACAAATCTCACAAACGATGAC	540
Qy	496	GCACCTACTCAAAACCTACGCGGCTGCTCTACTGCTTTCAGGAAGGACATGCAACAAAGTTCGAG	555
Db	541	GCACCTACTCAAAACCTACGCGGCTGCTCTACTGCTTTCAGGAAGGACATGCAACAAAGTTCGAG	600
Qy	556	ACATTCTCGCGCATGTCGACAGTGGCGCTCTGTTGGAAGGAGCGTGTGGCTTTGAG	609
Db	601	ACATTCTCGCGCATGTCGACAGTGGCGCTCTGTTGGAAGGAGCGTGTGGCTTTTTCAG	654

RESULT 2  
US-09-853-688-3  
; Sequence 3, Application US/09853688  
; Patent No. US20020081605A1

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1 GENERAL INFORMATION:
2 APPLICANT: COOPER, DAVID N.
3 APPLICANT: PROCTER, ANNIE M.
4 APPLICANT: GREGORY, JOHN
5 APPLICANT: MILLAR, DAVID S.
6 TITLE OF INVENTION: METHOD FOR DETECTING GROWTH HORMONE VARIATIONS IN
7 TITLE OF INVENTION: HUMANS, THE VARIATIONS AND THEIR USES
8 FILE REFERENCE: WCM/78
9 CURRENT APPLICATION NUMBER: US/09/853,688
10 CURRENT FILING DATE: 2001-05-14
11 NUMBER OF SEQ ID NOS: 66
12 SOFTWARE: PatentIn Ver. 2.1
13 SEQ ID NO 3
14 LENGTH: 654
15 TYPE: DNA
16 ORGANISM: Homo sapiens
17 FEATURE:
18 NAME/KEY: CDS
19 LOCATION: (1)..(651)
20 US-09-853-688-3

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Query Match      91.0%;  Score 554;  DB 9;  Length 654;
Best Local Similarity 93.1%;  Pred No.2.6e-164;
Matches 609;  Conservative 0;  Mismatches 0;  Indels 45;  Gaps 1;

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**Dy** 1 ATGGCTACAGGCTCCCGACGTCCTGTCTGGCTTTTGAACCTGCCTCCTGCCTGG 60  
Db 1 ATGGCTACAGGCTCCCGACGTCCTGTCTGGCTTTTGAACCTGCCTCCTGCCTGG 60

OY	61	TTTAAAGAGGGAGAGTGGCTTCCCAACAAATCCCTTATCCAGGCTTTTACAACAGCTAGT	120
Db	61	CTTCAAGAGGGAGAGTGGCTTCCCAACAAATCCCTTATCCAGGCTTTTACAACAGCTAGT	120
OY	121	CTCCGCGGCATCGTGTGACCCAGGTGGGCTTTGACCACTACCAAGAGTT-----	171
Db	121	CTCCGCGGCATCGTGTGACCCAGGTGGGCTTTGACCACTACCAAGAGTTGGGGAGCC	180
OY	172	-----AACCCGACACCTCCCTCTGTTTC	195
Db	181	TATATCCCAAGAGAACAGATGATTTCATTTCTGCAAGAACCCCAAGCTTCCTCTGTTTC	240
OY	196	TCAGAGTCTATTCGACACACCTTCACACGAGAGAAACCAACAGAAATCCAACTTAGAG	255
Db	241	TCAGAGTCTATTCGACACACCTTCACACGAGAGAAACCAACAGAAATCCAACTTAGAG	300
OY	256	CTGCTCGGCATCTCCCTGCTGCTCATTCAGTGTGGCTGGAGCCCGTGCAGTTCTCAGG	315
Db	301	CTGCTCGGCATCTCCCTGCTGCTCATTCAGTGTGGCTGGAGCCCGTGCAGTTCTCAGG	360
OY	316	AGTGTCTTTCGCCCAACAGCCTGTGTGTACGGCGCCTCTGACAGCAAGTCTATAGACTCTTA	375
Db	361	AGTGTCTTTCGCCCAACAGCCTGTGTGTACGGCGCCTCTGACAGCAAGTCTATAGACTCTTA	420
OY	376	AAGGACTTAGAGGAAGGCATCCAAACGCTGATGGGAGGCTGGAAAGATGGCAAGCCCGG	435
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OY	436	ACTGGGCGAGTCTTAAAGCAGACCTTACAGCAAGTTGCACACAACTCACACAAAGATGAC	495
Db	481	ACTGGGCGAGTCTTAAAGCAGACCTTACAGCAAGTTGCACACAACTCACACAGATGAC	540
OY	496	GCACATCTCAAGAACTAAGCGGCTGTCTAACTGCTTCAGGAAAGACATGGAACAAGGTCSAG	555
Db	541	GCACATCTCAAGAACTAAGCGGCTGTCTAACTGCTTCAGGAAAGACATGGAACAAGGTCSAG	600
OY	556	ACATTCTCGCGCATGTGACGAGTACCGCTCTGTGGAGGGGACGCTGTGGCTTTAG	609
Db	601	ACATTCTCGCGCATGTGACGAGTACCGCTCTGTGGAGGGGACGCTGTGGCTTTAG	654

RESULT 3  
US-10-788-318-1  
: Sequence 1, Application US/10788318

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1  Publication NO. US20040137510A1 .
2  GENERAL INFORMATION:
3  APPLICANT: COOPER, DAVID N.
4  APPLICANT: PROCTER, ANNIE M.
5  APPLICANT: GREGORY, JOHN
6  APPLICANT: MILLAR, DAVID S.
7  TITLE OF INVENTION: METHOD FOR DETECTING GROWTH HORMONE VARIATIONS IN
8  TITLE OF INVENTION: HUMANS, THE VARIATIONS AND THEIR USES
9  FILE REFERENCE: WCM78
10 CURRENT APPLICATION NUMBER: US/10/788,318
11 CURRENT FILING DATE: 2004-03-01
12 NUMBER OF SEQ. ID NOS.: 66
13 SOFTWARE: PatentIn Ver. 2.1
14 SEQ ID NO 1
15     LENGTH: 654
16     TYPE: DNA
17     ORGANISM: Homo sapiens
18     FEATURE:
19     NAME/KEY: CDS
20     LOCATION: (1)..(651)
21     US-10-788-318-1

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Query Match	91.0%;	Score 554;	DB 18;	Length 654;
Best Local Similarly	93.1%;	Pred. No. 2.6e-164;		
Matches 609; Conservative	0;	Mismatches 0;	Indels 45;	Gaps 1;

Qy 1 ATGCTACAGGCTCCCGGACGTCCTCCCTGCTTTGGCCCTGCTTGCCTGCGCTTG 60

Db 1 ATGCTACAGGCTCCCGGACGTCCTCCCTGCTTTGGCCCTGCTTGCCTGCGCTTG 60

Dp	1	ATGGCTACAGAGCTCCCGAGCGTCCCGTGGCTCTGGCTTTTGGCGCTGCTCGTGGCCCTGG	60
Qy	61	CTTCAAGAGGGAGAGTGGCTTCCCAACCATTTCCCTTATTCAGAGCTTTTGAACAACGCTAGT	120
Dp	61	CTTCAAGAGGGAGAGTGGCTTCCCAACCATTTCCCTTATTCAGAGCTTTTGAACAACGCTAGT	120
Qy	121	CTCCGCGCCATCGTCTGACACAGGTGGCTTTGACACTACACAGAGTTT-----	171
Dp	121	CTCCGCGCCATCGTCTGACACAGGTGGCTTTGACACTACACAGAGTTTGGGGAAGCC	180
Qy	172	-----AACCCCGAGCTCCCTCTCTTTTC	199
Dp	181	TATATCCAAAGGAACAGAGTATTCATTCTCGAGAAACCCCGAGCTCCCTCTCTTTTC	240
Qy	196	TCAGAGTCTATTCGACACACCTTCGAACGAGGAGAAACAAACAGAAATCCAACTTAGAG	255
Dp	241	TCAGAGTCTATTCGACACACCTTCGAACGAGGAGAAACAAACAGAAATCCAACTTAGAG	300
Qy	256	CTGCTCCGCATCTCCGCTGCTCATTCACAGTGTGGCTGGAGCCCGTGGAGTTCCCTAGG	315
Dp	301	CTGCTCCGCATCTCCGCTGCTCATTCACAGTGTGGCTGGAGCCCGTGGAGTTCCCTAGG	360
Qy	316	AGTGTCTTTCGCCAACAGGCTGGTGTACGGCGCTCTGACAGCAACGTTATGACACTCTTA	375
Dp	361	AGTGTCTTTCGCCAACAGGCTGGTGTACGGCGCTCTGACAGCAACGTTATGACACTCTTA	420
Qy	376	AAGGACCTTAGAGGAAGGATCCAAACGCTGATGGGGAGGCTGGAAGATGGACGCCCCGG	435
Dp	421	AAGGACCTTAGAGGAAGGATCCAAACGCTGATGGGGAGGCTGGAAGATGGACGCCCCGG	480
Qy	436	ACTGGGCGAGATCTTCAAGCAGACCTACAGCAAGTTCCGACACAACTCCACAAACGATGAC	495
Dp	481	ACTGGGCGAGATCTTCAAGCAGACCTACAGCAAGTTCCGACACAACTCCACAAACGATGAC	540
Qy	496	GCACTACTCAAGAACTACGGGCTGCTCTACTGCTTCAGAAAGACATGACCAAGTTCGAG	555
Dp	541	GCACTACTCAAGAACTACGGGCTGCTCTACTGCTTCAGAAAGACATGACCAAGTTCGAG	600
Qy	556	ACATTTCGCGCAATCGTGCATGTCCGCTCTGTGGAGGGCAGCTTGGCTTTTAG	609
Dp	601	ACATTTCGCGCAATCGTGCATGTCCGCTCTGTGGAGGGCAGCTTGGCTTTTAG	654

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RESULT 5
US-09-969-748C-3
; Sequence 3, Application US/09969748C
; Publication No. US20030161809A1
; GENERAL INFORMATION:
; APPLICANT: ARIZEKE PHARMACEUTICALS, INC.
; APPLICANT: HOUSTON, Lou, L.
; APPLICANT: SHERIDAN, Philip, J.
; APPLICANT: HAMLEY, Stephen
; APPLICANT: GLYNN, Jacqueline, M.
; APPLICANT: CHAPIN, Steven
; APPLICANT: BASU, Amarendra
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE TRANSPORT OF BIOLOGICALLY ACTIVE
; FILE OF INVENTION: AGENTS ACROSS CELLULAR BARRIERS
; FILE REFERENCE: 057220-0303
; CURRENT APPLICATION NUMBER: US/09/969,748C
; PRIOR FILING DATE: 2002-12-10
; PRIOR APPLICATION NUMBER: US 60/267,601
; PRIOR FILING DATE: 2001-02-09
; PRIOR APPLICATION NUMBER: US 60/248,819
; PRIOR FILING DATE: 2000-11-14
; PRIOR APPLICATION NUMBER: US 60/248,478
; PRIOR FILING DATE: 2000-11-13
; PRIOR APPLICATION NUMBER: US 60/237,929
; PRIOR FILING DATE: 2000-10-02
; NUMBER OF SEQ ID NOS: 115
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 3
; LENGTH: 821
; TYPE: DNA

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Query Match      91.0%; Score 554; DB 18; Length 654;
Best Local Similarity 93.1%; Pred. NO. 2.6e-164;
Matches 609; Conservative 0; Mismatches 0; Indels 45; Gaps 1
QY      1 ATGCTACAGAGCTCCCGAGCGTCCGTGCTGGCTTTGGCTGCTGCTGCTGCGG 60
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Query Match : 90.2%; Score 549.2; DB 9; Length 799;

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RESULT 7
US-10-411-037-47
/ Sequence 47, Application US/10411037
/ Publication No. US20040043446A1
/ GENERAL INFORMATION:
/ APPLICANT: Neose Technologies, Inc.
/ APPLICANT: Defrees, Shawn
/ APPLICANT: Zopf, David
/ APPLICANT: Bayer, Robert
/ APPLICANT: Hakes, David
/ APPLICANT: Chen, Xi
/ APPLICANT: Bove, Xayn
/ TITLE OF INVENTION: ALPHA GALACTOSIDASE A: REMODELING AND GLYCOCONJUGATION OF ALPHA
/ FILE REFERENCE: 040853-01-5082
/ CURRENT APPLICATION NUMBER: US/10/411,037
/ CURRENT FILING DATE: 2003-04-09
/ PRIOR APPLICATION NUMBER: US 60/328,523
/ PRIOR FILING DATE: 2001-10-10
/ PRIOR APPLICATION NUMBER: US 60/344,692
/ PRIOR FILING DATE: 2001-10-19
/ PRIOR APPLICATION NUMBER: US 60/387,292
/ PRIOR FILING DATE: 2002-06-07
/ PRIOR APPLICATION NUMBER: US 60/391,777
/ PRIOR FILING DATE: 2002-06-25

```

```

; GENERAL INFORMATION:
; APPLICANT: Neose Technologies, Inc.
; APPLICANT: Defrees, Shawn
; APPLICANT: Zopf, David
; APPLICANT: Bayer, Robert
; APPLICANT: Hakes, David

```

556 ACATTCCGCGCATCGTGACAGTCCCGCTCTGTGGAGGGCAGCTGTGGCTTCTAG 609





Query 172 -----AACCCGACCTCCCTGTTTC 195  
Db 221 TATATCCAAAGAAAGAGATATTCTTCGAGAACCCCGACCTCCCTGTTTC 280  
Query 196 TCAGAGTATTTCGACACCTCCGACGAGGAGAAACAAACAAATCCAGCTAGAG 255  
Db 281 TCAGAGTATTTCGACACCTCCGACGAGGAGAAACAAACAAATCCAGCTAGAG 340  
Query 256 CTGCTCCGATCTCCCTGCTGCTCATCCAGTGTGGGCTGAGGCCCGGTCAGTCTCAGG 315  
Db 341 CTGCTCCGATCTCCCTGCTGCTCATCCAGTGTGGGCTGAGGCCCGGTCAGTCTCAGG 400  
Query 316 AGTGTCTTCCGCAACAGCTGATGACGCGCTCTGACAGCAACGTATGACCTCTTA 375  
Db 401 AGTGTCTTCCGCAACAGCTGATGACGCGCGCTCTGACAGCAACGTATGACCTCTTA 460  
Query 376 AAGGACCTAGAGAGAGGATCCAAACGCTGATGGGAGGCTGAAAGATGGACGCCCGG 435  
Db 461 AAGGACCTAGAGAGAGGATCCAAACGCTGATGGGAGGCTGAAAGATGGACGCCCGG 520  
Query 436 ACTGGGAGATCTTCAGACAGCAAGCTTACAGCAAACTCACAAGATGAC 495  
Db 521 ACTGGGAGATCTTCAGACAGCAAGCTTACAGCAAACTCACAAGATGAC 580  
Query 496 GCACCTACAGAACTACGAGGCTGCTACGCTTACAGGAGGACATGAGAGGTCAG 555  
Db 581 GCACCTACAGAACTACGAGGCTGCTACGCTTACAGGAGGACATGAGAGGTCAG 640  
Query 556 ACATTCCTGCGCATGCTGACAGTGCAGCTCTGTGAGGAGGACGCTGCTTAG 609  
Db 641 ACATTCCTGCGCATGCTGACAGTGCAGCTCTGTGAGGAGGACGCTGCTTAG 694

RESULT 11  
US-10-410-930-47  
Sequence 47, Application US/10410930  
Publication No. US20040115168A1  
GENERAL INFORMATION:  
APPLICANT: Neose Technologies, Inc.  
APPLICANT: Zopf, David  
APPLICANT: Bayez, Robert  
APPLICANT: Hakes, David  
APPLICANT: Chen, X1  
TITLE OF INVENTION: INTERFERON BETA: REMODELING AND GLYCOCONJUGATION OF INTERFERON  
FILE REFERENCE: 040853-01-5056  
CURRENT APPLICATION NUMBER: US/10/410,930  
PRIOR FILING DATE: 2003-04-09  
PRIOR APPLICATION NUMBER: US 60/328,523  
PRIOR FILING DATE: 2001-10-10  
PRIOR APPLICATION NUMBER: US 60/344,692  
PRIOR FILING DATE: 2001-10-19  
PRIOR APPLICATION NUMBER: US 60/387,292  
PRIOR FILING DATE: 2002-06-07  
PRIOR APPLICATION NUMBER: US 60/391,777  
PRIOR FILING DATE: 2002-06-25  
PRIOR APPLICATION NUMBER: US 60/396,594  
PRIOR FILING DATE: 2002-07-17  
PRIOR APPLICATION NUMBER: US 60/404,249  
PRIOR FILING DATE: 2002-08-16  
PRIOR APPLICATION NUMBER: US 60/407,527  
PRIOR FILING DATE: 2002-08-28  
NUMBER OF SEQ ID NOS: 75  
SOFTWARE: PatentIn version 3.2  
SEQ ID NO 47  
LENGTH: 799  
TYPE: DNA  
ORGANISM: Homo sapiens  
US-10-410-930-47

Query Match 90.2%; Score 549.2; DB 18; Length 799;  
Best Local Similarity 92.7%; Pred. No. 9,1e-163;  
Matches 606; Conservative 0; Mismatches 3; Indels 45; Gaps 1;  
Query 1 ATGGCTACAGGCTCCCGAGCGTCCCTGCTCTGCTGCTTTGGCCGCTGCTGCTGCGCCG 60  
Db 41 ATGGCTACAGGCTCCCGAGCGTCCCTGCTCTGCTGCTTTGGCCGCTGCTGCTGCGCCG 100  
Query 61 CTTCAGAGGAGGAGTGCCTTCCCAACATTCCTTTATCCAGGCTTTTGAACAAGCTAGT 120  
Db 101 CTTCAGAGGAGGAGTGCCTTCCCAACATTCCTTTATCCAGGCTTTTGAACAAGCTATG 160  
Query 121 CTCGCGGCCATCGTCTGACACAGCTGCGCTTTTGAACCTTACACAGAGTTT----- 171  
Db 161 CTCGCGGCCATCGTCTGACACAGCTGCGCTTTTGAACCTTATACACAGAGTTTGAAGAGCC 220  
Query 172 -----AACCCGACCTCCCTGTTTC 195  
Db 221 TATATCCAAAGAAAGAGATATTCTTCGAGAACCCCGACCTCCCTGTTTC 280  
Query 196 TCAGAGTATTTCGACACCTCCGACGAGGAGAAACAAACAAATCCAGCTAGAG 255  
Db 281 TCAGAGTATTTCGACACCTCCGACGAGGAGAAACAAACAAATCCAGCTAGAG 340  
Query 256 CTGCTCCGATCTCCCTGCTGCTCATCCAGTGTGGGCTGAGGCCCGGTCAGTCTCAGG 315  
Db 341 CTGCTCCGATCTCCCTGCTGCTCATCCAGTGTGGGCTGAGGCCCGGTCAGTCTCAGG 400  
Query 316 AGTGTCTTCCGCAACAGCTGATGACGCGCTCTGACAGCAACGTATGACCTCTTA 375  
Db 401 AGTGTCTTCCGCAACAGCTGATGACGCGCGCTCTGACAGCAACGTATGACCTCTTA 460  
Query 436 ACTGGGAGATCTTCAGACAGCAAGCTTACAGCAAACTCACAAGATGAC 495  
Db 521 ACTGGGAGATCTTCAGACAGCAAGCTTACAGCAAACTCACAAGATGAC 580  
Query 496 GCACCTACAGAACTACGAGGCTGCTACGCTTACAGGAGGACATGAGAGGTCAG 555  
Db 581 GCACCTACAGAACTACGAGGCTGCTACGCTTACAGGAGGACATGAGAGGTCAG 640  
Query 556 ACATTCCTGCGCATGCTGACAGTGCAGCTCTGTGAGGAGGACGCTGCTTAG 609  
Db 641 ACATTCCTGCGCATGCTGACAGTGCAGCTCTGTGAGGAGGACGCTGCTTAG 694

RESULT 12  
US-10-410-997-47  
Sequence 47, Application US/10410997  
Publication No. US20040126838A1  
GENERAL INFORMATION:  
APPLICANT: Neose Technologies, Inc.  
APPLICANT: Zopf, David  
APPLICANT: Bayez, Robert  
APPLICANT: Hakes, David  
APPLICANT: Chen, X1  
TITLE OF INVENTION: POLYCLE STIMULATING HORMONE: REMODELING AND GLYCOCONJUGATION OF  
FILE REFERENCE: 040853-01-5059  
CURRENT APPLICATION NUMBER: US/10/410,997  
PRIOR FILING DATE: 2003-04-09  
PRIOR APPLICATION NUMBER: US 60/328,523  
PRIOR FILING DATE: 2001-10-10  
PRIOR APPLICATION NUMBER: US 60/344,692  
PRIOR FILING DATE: 2001-10-19  
PRIOR APPLICATION NUMBER: US 60/387,292  
PRIOR FILING DATE: 2002-06-07  
PRIOR APPLICATION NUMBER: US 60/391,777



QY 556 ACATTCCTGCGCATGTCGACATGCGCGCTCTGTGAGAGGAGCGATGTCGCTTCTAG 609  
DB 641 ACATTCCTGCGCATGTCGACATGCGCGCTCTGTGAGAGGAGCGATGTCGCTTCTAG 694

RESULT 14  
US-10-287-994-47  
; Sequence 47, Application US/10287994  
; Publication No. US20040137557A1  
; GENERAL INFORMATION:  
; APPLICANT: Neose technologies, Inc.  
; APPLICANT: Defrees, Shawn  
; APPLICANT: Zopf, David  
; APPLICANT: Bayer, Robert  
; APPLICANT: Bower, Caryn  
; APPLICANT: Hakes, David  
; APPLICANT: Chen, Xi  
; TITLE OF INVENTION: REMODELING AND GLYCOCONJUGATION OF PEPTIDES  
; FILE REFERENCE: 040853-01-5052-00  
; CURRENT APPLICATION NUMBER: US/10/287,994  
; CURRENT FILING DATE: 2002-11-05  
; PRIOR APPLICATION NUMBER: US 60/328,523  
; PRIOR FILING DATE: 2001-10-10  
; PRIOR APPLICATION NUMBER: US 60/344,692  
; PRIOR FILING DATE: 2001-10-19  
; PRIOR APPLICATION NUMBER: US 60/387,292  
; PRIOR FILING DATE: 2002-06-07  
; PRIOR APPLICATION NUMBER: US 60/391,777  
; PRIOR FILING DATE: 2002-06-25  
; PRIOR APPLICATION NUMBER: US 60/396,594  
; PRIOR FILING DATE: 2002-07-17  
; PRIOR APPLICATION NUMBER: US 60/404,249  
; PRIOR FILING DATE: 2002-08-16  
; PRIOR APPLICATION NUMBER: US 60/407,527  
; PRIOR FILING DATE: 2002-08-28  
; NUMBER OF SEQ ID NOS: 62  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 47  
; LENGTH: 799  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
US-10-287-994-47

Query Match 90.2%; Score 549.2; DB 18; Length 799;  
Best Local Similarity 92.7%; Pred. No. 9,1e-163;  
Matches 606; Conservative 0; Mismatches 3; Indels 45; Gaps 1;

QY 1 ATGGCTACAGGCTCCCGAGCGTCCCTGCTCTGCGCTTTTGGCTGTGCTGCTGCGCTTGG 60  
DB 41 ATGGCTACAGGCTCCCGAGCGTCCCTGCTCTGCGCTTTTGGCTGTGCTGCTGCGCTTGG 100  
QY 61 CTTCAAGAGGAGGAGGCTTCCCAACCATTCCTTATCCAGGCTTTTGAACAAGCTAGT 120  
DB 101 CTTCAAGAGGAGGAGGCTTCCCAACCATTCCTTATCCAGGCTTTTGAACAAGCTAGT 160  
QY 121 CTCGCGGCCCATGCTGTGACACGAGCTGGGCTTTGACACTTACAGAGAGTT----- 171  
DB 161 CTCGCGGCCCATGCTGTGACACGAGCTGGGCTTTGACACTTACAGAGAGTTTGAAGAGGCC 220  
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DB 221 TATATCCAAAGAGACAGAGATTCATTCTGCAAGAACCCGAGAGCTCCCTCTGTTTC 280  
QY 196 TCAAGATCTATTCCGACACCTCTCAACAGGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 255  
DB 281 TCAAGATCTATTCCGACACCTCTCAACAGGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 340  
QY 256 CTGCTCCGAGATCTCTGCTGCTCATTCAGTGTGCTGAGAGCCGCTGAGTTCCTAGG 315  
DB 341 CTGCTCCGAGATCTCTGCTGCTCATTCAGTGTGCTGAGAGCCGCTGAGTTCCTAGG 400  
QY 316 AGTGTCTTGCAAGAGCGTGTGTATAGGCGGCTCTGACAGAGAGTGTATAGACTCTCA 375

DB 401 AGTGTCTTGCAAGAGCGTGTGTATAGGCGGCTCTGACAGAGAGTGTATAGACTCTCA 460  
QY 376 AAGAGCTAGAGAGAGCGATCCAAACGCTGATGAGGAGAGGCTGAGAGATGAGAGCCCGG 435  
DB 461 AAGAGCTAGAGAGAGCGATCCAAACGCTGATGAGGAGAGGCTGAGAGATGAGAGCCCGG 520  
QY 436 ACTGGGAGATCTTCAACAGAGCTTACAGAGAGTTCGACAGAACTCAACAGCATGAC 495  
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QY 496 GCATCTCAAGAGACTACGAGGCTGCTTACTGCTTCAAGAGAGAGATGAGAGAGTTCGAG 555  
DB 581 GCATCTCAAGAGACTACGAGGCTGCTTACTGCTTCAAGAGAGAGATGAGAGAGTTCGAG 640  
QY 556 ACATTCCTGCGCATGTCGACATGCGCGCTCTGTGAGAGGAGCGATGTCGCTTCTAG 609  
DB 641 ACATTCCTGCGCATGTCGACATGCGCGCTCTGTGAGAGGAGCGATGTCGCTTCTAG 694

RESULT 15  
US-10-410-913-47  
; Sequence 47, Application US/10410913  
; Publication No. US20040142856A1  
; GENERAL INFORMATION:  
; APPLICANT: Neose Technologies, Inc.  
; APPLICANT: Defrees, Shawn  
; APPLICANT: Zopf, David  
; APPLICANT: Bayer, Robert  
; APPLICANT: Hakes, David  
; APPLICANT: Chen, Xi  
; APPLICANT: Bower, Caryn  
; TITLE OF INVENTION: GLYCOCONJUGATION METHODS AND PROTEINS/PEPTIDES PRODUCED BY THE  
; FILE REFERENCE: 040853-01-5081  
; CURRENT APPLICATION NUMBER: US/10/410,913  
; CURRENT FILING DATE: 2003-04-09  
; PRIOR APPLICATION NUMBER: US 60/328,523  
; PRIOR FILING DATE: 2001-10-10  
; PRIOR APPLICATION NUMBER: US 60/344,692  
; PRIOR FILING DATE: 2001-10-19  
; PRIOR APPLICATION NUMBER: US 60/387,292  
; PRIOR FILING DATE: 2002-06-07  
; PRIOR APPLICATION NUMBER: US 60/391,777  
; PRIOR FILING DATE: 2002-06-25  
; PRIOR APPLICATION NUMBER: US 60/396,594  
; PRIOR FILING DATE: 2002-07-17  
; PRIOR APPLICATION NUMBER: US 60/404,249  
; PRIOR FILING DATE: 2002-08-16  
; PRIOR APPLICATION NUMBER: US 60/407,527  
; PRIOR FILING DATE: 2002-08-28  
; NUMBER OF SEQ ID NOS: 75  
; SOFTWARE: PatentIn version 3.2  
; SEQ ID NO 47  
; LENGTH: 799  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
US-10-410-913-47

Query Match 90.2%; Score 549.2; DB 18; Length 799;  
Best Local Similarity 92.7%; Pred. No. 9,1e-163;  
Matches 606; Conservative 0; Mismatches 3; Indels 45; Gaps 1;

QY 1 ATGGCTACAGGCTCCCGAGCGTCCCTGCTCTGCGCTTTTGGCTGTGCTGCTGCGCTTGG 60  
DB 41 ATGGCTACAGGCTCCCGAGCGTCCCTGCTCTGCGCTTTTGGCTGTGCTGCTGCGCTTGG 100  
QY 61 CTTCAAGAGGAGGAGGCTTCCCAACCATTCCTTATCCAGGCTTTTGAACAAGCTAGT 120  
DB 101 CTTCAAGAGGAGGAGGCTTCCCAACCATTCCTTATCCAGGCTTTTGAACAAGCTAGT 160  
QY 121 CTCGCGGCCCATGCTGTGACACGAGCTGGGCTTTGACACTTACAGAGAGTT----- 171

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Db 161 CTCGCGCCCATGCTGTGACACAGCTGSCCTTTGACACTACAGAGATTGAAAGCC 220
QY 172 -----AACCCCGACCTCCCTCTGTTTC 195
Db 221 TATATCCAAAGGAAACAGATTCATTCCTGAGAAACCCCGACCTCCCTGTGTTTC 280
QY 196 TCAGAGTCAATTCGACACCCCTCCAAAGGAGGAAACACACAGAAATCCAACTAGAG 255
Db 281 TCAGAGTCAATTCGACACCCCTCCAAAGGAGGAAACACACAGAAATCCAACTAGAG 340
QY 256 CTGCTCCGATCTCCCTGCTGCTCATCAAGTCGTGCTGAGCCCGTGCAATTCTCAGG 315
Db 341 CTGCTCCGATCTCCCTGCTGCTCATCAAGTCGTGCTGAGCCCGTGCAATTCTCAGG 400
QY 316 AGTGTCTTCCCAACAGCCTGTGTACAGGCGCTTGACAGCAACGTCTATGACCTCTA 375
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QY 376 AAGGACCTAGAGGAAAGGCAATCCAAAGCTGATGGGAGGCTGGAAGATGGAGCCCGG 435
Db 461 AAGGACCTAGAGGAAAGGCAATCCAAAGCTGATGGGAGGCTGGAAGATGGAGCCCGG 520
QY 436 ACTGGGAGATCTTCAAGCAGACCTACAGAGTTGACAACTGACAAACGATGAC 495
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QY 496 GCACTACTCAAGAACTACGGGCTGCTCTACTGCTTCAGAAAGGACATGACAAAGTGCAG 555
Db 581 GCACTACTCAAGAACTACGGGCTGCTCTACTGCTTCAGAAAGGACATGACAAAGTGCAG 640
QY 556 ACATTCTGCGGATCGTGCAGTGCAGCTCTGTGAGGGGCACTGTGCTTCTAG 609
Db 641 ACATTCTGCGGATCGTGCAGTGCAGCTCTGTGAGGGGCACTGTGCTTCTAG 694
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Search completed: February 7, 2005, 13:39:05  
Job time : 482 secs

GenCore version 5.1.6  
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# OM nucleic - protein search, using frame\_plus\_n2p model

Run on: February 6, 2005, 13:14:30 (Search time 36 Seconds  
(without alignments)  
3255.334 Million cell updates/sec

Title: US-09-856-796B-1  
Perfect score: 1112  
Sequence: 1 atggctacagctccggac.....agggcagctgtgcttctag 609

Scoring table:  
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Xgapop 10.0, Xgapext 0.5  
Ygapop 10.0, Ygapext 0.5  
Fgapop 6.0, Fgapext 7.0  
Delop 6.0, Delext 7.0

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 566832

Minimum DB seq length: 0  
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Command line parameters:  
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-O=/sgn2.1/USFO-epool\_p/US09856796/rnat\_06022005\_124620\_3493/app\_query.fasta\_1.775  
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-UNITS=bits -START=1 -END=-1 -MATRIX=bloms62 -TRANS=human40.cdi -LIST=45  
-DOCALLIGN=200 -THR SCORE=DCT -THR MAX=100 -THR MIN=0 -ALIGN=15 -MODE=LOCAL  
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-NO MAP -LARGEQUERY -NEG\_SCORES=0 -WAIT -DSBLOCK=100 -LONGLOC  
-DEV TIMEOUT=120 -WARN TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6  
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database :  
1: PIR\_79:\*  
2: PIR1:\*  
3: PIR3:\*  
4: PIR4:\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1024.5	92.1	217	1	STHU
2	981.5	88.3	217	1	somatotropin 1 pre
3	939.5	84.5	217	1	somatotropin - the
4	873.5	78.6	217	1	somatotropin 2 pre
5	872.5	78.5	217	1	choriomammotropin
6	866.5	77.9	217	1	choriomammotropin
7	850.5	76.5	217	2	chorionic somatoma
8	843.5	75.9	217	2	somatotropin - the
9	842.5	75.8	215	2	choriomammotropin
10	831.5	74.8	212	2	chorionic somatoma
11	779.5	70.1	199	2	choriomammotropin
12	698	62.8	216	2	somatotropin precu
13	694	62.4	216	1	STPG
14	687	61.8	216	2	somatotropin precu

15	682	61.3	216	2	S49483	somatotropin precu
16	682	61.3	216	2	B49159	somatotropin - gol
17	679	61.1	216	1	STMS	somatotropin precu
18	677	60.9	217	1	STBO	somatotropin precu
19	672	60.4	216	2	A37782	somatotropin precu
20	666	59.9	217	1	STGT	somatotropin precu
21	666	59.9	217	1	STSH	somatotropin precu
22	666	59.9	217	2	S32682	somatotropin - dom
23	661	59.4	216	1	STRT	somatotropin precu
24	643.5	57.9	256	1	STHV2	somatotropin 2 pre
25	603	54.2	190	2	UK0219	somatotropin - Afr
26	602	54.1	190	2	PM0140	somatotropin - sei
27	601	54.0	190	1	A61584	somatotropin - alp
28	598	53.8	190	2	JS0429	somatotropin - Arc
29	596	53.6	190	1	STHO	somatotropin - hor
30	551	49.6	216	2	S04929	somatotropin precu
31	550	49.5	216	2	A60509	somatotropin precu
32	542	48.7	216	2	JC1514	somatotropin - gre
33	536	48.2	191	2	A60625	somatotropin - gre
34	480	43.2	190	2	S21750	somatotropin - Rus
35	471.5	42.4	215	2	US0037	somatotropin precu
36	467.5	42.0	215	2	IS1188	somatotropin - bul
37	465	41.8	195	2	IS1250	somatotropin - bow
38	449	40.4	190	2	A56816	somatotropin - bul
39	421.5	37.9	163	2	JN0387	somatotropin A - sei
40	394.5	35.5	139	2	S04353	somatotropin A - A
41	386.5	34.8	209	2	UT0483	somatotropin I pre
42	374.5	33.7	183	2	A60623	somatotropin - blu
43	279.5	25.1	210	2	IS0763	somatotropin - nob
44	279.5	25.1	210	2	S21915	somatotropin - sll
45	278.5	25.0	210	2	S69262	growth hormone I p

## ALIGNMENTS

RESULT 1  
STHU  
N:Alternates names: growth hormone 1; hGH-N; pituitary somatotropin  
N:Contains: growth hormone 5K peptide; somatotropin 1, long form; somatotropin 1, short  
C:Species: Homo sapiens (man)  
C:Date: 24-Apr-1984 #sequence revision 10-Feb-1995 #text change 09-Jul-2004  
C:Accession: A93731; A32435; A93694; A94247; A90051; A93397; A93778; A91764; A90217; A92  
R:Denoto, F.M.; Moore, D.D.; Goodman, H.M.  
Nucleic Acids Res. 9, 3719-3730, 1981  
A>Title: Human growth hormone DNA sequence and mRNA structure: possible alternative splicing  
A:Reference number: A93731; MUID:82014939; PMID:6269091  
A:Accession: A93731  
A:Molecule type: DNA  
A:Residues: 1-217 <DEN>  
A:Cross-references: UNIPROT:P01241; GB:V00520  
A>Note: The 20K short form somatotropin lacks residues 58-72 (32-46 in the active hormone  
R:Chen, E.Y.; Liao, Y.C.; Smith, D.H.; Barrera-Saldana, H.A.; Gelinae, R.E.; Seeburg, P.  
Genomics 4, 479-497, 1989  
A>Title: The human growth hormone locus: nucleotide sequence, biology, and evolution.  
A:Reference number: A32435; MUID:89307277; PMID:2744760  
A:Accession: A32435  
A:Molecule type: DNA  
A:Residues: 1-217 <CHE>  
A:Cross-references: GB:J03071; NID:G183148; PIDN:AA52549.1; PID:G183149  
R:Rooskam, W.; Rougeon, F.  
Nucleic Acids Res. 7, 305-320, 1979  
A>Title: Molecular cloning and nucleotide sequence of the human growth hormone structure  
A:Reference number: A93694; MUID:80034477; PMID:386281  
A:Accession: A93694  
A:Molecule type: mRNA  
A:Residues: 1-217 <ROS>  
A:Cross-references: GB:V00519  
A>Note: 35-Pro was also found  
R:Marshall, J.A.; Halliwell, R.A.; Baxter, J.D.; Goodman, H.M.  
Science 205, 602-607, 1979  
A>Title: Human growth hormone: complementary DNA cloning and expression in bacteria.  
A:Reference number: A94247; MUID:79203293; PMID:377496

A:Accession: A94247  
A:Molecule type: mRNA  
A:Residues: 1-217 <MAR>  
R:Li, C.H.; Dixon, J.S.; Liu, W.K.  
Arch. Biochem. Biophys. 133, 70-91, 1969  
A:Title: Human pituitary growth hormone.  
A:Reference number: A90048; MUID:69289202; PMID:5610834  
A:Contents: annotation  
R:Li, C.H.; Dixon, J.S.  
Arch. Biochem. Biophys. 146, 233-236, 1971  
A:Title: Human pituitary growth hormone. XXXII. The primary structure of the hormone.  
A:Reference number: A90051; MUID:72143935; PMID:5144027  
A:Accession: A90051  
A:Molecule type: protein  
A:Residues: 27-94; 96-217 <LIC>  
R:Niall, H.D.  
Nature New Biol. 230, 90-91, 1971  
A:Title: Revised primary structure for human growth hormone.  
A:Reference number: A93397; MUID:71139765; PMID:5279546  
A:Accession: A93397  
A:Molecule type: protein  
A:Residues: 27-51 <NTA>  
R:Niall, H.D.; Hogan, M.L.; Sauer, R.; Rosenblum, I.Y.; Greenwood, F.C.  
Proc. Natl. Acad. Sci. U.S.A. 68, 866-869, 1971  
A:Title: Sequences of pituitary and placental lactogenic and growth hormones: evolution  
A:Reference number: A93778; MUID:71153968; PMID:5279528  
A:Accession: A93778  
A:Molecule type: protein  
A:Residues: 119-120; 157-159 <NT2>  
R:Niall, H.D.  
In Prolactin and Carcinogenesis, Proc. Fourth Tencovs Workshop Prolactin, Griffiths, K.,  
A:Title: The chemistry of the human lactogenic hormones.  
A:Reference number: A94427  
A:Contents: annotation; somatotropin revision  
R:Bewley, T.A.; Dixon, J.S.; Li, C.H.  
Int. J. Pept. Protein Res. 4, 281-287, 1972  
A:Title: Sequence comparison of human pituitary growth hormone, human chorionic somatoma  
A:Reference number: A91764; MUID:73092028; PMID:4675454  
A:Accession: A91764  
A:Molecule type: protein  
A:Residues: 27-217 <BEW>  
R:Lewis, U.J.; Bonewald, L.F.; Lewis, L.J.  
Biochem. Biophys. Res. Commun. 92, 511-516, 1980  
A:Title: The 20,000-dalton variant of human growth hormone: location of the amino acid  
A:Reference number: A90217; MUID:80130196; PMID:7356479  
A:Accession: A90217  
A:Contents: somatotropin, 20K short variant  
A:Molecule type: protein  
A:Residues: 46-57; 73-80 <LEW>  
R:Chapman, G.E.; Rogers, K.M.; Birttain, T.; Bradshaw, R.A.; Bates, O.J.; Turner, C.; Ca  
J. Biol. Chem. 256, 2395-2401, 1981  
A:Title: The 20,000 molecular weight variant of human growth hormone. Preparation and st  
A:Reference number: A92311; MUID:8117361; PMID:7462247  
A:Contents: somatotropin, 20K short variant  
A:Accession: A92311  
A:Molecule type: protein  
A:Residues: 27-57; 73-79 <CHA>  
R:Singh, R.N.P.; Seavey, B.K.; Lewis, L.J.; Lewis, U.J.  
J. Protein Chem. 2, 423-436, 1983  
A:Title: Human growth hormone peptide 1-43: isolation from pituitary glands.  
A:Reference number: A61466  
A:Accession: A61466  
A:Molecule type: protein  
A:Residues: 27-69 <SIN>  
A:Note: growth hormone 5K peptide has insulin potentiating activity; its physiological p  
R:Robson, V.M.J.; Rae, I.D.; NG, F.  
J. Biol. Chem. Hoppe-Seyler 371, 423-431, 1990  
A:Title: Identification of the aspartimide structure in a previously-reported peptide.  
A:Reference number: S09685; MUID:90334745; PMID:2376679  
A:Accession: S09685  
A:Molecule type: protein  
A:Residues: 27-34; 71, 36-47 <ROB>  
R:de Vos, A.M.; Uitsch, M.; Kossiakoff, A.A.

A>Title: Human growth hormone and extracellular domain of its receptor: crystal structure  
 Science 255, 306-312, 1992  
 A:Reference number: A41728; MUID:92196577; PMID:1549776  
 A:Contents: annotation, X-ray crystallography, 2.8 angstroms  
 A>Note: The structure of the complex with growth hormone receptor is described  
 R:Gray, G.L.; Baldridge, J.S.; McKeown, K.S.; Heyneker, H.L.; Chang, C.N.  
 Gene 39, 247-254, 1985  
 A>Title: Periplasmic production of correctly processed human growth hormone in *Escherichia*  
 A:Reference number: I41126; MUID:86137393; PMID:3912621  
 A:Accession: 184549  
 A:Status: preliminary; translated from GB/EMBL/DBJ  
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 C:Comment: About 90% of somatotropin is the 22K long form.  
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 A:Cross-references: GDB:119982; OMIM:139250  
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 A:Introns: 4/1; 57/3; 97/3; 152/3  
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 C:Keywords: alternative splicing; hormone; pituitary  
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 F:27-69/Product: growth hormone 5K peptide #status experimental <SKP>  
 F:27-57, 73-217/Product: somatotropin 1, short form #status experimental <SOS>  
 F:79-191, 208-215/Disulfide bonds: #status experimental

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Percent Similarity:	92.63%
Best Local Similarity:	92.63%
Query Match:	92.13%
DB:	1
US-09-856-796B-1 (1-609)	x STNU (1-217)
Length:	217
Matches:	201
Conservative:	0
Mismatches:	1
Indels:	15
Gaps:	1

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QY	61	CTTCAAGAGGGCAGTGCCTTCCCAACATTCCTTATCCAGAGCTTTTGGACAGCTTAGT	120
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QY	376	AAGACCTTAGAGAAAGGACATCCAAACGCTGATGGGAGAGGCTGAGAAATGGCAGCCCGG	435
Db	141	LysAspLeuGlnGlnGlyIleGlnThrLeuMetGlyArgLeuGlnAspGlySerProArg	160
QY	436	ACTGGGCGAGTCTTAAACACACTTACAGCAAGTTTCGACACAACTACACCAACATGAC	495

Db 161 ThrGlyGlnIlePheLysGlnThrTySerLysPheAspThrAsnSerHisAsnAsp 180  
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 RESULT 2  
 167410  
 somatotropin - rhesus macaque  
 N:Alternate names: growth hormone  
 C:Species: Macaca mulatta (rhesus macaque)  
 C>Date: 31-May-1996 #sequence\_revision 31-May-1996 #text\_change 09-Jul-2004  
 C:Accession: 167410; A05094  
 R:Golios, T.G.; Durning, M.; Fisher, J.M.; Fowler, P.D.  
 A>Title: Cloning of four growth hormone/chorionic somatomammotropin-related complementat  
 A:Reference number: 153267; MUID:94008724; PMID:8404617  
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 A:Cross-references: UNIPROT:P33093; GB:LI6556; NID:G293114; PIDN:AAA18842.1; PID:G293115  
 R:Li, C.H.; Chung, D.; Lahm, H.W.; Stein, S.  
 Arch. Biochem. Biophys. 245, 287-291, 1986  
 A>Title: The primary structure of monkey pituitary growth hormone.  
 A:Reference number: A05094; MUID:86129460; PMID:3080959  
 A:Accession: A05094  
 A:Molecule type: protein  
 A:Residues: 27-99, 'Q', 101-178, 'D', 180-217 <LIC>  
 A>Note: the monkey species is not identified in the reference  
 R:Raben, M.S.  
 Science 125, 883-884, 1957  
 A>Title: Preparation of growth hormone from pituitaries of man and monkey.  
 A:Reference number: A44774  
 A:Contents: annotation; identification of source organism  
 C:Superfamily: prolactin  
 Alignment Scores:  
 Pred. No.: 5,49e-74 Length: 217  
 Score: 981.50 Matches: 133  
 Percent Similarity: 90.32% Conservative: 3  
 Best Local Similarity: 88.94% Mismatches: 6  
 Query Match: 88.26% Indels: 15  
 DB: 2 Gaps: 1  
 US-09-856-796b-1 (1-609) x 167410 (1-217)  
 Qy 1 ATGGCTACAGGCTCCCGACGCTGCTGCTTGGCTGCTGCTGCTGCTGCTGCTGCTG 60  
 Db 1 MetalAlaGlySerArgThrSerLeuLeuAlaPheAlaLeuLeuCysLeuProTrp 20  
 Qy 61 CTTGAAGAGGAGGAGGCTTCCCAACCATTCCTTACAGGCTTTTACAAAGCTACT 120  
 Db 21 LeuGlnGlnGlySerLysPheProThrLysPheLeuSerArgLeuPheAspAlaMet 40  
 Qy 121 CTCGCGCCCATCGTCTGACACGAGTGCCTTGAACCTTACACGAGGAGTTT----- 171  
 Db 41 LeuArgAlaHisArgLeuHisGlnLeuAlaPheAspThrTyrcysGlnIlePheGlnGlnAla 60  
 Qy 172 -----AACCCCGACGCTTCTGCTGCTTCTGCTTCTGCTTCTGCTTCTGCTTCT 195  
 Db 61 TyrlleProLysGlnGlnIleTyrcysPheLeuGlnAsnProGlnThrSerLeuCysPhe 80  
 Qy 196 TCAAGATCTATTCCGACACCTTCCACAGGAGGAGAAACACACAGAAATCCAACTTACAG 255  
 Db 81 SerGlnSerLysPheProThrProSerAsnArgGlnGlnThrGlnGlnIleLysSerAsnLeuGln 100  
 Qy 256 CTGCTCCGATCTCCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 315

Db 101 LeuLeuArgIleSerLeuLeuLeuIleGlnSerTrpLeuGlnProValGlnPheLeuArg 120  
 Qy 316 AGTGCTTTCGCGCAACAGCCTGTGTGACGCGCCCTCTGACAGCAAGTATGACCTCTA 375  
 Db 121 SerValPheAlaHisSerLeuLeuValTyrcysThrSerTyrcysAspValTyrcysPheLeu 140  
 Qy 376 AAGACCTTGAAGAGGAGCATCCAAAGCTGATGCGGAGGCTGTGAGAAATGACGACCCCGG 435  
 Db 141 LysAspLeuGlnGlnGlnIleGlnThrLeuMetGlyArgLeuGlnAspGlySerSerArg 160  
 Qy 436 ACTGGGCGATCTTACACACAGCTTACAGCAAGTTCGACAACTCAGACAGCATGAC 495  
 Db 161 ThrGlyGlnIlePheLysGlnThrTySerLysPheAspThrAsnSerHisAsnAsp 180  
 Qy 496 GCACCTACCAAGAACTACGAGGCTGCTACTGCTTACAGAAAGACATGACAGGTCGAG 555  
 Db 181 AlaLeuLeuLysHentyrGlyLeuLeuTyrcysPheArgLysAspMetAspLysValGln 200  
 Qy 556 ACATTCCTGCGCATGTCGACAGTCCGCTCTGTGAGGAGGACGCTGTGCTTC 606  
 Db 201 ThrPheLeuArgIleValGlnCysArgSerValGlnGlySerCysGlyPhe 217  
 RESULT 3  
 STHUV  
 somatotropin 2 precursor - human  
 N:Alternate names: growth hormone 2; growth hormone variant; hGH-V; placental somatotrop  
 N:Comments: somatotropin 2, long splice form; somatotropin 2, short splice form  
 C:Species: Homo sapiens (man)  
 C>Date: 17-Dec-1982 #sequence\_revision 10-Feb-1995 #text\_change 09-Jul-2004  
 C:Accession: D32435; B28072; A01511; I52104; A60711  
 R:Chen, B.Y.; Liao, Y.C.; Smith, D.H.; Barrera-Saldana, H.A.; Gelinas, R.E.; Seeburg, P.  
 Genomics 4, 479-497, 1989  
 A>Title: The human growth hormone locus: nucleotide sequence, biology, and evolution.  
 A:Reference number: A32435; MUID:89307277; PMID:2744760  
 A:Accession: D32435  
 A:Molecule type: DNA  
 A:Residues: 1-217 <CHS>  
 A:Cross-references: UNIPROT:P01242; GB:J03071; NID:G183148; PIDN:AAA52552.1; PID:G183152  
 R:Cooper, N.E.; Ray, J.; Emery, J.G.; Liebhafner, S.A.  
 J. Biol. Chem. 263, 9001-9006, 1988  
 A>Title: Two distinct species of human growth hormone-variant mRNA in the human placenta  
 A:Reference number: A92725; MUID:88243769; PMID:3379057  
 A:Accession: B28072  
 A:Molecule type: mRNA  
 A:Residues: 1-217 <COO>  
 R:Seeburg, P.H.  
 DNA 1, 239-249, 1982  
 A>Title: The human growth hormone gene family: nucleotide sequences show recent divergen  
 A:Reference number: A01511; MUID:83182010; PMID:7169009  
 A:Accession: A01511  
 A:Molecule type: DNA  
 A:Residues: 1-34, 'P', 36-217 <SEE>  
 R:Ignot, A.; Scippo, M.L.; Frankenne, F.; Hennen, G.  
 Arch. Int. Physiol. Biochem. 96, 63-67, 1988  
 A>Title: Cloning and nucleotide sequence of placental hGH-V cDNA.  
 A:Reference number: I52104; MUID:89024984; PMID:2460050  
 A:Accession: I52104  
 A:Status: preliminary; translated from GB/EMBL/DBJ  
 A:Molecule type: mRNA  
 A:Residues: 1-217 <IGO>  
 A:Cross-references: GB:M38451; NID:G183179; PIDN:AAA5891.1; PID:G183180  
 R:Frankenne, F.; Scippo, M.L.; Van Beunnen, J.; Ignot, A.; Hennen, G.  
 J. Clin. Endocrinol. Metab. 71, 15-18, 1990  
 A>Title: Identification of placental human growth hormone as the growth hormone-V gene e  
 A:Reference number: A60711; MUID:90317018; PMID:2196278  
 A:Accession: A60711  
 A:Molecule type: protein  
 A:Residues: 27-44/46-57 <PRA>  
 A:Experimental source: tissue placenta  
 A>Note: partial glycosylation was demonstrated by lectin binding  
 C:Comment: This gene is expressed by the placenta.  
 C:Genetics:  
 A:Gene: GDB:GH2

A:Cross-references: GDB:119983; OMIM:139240  
A:Map position: 17q22-17q24  
A:Introns: 4/1; 57/3; 97/3; 152/3  
C:Superfamily: prolactin  
C:Keywords: alternative splicing; glycoprotein; hormone; placenta  
F:1-26/Domain: signal sequence #status predicted <SIG-  
F:27-217/Product: somatotropin 2, long splice form #status predicted <SOL-  
F:27-57,73-217/Product: somatotropin 2, short splice form #status predicted <SOS-  
F:79-191,208-215/Disulfide bonds: #status predicted  
F:166/Binding site: carbonylrate (Asn) (covalent) #status predicted

**Alignment Scores:**

Pred. No.:	1,75e-70	Length:	217
Score:	939.50	Matches:	187
Percent Similarity:	88.02%	Conservative:	4
Best Local Similarity:	86.18%	Mismatches:	11
Query Match:	84.49%	Indels:	15
DB:	1	Gaps:	1

US-09-856-796B-1 (1-609) x STHUV (1-217)

QY	1	ATGGCTACAGAGGCTCCCGAGACGTCCTCGCTCTGGCTTTTGGCCGTGCTCGCTCCG	60
Db	1	MetAlaAlaAglySerThrArgThrSerLeuLeuAlaPheGlyLeuLeuCySLeuSerTrp	20
QY	61	CTTCAGAGGCGAGTCCCTCCCAACCAATCCCTTATCCAGGCTTTTGGACCAAGCTAGT	120
Db	21	LeuGlnGlnGlySerAlaPheProTrpIleProLeuSerArgLeuPheAspAlaMet	40
QY	121	CTCCGGCGCCATCGTCTGACACGAGCGGCTTTGACCACTACAGAGATT-----	177
Db	41	LeuArgAlaArgArgLeuTrpGlnLeuAlaTrpAspThrTrpGlnGlnPheGlnAla	60
QY	172	-----AACCCCGACCTCCCTCTGTTTC	195
Db	61	TyrIleLeuLysGlnGlnLysTrpSerPheLeuGlnAsnProGlnIntrSerLeuCyPhe	80
QY	196	TCAGAGTCTATTCGACACACCTTCACAGGAGAGAAACACACAAATCCAACTTAG	255
Db	81	SerGlnSerIleProThrProSerAsnArgValIleThrGlnGlnLysSerAsnLeuGln	100
QY	256	CTGCTCCCATCTCCCTCGCTCAACCCAGTCGTGGCTGGAGCCCGACGTTCCTAG	315
Db	101	LeuLeuAlaGlyIleSerLeuLeuLeuIleGlnSerTrpLeuGlnProValGlnLeuLeuArg	120
QY	316	AGTGTCTTCGCCAACAGCCTGTGTGACGGCGCCTTGACAGCAACGTCTATGACCTTCTA	375
Db	121	SerValPheAlaAsnSerLeuValTrpGlyAlaSerAspSerAsnValTyrArgHisLeu	140
QY	376	AAGACCTTAGAGGAAGGATCCAAACGCTGATGGGAGAGCTGGAGAATGGCAGCCCCGG	435
Db	141	LysAspLeuGlnGlnGlyIleGlnThrLeuMetTrpArgLeuGlnAspGlySerProArg	160
QY	436	ACTGGGCGAGATCTTCAAGCAGACCTTCACACAATTTGACACCAACTCACACAAGATGAC	495
Db	161	ThrGlyGlnIlePheAsnGlnSerTrpSerLysPheAspThrTrpLysSerHisAsnAspAsp	180
QY	496	GCACTACTCAAGAACTACGGGCTGCTCTACTGCTTCAAGAGAGACATGACAAAGTTGAG	555
Db	181	AlaLeuLeuLysAsnTrpGlyLeuLeuLysTrpCySPhaArgLysAspMetAspLysValGln	200
QY	556	ACATTTCCCGCGCATGTGAGAGCGCGCTCTGACAGGCGACGCTGGCTTC	606
Db	201	ThrPheLeuAlaGlyLeuValGlnCySAspSerValGlnGlySerCySgLyPhe	217

## RESULT 4

E32435

choriomammotropin B precursor - human

N;Alternate names: chorionic somatomammotropin 2

C;Species: Homo sapiens (man)

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C:\Accession: E32435
C:\date: 29-Dec-1989 #sequence_revision 29-Dec-1989 #text_change 09-Jul-2004
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R:Chen, E.Y.: Liao, Y.C.: Smith, D.H.: Barrera-Saldana H.A.: Gelinas P.F.

Barbara, M.A.; Director, D.M.; Patricia-Savanna, M.A.; Gerling, R.E.; Seeburg, E.

Genomics 4, 479-497, 1989

**A/Title:** The human growth hormone locus: nucleotide sequence, biology, and evolution

A/Accession: E32A35  
A/Reference number: A32435; MUID:8930/211; PMID:2144760

A:Status: Preliminary  
A:ACCESSION: E32433

A:Molecule type: DN

A;Residues: 1-217 <CHE>

A;Cross-references: UNI

C/Genetics:

A;Gene: GDB:CSH

A;Cross-references: GDB:119813; OMIM:118820

A;Map position: 17q22-17q24

C;superfamily: prolactin

### Alignment Scores:

**Alignment Scores:**

Pred. No.:	5.57e-65	Length:	217
Score:	873.50	Matches:	172
Percent Similarity:	84.33%	Conservative:	11
Best Local Similarity:	79.26%	Mismatches:	19
Query Match:	78.55%	Indels:	15
DB:	2	Gaps:	1

US-09-856-796B-1 (1-609) x E32435 (1-217)

[illegible]

## RESULT

LSHUC

choriomammotropin A precursor [validated] - human

N/Alternate names: chorionic somatomammotropin 1; placental lactogen

C;species: Homo sapiens (man,



C>Date: 23-Oct-981 #sequence revision 23-Oct-1981 #text change 09-Jul-2004  
A:Accession: C32435, A94422, T52342, A93833, A93192, A90054, A94427, A61283, I55229, I5  
R:Chen, E.Y.; Liao, Y.C.; Smith, D.H.; Barreira-Saldana, H.A.; Gellinas, R.E.; Seeburg, P.  
Genomics 4, 479-497, 1989  
A>Title: The human growth hormone locus: nucleotide sequence, biology, and evolution.  
A:Reference number: A32435, MUID:89307277, PMID:2744760  
A:Accession: C32435  
A:Molecule type: DNA  
A:Residues: 1-217 <CHE>  
A:Cross-references: UNIPROT:P01243; GB:J03071; NID:g183148; PIDN:AA52551.1; PID:g183151  
R:Goodman, H.M.; Delotto, F.; Fiddes, J.C.; Halliwell, R.A.; Page, G.S.; Smith, S.; Tisch  
in Mobilization and Reassembly of Genetic Information, Scott, W.A., Werner, R., Joseph,  
A:Reference number: A94422  
A:Accession: A94422  
A:Molecule type: mRNA  
A:Residues: 1-217 <GOO>  
R:Tanaka, M.; Masuda, N.; Watabiki, M.; Yamakawa, M.; Shimizu, K.; Nagai, J.; Nakashima,  
Biochem. Int. 16, 287-292, 1988  
A>Title: cDNA cloning of human chorionic somatomammotropin-1 mRNA whose transcription wa  
A:Reference number: I52342, MUID:88209096, PMID:2835050  
A:Accession: I52342  
A>Status: translated from GB/EMBL/DBD  
A:Molecule type: mRNA  
A:Residues: 1-3 <TAN>  
A:Cross-references: GB:M35419; NID:9506822  
R:Sherwood, L.M.; Burrestein, Y.; Schechter, I.  
Proc. Natl. Acad. Sci. U.S.A. 76, 3819-3823, 1979  
A>Title: Primary structure of the NH-2-terminal extra piece of the precursor to human pl  
A:Reference number: A93833; MUID:80034970; PMID:291043  
A:Accession: A93833  
A:Molecule type: protein  
A:Residues: 1,3-26 <SHE>  
A:Experimental source: placenta  
R:Shine, J.; Seeburg, P.H.; Martial, J.A.; Baxter, J.D.; Goodman, H.M.  
Nature 270, 494-499, 1977  
A>Title: Construction and analysis of recombinant DNA for human chorionic somatomammotro  
A:Reference number: A93192; MUID:78071761, PMID:593368  
A:Accession: A93192  
A:Molecule type: DNA  
A:Residues: 50-217 <SHI>  
R:Li, C.H.; Dixon, J.S.; Chung, D.  
Arch. Biochem. Biophys. 155, 95-110, 1973  
A>Title: Amino acid sequence of human chorionic somatomammotropin.  
A:Reference number: A90054; MUID:73201971; PMID:4712450  
A:Accession: A90054  
A:Molecule type: protein  
A:Residues: 27-217 <LIC>  
A:Experimental source: placenta  
R:Niall, H.D.  
in Prolactin and Carcinogenesis, Proc. Fourth Tenovus Workshop Prolactin, Griffiths, K.,  
A>Title: The chemistry of the human lactogenic hormones.  
A:Reference number: A94427  
A:Accession: A94427  
A:Molecule type: protein  
A:Residues: 27-217 <NIA>  
R:McAuliffe, N.; Tipton, K.F.  
Biochem. Soc. Trans. 19, 205, 1991  
A>Title: Catechol-O-methyltransferase from human placenta: purification and some proper  
A:Reference number: A61283; MUID:91244006; PMID:2037148  
A:Accession: A61283  
A:Molecule type: protein  
A:Residues: 27-46 <NIC>  
A>Note: chloramphenicol apparently copurified with placental catechol-O-methyltransferase  
R:Sherwood, L.M.; Handwerker, S.; McLaurin, W.D.; Lanner, M.  
Nature New Biol. 233, 59-61, 1971  
A>Title: Amino-acid sequence of human placental lactogen.  
A:Reference number: A93401; MUID:72016313; PMID:5286363  
A:Accession: A93401  
R:Sherwood, L.M.; Handwerker, S.; McLaurin, W.D.; Lanner, M.  
Nature New Biol. 235, 64, 1972  
A:Reference number: A93405

A:Contents: annotation  
 R.Schneider, A.B.; Kowalski, K.; Russell, J.; Sherwood, L.M.  
 U.Biol. Chem. 254, 3782-3787, 1979  
 Article: Identification of the interchain disulfide bonds of dimeric human placental lactoferrin  
 A:Reference number: A92251; MID:79173081; PMID:438159  
 A:Contents: annotation; dimeric disulfide bonds  
 R.Selby, M.J.; Barta, A.; Baxter, J.D.; Bell, G.I.; Eberhardt, N.L.  
 U.Biol. Chem. 259, 13331-13338, 1984  
 Article: Analysis of a major human chorionic somatomammotropin gene. Evidence for two functional alleles  
 A:Reference number: I55229; MID:85030426; PMID:6208192  
 A:Accession: I55229  
 A:Status: translated from GB/EMBL/DBJ  
 A:Molecule type: DNA  
 A:Residues: 1-217 <RES>  
 A:Cross-references: GB:K02401; NID:g181120; PIDN:AAA52115.1; PID:g181121  
 R.Selby, M.J.; Shine, J.; Martini, J.A.; Ullrich, A.; Goodman, H.  
 Trans. Assoc. Am. Physicians 90, 109-116, 1977  
 Article: Nucleotide sequence of a human gene coding for a polypeptide hormone.  
 A:Reference number: I59658; MID:78160787; PMID:611657  
 A:Accession: I59658  
 A:Status: translated from GB/EMBL/DBJ  
 A:Molecule type: mRNA  
 A:Residues: 160-217 <RES>  
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 A:Gene: GDB:CSH1  
 A:Cross-references: GDB:119084; OMIM:150200  
 A:Map position: 17q22-17q24  
 A:introns: 4/1; 57/3; 97/3; 152/3  
 C:Superfamily: prolactin  
 C:Keywords: hormone; placenta  
 F.1-36/Domains: signal sequence #status experimental <SIG>  
 F.127-217/Product: chorionmammotropin A #status experimental <MAT>  
 F.79-191/Disulfide bonds: #status experimental  
 F.79-191/Disulfide bonds: (in monomeric form) #status experimental  
 F.208/Disulfide bonds: interchain (to 215 in dimeric form) #status experimental  
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QY 61 CTTCAGAGGGGAGTGCCTTCCCAACCATTTCCCTTAATCCAGAGCTTTTTCAGACGGTAGT 120  
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QY 172 -----AACCCCAAGACCTCCCTCTGTTTC 195  
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QY 256 CTGCTCCGCGCATCTCCCTGGCTGCATCCAGATCGCTGGAGCCCGTGCAGTTCTCAGG 315  
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Dd	21	LeuGlnGln	AaAaGlyAaAaValGlnThrValProLeuSerArgLeuPheAspHisAlaMet	40
Oy	121	CTCGCGG	CGCCATCGCTGTGACACGAGTGGCCTTTGACACTACAGAGATT-----	171
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Oy	172	-----	AAACCCCAAGACCTCCCTCTGTTTC	195
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Dd	81	SerAspSer	LeuProThrProSerAsnMetGlnGlnThrGlnGlnLysSerAsnLeuGln	100
Oy	256	CTGCTCG	GCATCTCCCTGCTGCTATCCAGTGTGGCTGGAGCCCGTGAGATTTCCTCAG	315
Dd	101	LeuLeuAa	GluLeu-----LeuLeuLeuLeuGlnSerTrpLeuGlnPro-----ArgPheLeuAaG	118
Oy	316	AGTGTCTT	CGCCCAACAGCGCTGTGTACGAGCGCTCTGAACAGCAAGCTCTTAGACCTCTTA	375
Dd	119	SerMetPhe	AaAaAsnAaAsnLeuValTyrAspThrSerAspSerAspAspTyrHisLeuLeu	138
Oy	376	AAGGACCT	TAAGAGAGATCCAAACGTATAGGGAGAGCTTGAAGATAGGCAAGCCCCGG	435
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## RESULT 12

146145  
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 N:Alternate names: growth hormone  
 C:Species: Canis lupus familiaris (dog)  
 C>Date: 19-Dec-1997 #sequence\_revision 19-Dec-1997 #text\_change 09-Jul-2004  
 C:Accession: I46145; S35790  
 R:Ascacio-Martinez, J.A.; Barrera-Saldana, H.A.  
 Gene 143, 277-280, 1994  
 A:Title: A dog growth hormone cDNA codes for a mature protein identical to pig growth hormone  
 A:Reference number: I46145; MUID:94266166; PMID:8206387  
 A:Accession: I46145  
 A:Status: preliminary; translated from GB/EMBL/DBJ  
 A:Molecule type: mRNA  
 A:Residues: 1-216 <ASC>  
 A:Cross-references: UNIPROT:P33711; EMBL:Z23067; NID:g312195; PIDN:CAA80601.1; PID:g3121  
 A>Note: submitted to the EMBL Data Library, June 1993  
 C:Superfamily: prolactin  
 C:Keywords: hormone; pituitary  
 F:1-26/Domain: signal sequence #status predicted <SIG>  
 F:27-216/Product: somatotropin #status predicted <MT>  
 F:78-189,206-214/Disulfide bonds: #status predicted

## Alignment Scores:

Pred. No.:	2,4e-50	Length:	216
Score:	698.00	Matches:	140
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Best Local Similarity:	64.52%	Mismatches:	41
Query Match:	62.77%	Indels:	16
	2	Gaps:	3

US-09-856-796B-1 (1-609) x I46145 (1-216)

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 Db 1 MetAlaAlaGlyProArgThrSerValLeuAlaPheAlaLeuLeuCysLeuProTrp 20  
 QY 61 CTTCAGAGGGGAGGCTTCCCAACCATTCCTTATCCAGGCTTTTGGACAGCTAGT 120  
 Db 21 ProGInGluValGIuAlaPheProAlaMetProLeuSerSerLeuPheAlaAlaVal 40  
 QY 121 CTCGGCGCCGACATCGCTGCACAGCTGGGCTTTGACCTTACCAAGAGTT----- 171  
 Db 41 LeuArgAlaGInHisLeuHisLeuAlaAlaAspPheTrpTyrGluPheGluArgAla 60  
 QY 172 -----AACCCGAGACCTCCCTCTCTCTCA 198  
 Db 61 TyrIleProGIuGIuGlyGlnArgTyrSerIleGlnHisAlaGlnAlaAlaPheCysPheSer 80  
 QY 199 GAGGTATATCCGACACCTCCCAAGGAGGAGAACACACAAAGAAATCCAACTAGAGTG 258  
 Db 81 GluThrIleProAlaProThrGlyLysAspGluAlaGInGlnArgSerAspValGluLeu 100  
 QY 259 CTCGGCATCTCCGCTGCTCATCGATCGTGGGCTGGAGCCCGTCACTTCTCTAGAGT 318  
 Db 101 LeuArgPheSerLeuLeuLeuIleGlnSerTrpLeuGlyProValGlnPheLeuSerArg 120  
 QY 319 GTCTTGCCCAACAGGCTGTGATGAGCGGCTCTGACAGCAAGTATATGACTCTTAAG 378  
 Db 121 ValPheThrAsnSerLeuValPheGlyThrSerPhe---ArgValTyrGluIuIysLeu 139  
 QY 379 GACCTAGAGGAGGAGCATCAACGCTGATGGGAGAGGCTGGAAGATGAGGCCCGGAGT 438  
 Db 140 AspLeuGIuGIuGlyIleGlnAlaLeuMetArgIuLeuGIuAspGlySerProArgAla 159

QY 439 GGGCAGATCTTCAAGCAGACCTTACAGCAAGTTGCACAAACTCACACAGCATGACGA 498  
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## RESULT 13

STPG  
 somatotropin precursor - pig  
 N:Alternate names: growth hormone  
 C:Species: Sus scrofa domestica (domestic pig)  
 C>Date: 30-Jun-1992 #sequence\_revision 30-Jun-1992 #text\_change 09-Jul-2004  
 C:Accession: J00015; S09015; I46584; I46585; PC1063; A01516; A94594  
 R:Vize, P.D.; Wells, J.R.E.  
 Gene 55, 339-344, 1987  
 A:Title: Isolation and characterization of the porcine growth hormone gene.  
 A:Reference number: J00015; MUID:88030700; PMID:3666458  
 A:Accession: J00015  
 A:Molecule type: DNA  
 A:Residues: 1-216 <VIZ>  
 A:Cross-references: UNIPROT:P01248; GB:M17704; NID:G164475; PIDN:AAA31044.1; PID:g164476  
 R:Kato, Y.; Shimokawa, N.; Kato, T.; Hirai, T.; Yoshihama, K.; Kawai, H.; Hattori, M.A.;  
 Blochum. Biophys. Acta 1048, 290-293, 1990  
 A:Title: Porcine growth hormone: molecular cloning of cDNA and expression in bacterial a  
 A:Reference number: S09015; MUID:90212663; PMID:2182128  
 A:Accession: S09015  
 A:Molecule type: mRNA  
 A:Residues: 1-216 <KAT>  
 A:Cross-references: GB:X53325; NID:g288361; PIDN:CAA37411.1; PID:g288362  
 R:Seeburg, P.H.; Sias, S.; Adelman, J.P.; de Boer, H.A.; Hayflick, J.; Jhurani, P.; Goed  
 DNA 2, 37-45, 1983  
 A:Title: Efficient bacterial expression of bovine and porcine growth hormones.  
 A:Reference number: I45898; MUID:83209123; PMID:6303731  
 A:Accession: I46584  
 A:Status: preliminary; translated from GB/EMBL/DBJ  
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 R:Su, T.  
 Gene 69, 81-89, 1988  
 A:Title: A multisite-directed mutagenesis using T7 DNA polymerase: application for recon  
 A:Reference number: I46585; MUID:89137997; PMID:3224824  
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 A:Cross-references: GB:M2761; NID:g164479; PIDN:AAA31046.1; PID:g164480  
 R:Yang, Q.; Zhu, B.L.; Zhou, S.W.; Qi, S.Z.  
 Chinese J. Biotechnol. 8, 318-323, 1992  
 A:Title: Cloning and partial sequencing of the porcine growth hormone (pGH) gene from pit  
 A:Reference number: PC1063  
 A:Accession: PC1063  
 A:Molecule type: mRNA  
 A:Residues: 97-108,'E',110-158 <YAN>  
 A:Experimental source: pituitary  
 R:Wills, J.B.; Howard, S.C.; Scapa, S.; Wilhelm, A.E.  
 J. Biol. Chem. 245, 3407-3415, 1970  
 A:Title: Cyanogen bromide cleavage and partial amino acid sequence of porcine growth hor  
 A:Reference number: A01516; MUID:70293161; PMID:4918150  
 A:Accession: A01516  
 A:Molecule type: Protein  
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 R:Wills, J.B.  
 submitted to the Atlas, May 1971  
 A:Reference number: A94594  
 A:Accession: A94594





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GenCore version 5.1.6  
Copyright (c) 1993 - 2005 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: February 7, 2005, 10:10:48 ? Search time 2871 Seconds  
(without alignments)  
8074.239 Million cell updates/sec

Title: US-09-856-796B-1

Perfect score: 609  
Sequence: 1 atggctacagctcccgagc.....agggcagctgtgctctag 609

Scoring table: IDENTITY\_NUC  
Gapop 10.0, Gapept 1.0

Searched: 34239544 seqs, 19032134700 residues

Total number of hits satisfying chosen parameters: 68479088

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database :

EST: \*  
1: gb\_est1: \*  
2: gb\_est2: \*  
3: gb\_hlc: \*  
4: gb\_est3: \*  
5: gb\_est4: \*  
6: gb\_est5: \*  
7: gb\_est6: \*  
8: gb\_gss1: \*  
9: gb\_gss2: \*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	* Query Match	Length	DB ID	Description
1	605.8	99.5	755	6	CD513951 AGENCOURT
2	605.8	99.5	759	6	CD106929 AGENCOURT
3	605.8	99.5	817	6	CD251386 AGENCOURT
4	604.2	99.2	770	6	CD105630 AGENCOURT
5	604.2	99.2	818	6	CD356434 AGENCOURT
6	594.8	97.7	768	6	CD108395 AGENCOURT
7	586.8	96.4	768	6	CD242555 AGENCOURT
8	577.6	94.8	738	6	CD251608 AGENCOURT
9	572	93.9	733	1	AV751954 AV751954
10	550.8	90.4	757	6	CD107947 AGENCOURT
11	550.8	90.4	798	6	CD107985 AGENCOURT
12	550.8	90.4	800	6	CD251158 AGENCOURT
13	550.8	90.4	801	6	CD108743 AGENCOURT
14	550.8	90.4	802	6	CD513888 AGENCOURT
15	550.8	90.4	803	6	CD106442 AGENCOURT
16	550.8	90.4	803	6	CD108431 AGENCOURT
17	550.8	90.4	804	6	CD105346 AGENCOURT
18	550.8	90.4	808	6	CD105855 AGENCOURT
19	550.8	90.4	808	6	CD251173 AGENCOURT
20	550.8	90.4	810	6	CD107812 AGENCOURT
21	550.8	90.4	810	6	CD109024 AGENCOURT
22	550.8	90.4	811	6	CD108773 AGENCOURT
23	550.8	90.4	816	6	CD108302 AGENCOURT
24	550.8	90.4	817	6	CD513464 AGENCOURT

25	550.8	90.4	818	6	CD105554 AGENCOURT
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27	550.8	90.4	818	6	CD106416 AGENCOURT
28	550.8	90.4	819	6	CD106646 AGENCOURT
29	550.8	90.4	819	6	CD108015 AGENCOURT
30	550.8	90.4	819	6	CD108038 AGENCOURT
31	550.8	90.4	820	6	CD108957 AGENCOURT
32	550.8	90.4	822	6	CD105685 AGENCOURT
33	550.8	90.4	822	6	CD251169 AGENCOURT
34	550.8	90.4	824	6	CD107683 AGENCOURT
35	550.8	90.4	825	6	CD513803 AGENCOURT
36	550.8	90.4	833	6	CD251579 AGENCOURT
37	550.8	90.4	851	6	CD512835 AGENCOURT
38	550.8	90.4	856	6	CD106037 AGENCOURT
39	550.8	90.4	861	6	CD513266 AGENCOURT
40	550.8	90.4	867	6	CD250877 AGENCOURT
41	550.8	90.4	867	6	CD513076 AGENCOURT
42	550.8	90.4	871	6	CD108762 AGENCOURT
43	550.8	90.4	873	6	CD108142 AGENCOURT
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#### ALIGNMENTS

RESULT 1  
LOCUS CD513951 755 bp mRNA linear EST 06-JUN-2003  
DEFINITION AGENCOURT\_14375351 NIH\_MGC\_179 Homo sapiens cDNA clone  
IMAGE:30393581 5', mRNA sequence.

ACCESSION CD513951  
VERSION CD513951  
KEYWORDS EST.

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

REFERENCE 1 (bases 1 to 755)

AUTHORS NIH-MGC <http://mgs.nci.nih.gov/>.

JOURNAL National Institutes of Health, Mammalian Gene Collection (MGC)  
Unpublished (1999)

COMMENT Contact: Daniela S. Gerhard, Ph.D.  
Office of Cancer Genomics  
National Cancer Institute / NIH  
Bldg. 31 Rm10A07 Bethesda, MD 20892

Email: [cgabbs-r@mail.nih.gov](mailto:cgabbs-r@mail.nih.gov)  
Tissue Procurement: Dr. Michael Brownstein  
CDNA Library Preparation: Invitrogen Corp

CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)  
DNA Sequencing by: Agencourt Bioscience Corporation

Clone distribution: MGC clone distribution information can be  
found through the I.M.A.G.E. Consortium/LNL at:

<http://image.llnl.gov>  
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High quality sequence stop: 705.  
Location/Qualifiers

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/tissue\_type="Pituitary"  
/lab\_host="DH10B-Ton A ( T1 and T5 phage resistances) "

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/note="Organ: brain; Vector: PCMV-SPORE.1; Site 1: Scory  
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cloning). Average insert size 1.1 Kb. Library was  
constructed by (Invitrogen). Note: this is a NIH\_MGC  
Library."

ORIGIN

http://image.llnl.gov  
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High quality sequence stop: 730.

Location/Qualifiers  
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directionally cloned (EcoRV site is destroyed upon
cloning). Average insert size 1.1 kb. Library was
constructed by (Invitrogen). Note: this is a NIH_MGC
Library."

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QY	61	CTTCAAGAGGGGAGTGCTTCCCAACATTCCTTATCCAGGCTTTTGACACAGCTAGT	120
Db	103	CTTCAAGAGGGGAGTGCTTCCCAACATTCCTTATCCAGGCTTTTGACACAGCTAGT	162
QY	121	CTCCGCGGCCATCGTGTGACCAAGCTGGCTTTGACACCTAACAGAGATTAAACCCGAG	180
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QY	181	ACCTCCCTCTGTTTCTCAGAGCTTATTCGGACACCTTCMAACAGGAGGAAACACACAG	240
Db	223	ACCTCCCTCTGTTTCTCAGAGCTTATTCGGACACCTTCMAACAGGAGGAAACACACAG	282
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Db	283	AAATCCAACTAGAGCTGTCGCGACATCCCGTGGCTCAACCAAGTCGTGGCTGAAGCC	342
QY	301	GTGCAGTTCCTCAGAGATGCTTGGCCAAACAGCTGGGTACAGGAGGCTCTGACAGCAAC	360
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CD106929	759 bp	mRNA	linear	EST 15-MAY-2003
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IMAGE:30368973 5', mRNA sequence.

CD106929 1 GT.30760387

KEYWORDS EST.

**Homo sapiens**

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Cetartemata; Placentalia; Carnivora; Canidae; Felidae; Felis; Felis concolor

1 (bases 1 to 759)

NIH-MGC <http://mgc.nci.nih.gov/>.

National Institutes of Health, Mammalian Gene Collection (MGC)  
Unpublished (1999)

Contact: Robert Strausberg, Ph.D.

Email: [cgapbs-r@mail.nih.gov](mailto:cgapbs-r@mail.nih.gov)

Issue Procurement: Dr. Michael Brownstein  
cDNA Library Preparation: Invitrogen Corp  
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LINT)  
DNA Sequencing by: Agencourt Bioscience Corporation  
Clone Distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LINT at:

LOCUS	CD251386	817 bp	mRNA	linear	EST 22-MAY-2003
DEFINITION	AGENCOURT_14204245 NIH_MGC_179 Homo sapiens cDNA clone				

**FEATURES**  
**source**

**ORIGIN**

## FEATURES

Query Match	99.2%	Score 604.2	DB 6	Length 770
Best Local Similarity	99.5%	Pred. No. 3	3e-147	
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Qy 61 CTTCAGAGGGGAGTGCTCCCAACATTCCTTATCCAGCTTTTGACAAAGCTAGT 120

Db	446	GTCATGACCTCTCTAAAGCACTTAGAGGAAGGCAATCCAAACGCTGATGGGAGGCTGGAA	505
QY	421	GATGGCAGCCCCCGGACTGGGGCAGATCTTTCAAGCGACACTTAAGCAAGTTCCACAAC	480
Db	506	GATGGCAGCCCCCGGACTGGGGCAGATCTTTCAAGCGACCTTACAGCAAGTTCCACAAC	565
QY	481	TCACACACAGATGACGCACTACTCAAGAACTACGGGCTGCTTACTGCTTTCAGGAAGAC	540
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Db	626	ATGACCAAGTTCAGACATTTCTGGGCATCTGCGACTGCGCGCTCTGTGAGAGGCGACCTGT	685
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	IMAGE:30368235 5', mRNA sequence.			
ACCESSION	CD105630			
VERSION	CD105630.1			
KEYWORDS	GI:30758804			
SOURCE	Homo sapiens (human)			
ORGANISM	Homo sapiens			

REFERENCE	AUTHORS	TITLE	JOURNAL	COMMENT
1 (bases 1 to 710)	NIH-MGC	<a href="http://mgc.nci.nih.gov/">http://mgc.nci.nih.gov/</a> .		
	National Institutes of Health,	Mammalian Gene Collection (MGC)		
	Unpublished (1999)			
Contact:	Robert Strausberg, Ph.D.			
Email:	cgapbs-remail.nih.gov			
Tissue Procurement:	Dr. Michael Brownstein			
cDNA library Preparation:	Invitrogen Corp			
cDNA library Arrayed by:	The I.M.A.G.E. Consortium (LNL)			
DNA Sequencing by:	Agencourt Bioscience Corporation			
Clone distribution:	MGC clone distribution information can be			
found through the I.M.A.G.E. Consortium/LNL at:				
<a href="http://image.llnl.gov">http://image.llnl.gov</a>				
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Location/Qualifiers				

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cloning). Average insert size 1.1 kb. Library was
constructed by (Invitrogen). Note: this is a NIH_MGC
library."

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Db      103 CTTCAAGAGGGGAGGCGCTTCCCAACATCCCTTATCCAGGCTTTTGAACAAGCTTAG 162
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Db      283 AAATCCAACTAGAGCTGCTCCGACATCTCCCTGCTGCTATCCAGTCCGAGGAGCCG 342
QY      301 GTGCAAGTTCTCAGAGAGTCTTCCCAACAGCTGCTGTAAGGAGGCTCTGACAGCAAC 360
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QY      361 GTCTATGACCTCTCTAAAGAGACTTGAAGAGAGGACATCCAAACGCTGATGGGAGGCTGAA 420
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QY      421 GATGGAGAGCCCGGAGCTGGGCAATCTTCAAGAGACCTTACAGCAAGTTGACACAAAC 480
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DEFINITION AGENCOURT 14477422 NIH MGC 179 Homo sapiens cDNA clone
IMAGE:30353023 5', mRNA sequence.
CD556434

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ACCESSION CD556434.1 GI:31582502
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
REFERENCE 1 (bases 1 to 818)
AUTHORS NIH-MGC http://mgi.nci.nih.gov/
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Daniela S. Gerhard, Ph.D.
Office of Cancer Genomics
National Cancer Institute / NIH
Bldg. 31 Rm10A07 Bethesda, MD 20892
Email: cgabbs-r@mail.nih.gov
Tissue Procurement: Dr. Michael Brownstein
CDNA Library Preparation: Invitrogen Corp
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LNL at:
http://image.llnl.gov
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Location/Qualifiers
1: .818

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FEATURES

Source

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cloning). Average insert size 1.1 kb. Library was
constructed by (Invitrogen). Note: this is a NIH_MGC
Library."

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#### ORIGIN

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Query Match 99.2%; Score 604.2; DB 6; Length 818;
Best Local Similarity 99.5%; Pred. No. 3.3e-147;
Matches 606; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

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QY      301 GTGCAAGTTCTCAGAGAGTCTTCCGCAACAGGCTGCTGCTATCCAGTCTGTGAGAGCC 360
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QY      541 ATGACAAGGTCGAGACATCTCTGCGCATCTGTCAGAGTGCCTCTGTGAGAGGAGCTGT 600
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RESULT 6
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DEFINITION AGENCOURT 14016072 NIH MGC 179 Homo sapiens cDNA clone
IMAGE:30364686 5', mRNA sequence.
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ACCESSION CD108395
VERSION CD108395.1 GI:30761569
KEYWORDS EST.
SOURCE Homo sapiens (human)

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DB 571 GCACTACTCAGAACTACAGGCTGCTCTACTACTCTTCAGAGAGACATGACCAAGTCCAG 630  
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DB 631 ACATTCTGGCGCATGTCAGTCCGCTCTGTGAGAGGGGACGTGGCTTTCAG 684

RESULT 11  
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DEFINITION AGENCOURT\_13980152 NIH\_MGC\_179 Homo sapiens cDNA clone

ACCESSION CD107985 IMAGE:30367958 5', mRNA sequence.  
VERSION CD107985  
KEYWORDS EST, CD107985.1 GI:30761159

SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens

REFERENCE NIH-MGC http://mgi.nci.nih.gov/  
AUTHORS National Institutes of Health, Mammalian Gene Collection (MGC)  
TITLE Unpublished (1999)  
JOURNAL Contact: Robert Strausberg, Ph.D.

COMMENT Email: cgabbs-remail.nih.gov  
Tissue Procurement: Dr. Michael Brownstein  
cDNA Library Preparation: Invitrogen Corp  
DNA Sequencing by: Agencourt Bioscience Corporation  
Clone distribution: MGC clone distribution information can be  
found through the I.M.A.G.E. Consortium/LNL at:  
http://image.llnl.gov  
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High quality sequence stop: 765.

FEATURES  
source location/Qualifiers  
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/lab\_host="DH10B-Ton A ( T1 and T5 phage resistances) "  
/note="Organ: brain; Vector: PCMV-SPORT6.1; Site\_1: EcoRV  
(destroyed); Site\_2: NotI; Library is oligo-dT primed and  
directionally cloned (EcoRV site is destroyed upon  
cloning). Average insert size 1.1 kb. Library was  
constructed by (Invitrogen). Note: this is a NIH\_MGC  
Library."

ORIGIN  
Query Match 90.4%; Score 550.8; DB 6; Length 798;  
Best Local Similarity 92.8%; Pred. No. 3.2e-133;  
Matches 607; Conservative 0; Mismatches 2; Indels 45; Gaps 1;

QY 1 ATGGCTAAGGCTCCCGACGCTCCCTGCTGCTTGGCTTGGCTGCTGCTGCTGCTGCTG 60  
DB 31 ATGGCTAAGGCTCCCGACGCTCCCTGCTGCTTGGCTTGGCTGCTGCTGCTGCTGCTG 90  
QY 61 CTTCAAGAGGCGAGGCTTCCCAACCATTCCTTATCCAGGCTTTTGGACCAAGCTAGT 120  
DB 91 CTTCAAGAGGCGAGGCTTCCCAACCATTCCTTATCCAGGCTTTTGGACCAAGCTAGT 150  
QY 121 CTCGCGCCCATTCGCTCAGACAGGCTGGCTTGAACCTACCAAGAGTTT----- 171  
DB 151 CTCGCGCCCATTCGCTCAGACAGGCTGGCTTGAACCTACCAAGAGTTTGAAGAGCC 210

QY 172 -----AACCCCAAGACCTCTCTGTTTC 195  
DB 211 TATATCCCAAGAGACAGAAATATTCATTCCTGACAAACCCCAAGACCTCTCTGTTTC 270  
QY 196 TCAGAGTCTATTCGACACCTCTCACAAGGAGGAAACACACAGAAATCCAACTAGAG 255  
DB 271 TCAGAGTCTATTCGACACCTCTCACAAGGAGGAAACACACAGAAATCCAACTAGAG 330  
QY 256 CTGCTCCGACATCTCCCTGCTGCTCATCGAGTGTGCTGAGAGCCGCTGAGAGTTCTTCAG 315  
DB 331 CTGCTCCGACATCTCCCTGCTGCTCATCGAGTGTGCTGAGAGCCGCTGAGAGTTCTTCAG 390  
QY 316 AGTGTCTTGGCCACAGGCTGTGTATGAGGCGGCTCTGACAGCAAGCTATGACCTCTTA 375  
DB 391 AGTGTCTTGGCCACAGGCTGTGTATGAGGCGGCTCTGACAGCAAGCTATGACCTCTTA 450  
QY 376 AAGGACCTTAGAGAGAGGACATCCAAAGCTGATGGGAGGCTGGAAGATGCGACCCCGG 435  
DB 451 AAGGACCTTAGAGAGAGGACATCCAAAGCTGATGGGAGGCTGGAAGATGCGACCCCGG 510  
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DB 511 ACTGGGAGATCTTTCAGACAGACCTACAGCAAGTTGACACAACTCAGACCAAGATGAC 570  
QY 496 GCACTACTCAGAACTACAGGCTGCTCTACTACTCTTCAGAGAGACATGACCAAGTCCAG 555  
DB 571 GCACTACTCAGAACTACAGGCTGCTCTACTACTCTTCAGAGAGACATGACCAAGTCCAG 630  
QY 556 ACATTCTGGCGCATGTCAGTCCGCTCTGTGAGAGGGGACGTGGCTTTCAG 609  
DB 631 ACATTCTGGCGCATGTCAGTCCGCTCTGTGAGAGGGGACGTGGCTTTCAG 684

RESULT 12  
LOCUS CD251158 800 bp mRNA linear EST 22-MAY-2003  
DEFINITION AGENCOURT\_14214052 NIH\_MGC\_179 Homo sapiens cDNA clone  
ACCESSION CD251158 IMAGE:30383909 5', mRNA sequence.  
VERSION CD251158  
KEYWORDS EST, CD251158.1 GI:31011624

SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
AUTHORS NIH-MGC http://mgi.nci.nih.gov/  
TITLE Unpublished (1999)  
JOURNAL National Institutes of Health, Mammalian Gene Collection (MGC)  
COMMENT Contact: Daniela S. Gerhard, Ph.D.  
Office of Cancer Genomics / NIH  
National Cancer Institute / NIH  
Bldg. 31 Rm10A07 Bethesda, MD 20892  
Email: cgabbs-remail.nih.gov  
Tissue Procurement: Dr. Michael Brownstein  
cDNA Library Preparation: Invitrogen Corp  
DNA Sequencing by: Agencourt Bioscience Corporation  
Clone distribution: MGC clone distribution information can be  
found through the I.M.A.G.E. Consortium/LNL at:  
http://image.llnl.gov  
Plate: NDAM48 row: 1 column: 06  
High quality sequence stop: 634.

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source location/Qualifiers  
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/note="Organ: brain; Vector: PCMV-SPORT6.1; Site\_1: EcoRV



(destroyed) ; Site 2: NotI; Library is oligo-dT primed and directionally cloned (EcoRV site is destroyed upon cloning). Average insert size 1.1 kb. Library was constructed by (Invitrogen). Note: this is a NIH\_MGC library."

**ORIGIN**

Query Match	90.4%	Score 550.8;	DB 6;	Length 800;
Best Local Similarity	92.8%;	Pred. No. 3.2e-133;		
Matches 607;	Conservative	0;	Mismatches 2;	Indels 45;
				Gaps 1

OY	ATGGCTACAGAGCTCCGGAAGTCCCTGCTCTGGCTTTTGGCTGCTGCTGCTGCTG	60
Db	ATGGCTACAGAGCTCCGGAAGTCCCTGCTCTGGCTTTTGGCTGCTGCTGCTGCTG	99
OY	CTTCCAGAGGGCAGTGGCTTTCCCAACATTCCTTATCCAGGCTTTTGAACA	120
Db	CTTCCAGAGGGCAGTGGCTTTCCCAACATTCCTTATCCAGGCTTTTGAACA	159
OY	CTCCGCGCCATCGTCTGGACACAGCTGGCTTTGACACTTACAGAGATT	171
Db	CTCCGCGCCATCGTCTGGACACAGCTGGCTTTGACACTTACAGAGATTGAAGACC	219
OY	172 -----AACCCGACCTCCCTGTTTC	195
Db	220 TATATCCCAAGAACAGAAAGTATTCAATCTCGAAGACCCCAAGCTCTCTGTTTC	279
OY	196 TCAGAGTATTTCGACACCTCCCAAGAGGAGAAACACACAGAAATCCAACTT	255
Db	280 TCAGAGTATTTCGACACCTCCCAAGAGGAGAAACACACAGAAATCCAACTT	339
OY	256 CTGCTCCGCATCTCCCTGCTGCTCATCCAGTCGTGGCTGAGCCCTGGACGTTCT	315
Db	340 CTGCTCCGCATCTCCCTGCTGCTCATCCAGTCGTGGCTGAGCCCTGGACGTTCT	399
OY	316 AGTGTCTTTCGCCAACAGCTGGTGTACGGGCGCTCTGACAGCAACGTCTATGAC	375
Db	400 AGTGTCTTTCGCCAACAGCTGGTGTACGGGCGCTCTGACAGCAACGTCTATGAC	459
OY	376 AAGAACCTTAGAGGAAGCATCCAAACGTTGATGGGAGGCTGGAAGATGGAGCCCG	435
Db	460 AAGAACCTTAGAGGAAGCATCCAAACGTTGATGGGAGGCTGGAAGATGGAGCCCG	519
OY	436 ACTGGGCAAGATTTTGAAGAGACCTAACAGCAAGTTGACACAACTCACAAAGAT	495
Db	520 ACTGGGCAAGATTTTGAAGAGACCTAACAGCAAGTTGACACAACTCACAAAGAT	579
OY	496 GCACTACTCAAGAACTACGGGCTGCTACTAGCTTCAGGAAGGACATGACAGAGTC	555
Db	580 GCACTACTCAAGAACTACGGGCTGCTACTAGCTTCAGGAAGGACATGACAGAGTC	639
OY	556 ACATTCTTCGCAATCGTGCAGTCCGCTCTGTGAGAGGCACTGTGGCTTCTAG	609
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DEFINITION	CD108743	
ACCESSION	CD108743	
VERSION	CD108743.1	
KEYWORDS	EST.	
SOURCE	Homo sapiens (human)	
ORGANISM	Homo sapiens	
REFERENCE	1 (bases 1 to 801)	
TITLE	NIH-MGC http://mgi.nci.nih.gov/	
COMMENT	Unpublished (1999)	
	Contact: Robert Strauberg Ph.D.	

Email: c9apbs-r@mail.nih.gov  
Tissue Procurement: Dr. Michael Brownstein  
CDNA Library Preparation: Invitrogen Corp  
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)  
DNA Sequencing by: Agencourt Bioscience Corporation  
Clone distribution: MGC clone distribution information can be  
found through the I.M.A.G.E. Consortium/LLNL at:  
<http://image.llnl.gov>  
Plate: NDAM432 row: e column: 13  
High quality sequence stop: 635.  
Location/Qualifiers

## FEATURES

**Source**

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directionally cloned (Bscore site is destroyed upon
cloning). Average insert size 1.1 kb. Library was
constructed by (Invitrogen). Note: this is a NIH_MGC
library."

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## ORIGIN

Query Match	90.4%;	Score 550.8;	DB 6;	Length 801;
Best Local Similarity	92.8%;	Pred. No. 3.2e-133;		
Matches 607; Conservative	0;	Mismatches 2;	Indels 45;	Gaps 1

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Db	41	ATGCTTACAGGCTTCCCGAAGCTCCCTGCTCTTGCTTTTGACCTGCTCTGCTGCGCTGG	100
QY	61	CTTCAAGAGGCGCAGTGCCTTCCCAACATTCCTTATTCAGGCTTTTGAACAAGCTAGT	120
Db	101	CTTCAAGAGGCGCAGTGCCTTCCCAACATTCCTTATTCAGGCTTTTGAACAAGCTAGT	160
QY	121	CTCGCGCCCATGCTGTGACACAGCTGGCTTTTGACACTTACAGGATTT-----	171
Db	161	CTCGCGCCCATGCTGTGACACAGCTGGCTTTTGACACTTACAGGATTTGAAAGAGCC	220
QY	172	-----MACCCCAGACCTCCCTCTGTTTC	195
Db	221	TATATCCCAAGAACAGAGTATTCACTTCTCGAAGACCCCAAGCTCCTCTCTGTTTC	280
QY	196	TCAGAGCTTATTCGACACACCTCCAAAGGAGGAAACAACAAGAAATCCAACTAGAG	255
Db	281	TCAGAGCTTATTCGACACACCTCCAAAGGAGGAAACAACAAGAAATCCAACTAGAG	340
QY	256	CTGCTCGGCATCTCCCTGCTGCTATCCAGTGTGTGCTGTGAGCCCGTGAAGTTCCCTAG	315
Db	341	CTGCTCGGCATCTCCCTGCTGCTATCCAGTGTGTGAGCCCGTGAAGTTCCCTAG	400
QY	316	AGTGTCTTGCCTAACAGCTGTGTGACGGCGCTGTGACAGCAAGCTATATGACTCTTA	375
Db	401	AGTGTCTTGCCTAACAGCTGTGTGACGGCGCTGTGACAGCAAGCTATATGACTCTTA	460
QY	376	AAGAGCTTAGAGGAGGACTCCAAACGCTGATGTGGAGGCTGGAAGATGGACCCCGG	435
Db	461	AAGAGCTTAGAGGAGGACTCCAAACGCTGATGTGGAGGCTGGAAGATGGACCCCGG	520
QY	436	ACTGGGACAGATCTTCAAGCAGACTTACAGCAAGTTTGAACAACAACTCACACAGATGAC	495
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QY	496	GCACTACTCAAAACCTAAGGGGCTGCTCTA CTGCTT CAGGAAGGACATGACAAAGTCTGAG	555
Db	581	GCACTACTCAAAACCTAAGGGGCTGCTCTA CTGCTT CAGGAAGGACATGACAAAGTCTGAG	640
QY	556	ACATTCTCGCATCTGACAGTCCGCTCTGTGAGAGGCGAGCTGTGGCTTTCTAG	609

Db 641 ACATTCTGCGCATGTCGAGTGCCTCTGTGAGGAGAGCTGTGGCTTCTAG 694

RESULT 14  
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LOCUS 802 bp mRNA linear EST 06-JUN-2003

DEFINITION AGENCOURT 14365159 NIH MGC 179 Homo sapiens cDNA clone

ACCESSION IMAGE:30394616 5', mRNA sequence.  
CD513888

VERSION CD513888.1 GI:31445606

KEYWORDS EST.

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens

REFERENCE Mammalia; Euthera; Primates; Catarrhini; Homidae; Homo.  
1 (bases 1 to 802)  
NIH-MGC http://mgi.nci.nih.gov/.  
National Institutes of Health, Mammalian Gene Collection (MGC)  
Unpublished (1999).

AUTHORS Contact: Daniela S. Gerhard, Ph.D.  
Office of Cancer Genomics  
National Cancer Institute / NIH  
Bldg. 31 Rm10A07 Bethesda, MD 20892  
Email: cgabs-remail.nih.gov

JOURNAL Tissue Procurement: Dr. Michael Brownstein  
CDNA Library Preparation: Invitrogen Corp  
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)  
DNA Sequencing by: Agencourt Bioscience Corporation  
Clone distribution: MGC clone distribution information can be  
found through the I.M.A.G.E. Consortium/LNL at:  
http://image.llnl.gov

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/note="Organ: Brain; Vector: pCMV-Sport6.1; Site 1: EcoRV  
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directionally cloned (EcoRV site is destroyed upon  
cloning). Average insert size 1.1 kb. Library was  
constructed by (Invitrogen). Note: this is a NIH\_MGC  
Library."

FEATURES  
source

Query Match 90.4%; Score 550.8; DB 6; Length 802;  
Best Local Similarity 92.8%; Pred. No. 3.2e-133;  
Matches 607; Conservative 0; Mismatches 2; Indels 45; Gaps 1;

ORIGIN

1 ATGGCTACAGGCTCCCGAGCTCCCTGCTCTGCTTGGCTGCTCCGCTCCGCTCG 60  
23 ATGGCTACAGGCTCCCGAGCTCCCTGCTCTGCTTGGCTGCTCCGCTCCGCTCG 82  
61 CTTCAGAGGGAGTGCCTTCCCAACATTCCTTATCCAGGCTTTTGAACAAGCTAGT 120  
83 CTTCAGAGGGAGTGCCTTCCCAACATTCCTTATCCAGGCTTTTGAACAAGCTAGT 142  
121 CTTCAGAGGGAGTGCCTTCCCAACATTCCTTATCCAGGCTTTTGAACAAGCTAGT 171  
143 CTTCAGAGGGAGTGCCTTCCCAACATTCCTTATCCAGGCTTTTGAACAAGCTAGT 202  
172 -----AACCCCAAGCTTCCTCTGTTTC 195  
203 TATATCCCAAGGAACAGAGTATTCCTTCGAGAACCCCAAGCTTCCTCTGTTTC 262  
196 TCAGAGCTTATTCGACACCTCCCAACAGGAGGAGAAACAGAAATCCAACTAGAG 255  
263 TCAGAGCTTATTCGACACCTCCCAACAGGAGGAGGAGAAACAGAAATCCAACTAGAG 322

QY 256 CTGCTCGCATCTCCCTGCTGCTCATTCAGTGTGGAGCCCGTGCATTCCTCAGG 315  
DB 323 CTGCTCGCATCTCCCTGCTGCTCATTCAGTGTGGAGCCCGTGCATTCCTCAGG 362  
QY 316 AGTGTCTTGGCCCAACAGCTGCTGTGAAGGCGCTTGAACAGCAACTTATGACCTTCA 375  
DB 383 AGTGTCTTGGCCCAACAGCTGCTGTGAAGGCGCTTGAACAGCAACTTATGACCTTCA 442  
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DB 443 AAGGACTTGAAGGAAGGATCCAAAGCTGTATGGGAGGCTGGAAGATGGAGCCCGG 502  
QY 436 ACTGGGAGATCTTCAAGAGACCTTACAGCACTTGAACAACTCACAACAGATGAC 495  
DB 503 ACTGGGAGATCTTCAAGAGACCTTACAGCACTTGAACAACTCACAACAGATGAC 562  
QY 496 GCACTACTCAAGAACTACAGGCTGCTCTCTGCTTCAAGAGGAGGAGGAGGAGGAGG 555  
DB 563 GCACTACTCAAGAACTACAGGCTGCTCTCTGCTTCAAGAGGAGGAGGAGGAGGAGG 622  
QY 556 ACATTCTGCGCATGTCGAGTGCCTCTGTGAGAGGAGGAGGAGGAGGAGGAGGAGG 609  
DB 623 ACATTCTGCGCATGTCGAGTGCCTCTGTGAGAGGAGGAGGAGGAGGAGGAGGAGG 676

RESULT 15  
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LOCUS AGENCOURT 14018626 NIH MGC 179 Homo sapiens cDNA clone  
DEFINITION IMAGE:30367261 5', mRNA sequence.  
ACCESSION CD106442  
VERSION CD106442.1 GI:30759616

KEYWORDS EST.

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens

REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Euthera; Primates; Catarrhini; Homidae; Homo.  
1 (bases 1 to 803)  
NIH-MGC http://mgi.nci.nih.gov/.  
National Institutes of Health, Mammalian Gene Collection (MGC)  
Unpublished (1999).

AUTHORS Contact: Robert Strausberg, Ph.D.  
Email: cgabs-remail.nih.gov  
Tissue Procurement: Dr. Michael Brownstein  
CDNA Library Preparation: Invitrogen Corp  
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)  
DNA Sequencing by: Agencourt Bioscience Corporation  
Clone distribution: MGC clone distribution information can be  
found through the I.M.A.G.E. Consortium/LNL at:  
http://image.llnl.gov

COMMENT Plate: NDMA428 row: C column: 14  
High quality sequence stop: 638.  
Location/Qualifiers  
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/note="Organ: Brain; Vector: pCMV-Sport6.1; Site 1: EcoRV  
(destroyed); Site 2: NotI; Library is oligo-dT primed and  
directionally cloned (EcoRV site is destroyed upon  
cloning). Average insert size 1.1 kb. Library was  
constructed by (Invitrogen). Note: this is a NIH\_MGC  
Library."

FEATURES  
source

Query Match 90.4%; Score 550.8; DB 6; Length 803;  
Best Local Similarity 92.8%; Pred. No. 3.2e-133;  
Matches 607; Conservative 0; Mismatches 2; Indels 45; Gaps 1;

ORIGIN

1 ATGGCTACAGGCTCCCGAGCTCCCTGCTCTGCTTGGCTGCTCCGCTCCGCTCG 60  
23 ATGGCTACAGGCTCCCGAGCTCCCTGCTCTGCTTGGCTGCTCCGCTCCGCTCG 82  
61 CTTCAGAGGGAGTGCCTTCCCAACATTCCTTATCCAGGCTTTTGAACAAGCTAGT 120  
83 CTTCAGAGGGAGTGCCTTCCCAACATTCCTTATCCAGGCTTTTGAACAAGCTAGT 142  
121 CTTCAGAGGGAGTGCCTTCCCAACATTCCTTATCCAGGCTTTTGAACAAGCTAGT 171  
143 CTTCAGAGGGAGTGCCTTCCCAACATTCCTTATCCAGGCTTTTGAACAAGCTAGT 202  
172 -----AACCCCAAGCTTCCTCTGTTTC 195  
203 TATATCCCAAGGAACAGAGTATTCCTTCGAGAACCCCAAGCTTCCTCTGTTTC 262  
196 TCAGAGCTTATTCGACACCTCCCAACAGGAGGAGGAGAAACAGAAATCCAACTAGAG 255  
263 TCAGAGCTTATTCGACACCTCCCAACAGGAGGAGGAGGAGAAACAGAAATCCAACTAGAG 322

ORIGIN

Query Match 90.4%; Score 550.8; DB 6; Length 803;  
Best Local Similarity 92.8%; Pred. No. 3.2e-133;  
Matches 607; Conservative 0; Mismatches 2; Indels 45; Gaps 1;

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OY 1 ATGGCTACAGGCTCCCGGACGTCCTGCTCTGCGCTTTTGGCTCTGCTGCTGCTGG 60
DB 44 ATGGCTACAGGCTCCCGGACGTCCTGCTCTGCGCTTTTGGCTCTGCTGCTGCTGG 103
OY 61 CTTCAAGAGGGGAGTGGCTTCCCAACCATTCCTTATCCAGGCTTTTGAACAAGCTAGT 120
DB 104 CTTCAAGAGGGGAGTGGCTTCCCAACCATTCCTTATCCAGGCTTTTGAACAAGCTAGT 163
OY 121 CTCGGCGCCGACATCGTCTGACAGGCTGGCTTGAACACTACAGAGATT----- 171
DB 164 CTCGGCGCCGACATCGTCTGACAGGCTGGCTTGAACACTACAGAGATTGAAGAGCC 223
OY 172 -----AACCCGAGACTCCCTGTGTTTC 195
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OY 196 TCAGAGTCTATTCCGACACCTCTCCACAGGGAGGAAACACACAGAAATCCAACTAGAG 255
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DB 464 AAGGACTTAGAGAGGATCCAAACGCTGATGGGAGGCTGGAAAGTAGGCAAGCCCGG 523
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DB 524 ACTGGGCAAGTCTTCAAGCAGACCTACAGCAAGTTTGACACAACTCACAAAGATGAC 583
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DB 584 GCACTACTCAAGAACTACGGGCTGCTTACTGCTTCAGGAAGGACATGGAACAAGTCGAG 643
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GenCore version 5.1.6  
Copyright (c) 1993 - 2005 Compugen Ltd.

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4089.918 Million cell updates/sec

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Sequence: 1 atggtacagctcccgac.....aggcgactgtgcttcag 609

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Ygapop 10.0, Ygapext 0.5  
Fgapop 6.0, Fgapext 7.0  
Delop 6.0, Delext 7.0

Searched: 1612378 seqs, 512079187 residues

Total number of hits satisfying chosen parameters: 3224756

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Post-processing: Minimum Match 0%  
Maximum Match 100%

Listing first 45 summaries

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1: uniProt\_sprot.\*  
2: uniProt\_trembl.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1024.5	92.1	217	1	SOMA_HUMAN
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3	1018.5	91.6	217	1	SOMA_PANTR
4	1016.5	91.4	217	2	O61YF0
5	981.5	88.3	217	1	SOMA_MACMU
6	957	86.1	202	2	O14643
7	955.5	85.9	217	1	SOM2_PANTR
8	945.5	85.0	217	2	O6FHS4
9	939.5	84.5	217	1	SOM2_HUMAN
10	938.5	84.5	217	2	O6FHS2
11	908.5	81.7	217	2	Q8MND9
12	904.5	81.3	217	1	SOMA_SAIIB
13	895.5	80.5	217	1	SOMA_CALJA
14	888	79.9	245	2	O14644
15	882.5	79.4	217	2	O866U1
16	872.5	78.5	217	1	CSH_HUMAN

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19	855.5	76.9	217	2	O866T8	O866T8 pan troglod
20	853.5	76.8	217	2	O866U0	O866U0 pan troglod
21	850.5	76.5	217	2	O07367	O07367 macaca mula
22	831.5	74.8	212	2	O07368	O07368 macaca mula
23	829.5	74.6	217	1	SOM2_MACMU	Q07370 macaca mula
24	779.5	70.1	199	2	O14406	O14406 homo sapien
25	754.5	67.9	217	2	Q8MND9	Q8MND9 ateles geof
26	751.5	67.6	217	2	Q8M174	Q8M174 callithrix
27	728.5	65.5	217	2	O8M175	O8M175 pan troglod
28	726.5	65.3	184	2	O866T9	O866T9 balaenopter
29	702	63.1	216	1	SOMA_BALPH	O8M173 delphinus d
30	702	63.1	216	2	Q8M173	Q8M173 hippopotamu
31	701	63.0	216	2	Q7Y0B8	Q7Y0B8 camelus dro
32	696	62.6	216	2	Q7YR6	Q7YR6 sus scrofa
33	694	62.4	216	1	SOMA_PIG	P01248 equus cabal
34	693	62.3	216	1	SOMA_HORSE	O70615 spatax leuc
35	688	61.9	216	2	O70615	P33711 canis fami
36	687	61.8	216	1	SOMA_CANFA	P46404 felis silve
37	687	61.8	216	1	SOMA_FELCA	P37886 mesocricetu
38	682	61.3	216	1	SOMA_MESAU	P46407 oryctolagus
39	682	61.3	216	1	SOMA_RABIT	Q28957 sus scrofa
40	681	61.2	217	2	Q28957	Q28957 sus scrofa
41	679	61.1	216	1	SOMA_MOUSE	P06680 mus musculu
42	679	61.1	217	1	SOMA_CEREL	P56437 cervus elap
43	678	61.0	217	2	Q7Y0D2	Q7Y0D2 giraffa cam
44	677	60.9	217	1	SOMA_BOVIN	P01246 bos taurus
45	677	60.9	217	2	O864S7	O864S7 bos mutus g

## ALIGNMENTS

RESULT 1  
SOMA\_HUMAN STANDARD; PRT; 217 AA.  
ID P01241; Q14405; Q16631; Q9HB21; Q9DUM7; Q9UNL5;  
AC SOMA\_HUMAN  
DT 21-JUL-1986 (Rel. 01, Created)  
DT 01-MAR-1992 (Rel. 21, Last sequence update)  
DT 25-OCT-2004 (Rel. 45, Last annotation update)  
DE Somatotropin precursor (Growth hormone) (GH) (GH-N) (Pituitary growth hormone) (Growth hormone 1).  
GN Name=GH1;  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.  
OX NCBI\_Taxid=9606;  
RN [1]  
RP SEQUENCE FROM N.A. (ISOFORM 1).  
RX MEDLINE=80034477; PubMed=386281;  
RA Roskam W., Rougeon F.,  
RT "Molecular cloning and nucleotide sequence of the human growth hormone structural gene."  
RL Nucleic Acids Res. 7:305-320(1979).  
RN [2]  
RP SEQUENCE FROM N.A. (ISOFORM 1).  
RX MEDLINE=79203293; PubMed=377496;  
RA Martial J.A., Halliwell R.A., Baxter J.D., Goodman H.M.,  
RT "Human growth hormone: complementary DNA cloning and expression in bacteria."  
RL Science 205:602-607(1979).  
RN [3]  
RP SEQUENCE FROM N.A. (ISOFORM 1), AND POSSIBLE ALTERNATIVE SPLICING.  
RX MEDLINE=82014939; PubMed=6269091;  
RA Denoto F.M., Moore D.D., Goodman H.M.,  
RT "Human growth hormone DNA sequence and mRNA structure: possible alternative splicing."  
RL Nucleic Acids Res. 9:3719-3730(1981).  
RN [4]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=83182010; PubMed=7169009;  
RA Seeburg P.H.,  
RT "The human growth hormone gene family: nucleotide sequences show

- RT recent divergence and predict a new polypeptide hormone.";  
RL DNA 1:239-249(1982).  
RN [5]  
RX SEQUENCE FROM N.A.  
RA MEDLINE=89307277; PubMed=2744760;  
RA Chen B.Y., Liao Y.C., Smith D.H., Barrera-Saldana H.A., Gelinas R.E.,  
RA Seeburg P.H.;  
RT "The human growth hormone locus: nucleotide sequence, biology, and  
RT evolution.";  
RL Genomics 4:479-497(1989).  
RN [6]  
RX SEQUENCE FROM N.A. (ISOFORM 3).  
RA TISSUE=Pituitary;  
RA Gu J., Huang Q.-H., Li N., Xu S.-H., Han Z.-G., Fu G., Chen Z.;  
RT "A novel gene expressed in human pituitary.";  
RT Submitted (SEP-1999) to the EMBL/GenBank/DBJ databases.  
RN [7]  
RX SEQUENCE FROM N.A. (ISOFORM 4).  
RA TISSUE=Pituitary;  
RA MEDLINE=20402571; PubMed=10931946; DOI=10.1073/pnas.160270997;  
RA Hu R.-M., Han Z.-G., Song H.-D., Peng Y.-D., Huang Q.-H., Ren S.-X.,  
RA Gu B.-W., Dai M., Mao Y.-F., Gao G.-F., Rong R., Ye M., Zhou J.,  
RA Xu S.-H., Gu J., Shi J.-X., Jin W.-R., Zhang C.-K., Wu T.-M.,  
RA Huang G.-Y., Chen Z., Chen M.-D., Chen J.-L.;  
RT "Gene expression profiling in the human hypothalamus-pituitary-adrenal  
RT axis and full-length cDNA cloning.";  
RL Proc. Natl. Acad. Sci. U.S.A. 97:9543-9548(2000).  
RN [8]  
RX SEQUENCE OF 1-26 FROM N.A.  
RA MEDLINE=86137393; PubMed=3912261; DOI=10.1016/0378-1119(85)90319-1;  
RA Gray G.L., Balridge J.S., McKewen K.S., Heymeker H.L., Chang C.N.;  
RT "Periplasmic production of correctly processed human growth hormone in  
RT Escherichia coli: natural and bacterial signal sequences are  
RT interchangeable.";  
RL Gene 39:247-254(1985).  
RN [9]  
RX SEQUENCE OF 27-217.  
RA MEDLINE=69289202; PubMed=5810834;  
RA Li C.H., Dixon J.S., Liu W.-K.;  
RT "Human pituitary growth hormone. XIX. The primary structure of the  
RT hormone.";  
RL Arch. Biochem. Biophys. 133:70-91(1969).  
RN [10]  
RX SEQUENCE OF 27-217, AND REVISIONS.  
RA MEDLINE=72143935; PubMed=5144027;  
RA Li C.H., Dixon J.S.;  
RT "Human pituitary growth hormone. 32. The primary structure of the  
RT hormone: revision.";  
RL Arch. Biochem. Biophys. 146:233-236(1971).  
RN [11]  
RX REVISION.  
RA MEDLINE=73092028; PubMed=4675454;  
RA Bewley T.A., Dixon J.S., Li C.H.;  
RT "Sequence comparison of human pituitary growth hormone, human  
RT chorionic somatomammotropin, and ovine pituitary growth and lactogenic  
RT hormones.";  
RL Int. J. Pept. Protein Res. 4:281-287(1972).  
RN [12]  
RX SEQUENCE OF 27-61 AND 102-124.  
RA MEDLINE=71139765; PubMed=5279046;  
RA Niall H.D.;  
RT "Revised primary structure for human growth hormone.";  
RL Nature New Biol. 230:90-91(1971).  
RN [13]  
RX REVISIONS TO 119-120 AND 151-159.  
RA MEDLINE=71153968; PubMed=5279587;  
RA Niall H.D., Hogan M.L., Sauer R., Rosenblum I.Y., Greenwood F.C.;  
RT "Sequences of pituitary and placental lactogen and growth hormones:  
RT evolution from a primordial peptide by gene reduplication.";  
RL Proc. Natl. Acad. Sci. U.S.A. 68:866-869(1971).  
RN [14]  
RX REVISION.
- RA Niall H.D.;  
RT "The chemistry of the human lactogenic hormones.";  
RL (in) Griffiths K. (eds.);  
RL Prolactin and carcinogenesis. Proc. fourth tenovus workshop prolactin,  
RL pp.13-20. Alpha Omega Alpha Press, Cardiff (1972).  
RN [15]  
RX SEQUENCE OF 27-79 (ISOFORM 2).  
RA MEDLINE=8117361; PubMed=7462247;  
RA Chapman G.E., Rogers K.M., Brittain T., Bradshaw R.A., Bates O.J.,  
RA Turner C., Cary P.D., Crane-Robinson C.;  
RT "The 20,000 molecular weight variant of human growth hormone.  
RT Preparation and some physical and chemical properties.";  
RL J. Biol. Chem. 256:2395-2401(1981).  
RN [16]  
RX SEQUENCE OF 46-80 (ISOFORM 2).  
RA MEDLINE=80130196; PubMed=7356479;  
RA Lewis U.J., Bonewald L.F., Lewis L.J.;  
RT "The 20,000-dalton variant of human growth hormone: location of the  
RT amino acid deletions.";  
RL Biochem. Biophys. Res. Commun. 92:511-516(1980).  
RN [17]  
RX DEAMINATION OF GLN-163 AND ASN-178.  
RA MEDLINE=82052997; PubMed=7028740;  
RA Lewis U.J., Singh R.N., Bonewald L.F., Seavey B.K.;  
RT "Altered proteolytic cleavage of human growth hormone as a result of  
RT deamidation.";  
RL J. Biol. Chem. 256:11645-11650(1981).  
RN [18]  
RX PHOSPHORYLATION SITES SER-132 AND SER-176.  
RA TISSUE=Pituitary;  
RA PubMed=14997482; DOI=10.1002/pmic.200300584;  
RA Giorgianni F., Beranova-Giorgianni S., Desiderio D.M.;  
RT "Identification and characterization of phosphorylated proteins in the  
RT human pituitary.";  
RL Proteomics 4:587-598(2004).  
RN [19]  
RX REVIEW.  
RA MEDLINE=99321812; PubMed=10393484; DOI=10.1159/000053128;  
RA Baumann G.;  
RT "Growth hormone heterogeneity in human pituitary and plasma.";  
RL Horm. Res. 51 Suppl. 1:2-6(1999).  
RN [20]  
RX 3D-STRUCTURE MODELING.  
RA MEDLINE=88190073; PubMed=3447173;  
RA Cohen F.E., Kuntz I.D.;  
RT "Prediction of the three-dimensional structure of human growth  
RT hormone.";  
RL Proteins 2:162-166(1987).  
RN [21]  
RX X-RAY CRYSTALLOGRAPHY (2.8 ANGSTROMS).  
RA MEDLINE=92196577; PubMed=1549776;  
RA de Vos A.M., Ultsch M., Kosiakoff A.A.;  
RT "Human growth hormone and extracellular domain of its receptor:  
RT crystal structure of the complex.";  
RL Science 255:306-312(1992).  
RN [22]  
RX X-RAY CRYSTALLOGRAPHY (2.9 ANGSTROMS).  
RA MEDLINE=95075462; PubMed=7984244; DOI=10.1038/377478a0;  
RA Somers W., Ultsch M., de Vos A.M., Kosiakoff A.A.;  
RT "The X-ray structure of a growth hormone-prolactin receptor complex.";  
RL Nature 372:478-481(1994).  
RN [23]  
RX X-RAY CRYSTALLOGRAPHY (2.5 ANGSTROMS).  
RA Chantelat L., Chirgadze N.Y., Jones N., Korber F., Navaza J.,  
RA Pavlovsk A.G., Wlodawer A.;  
RT "The crystal structure of wild-type growth-hormone at 2.5-A  
RT resolution.";  
RL Protein Pept. Lett. 2:333-340(1995).  
RN [24]  
RX X-RAY CRYSTALLOGRAPHY (2.5 ANGSTROMS).  
RA MEDLINE=97113023; PubMed=8943276; DOI=10.1074/jbc.271.50.32197;  
RA Sundstrom M., Lundqvist T., Roedin J., Giebel L.B., Milligan D.,  
RA Norstedt G.;

RT "Crystal structure of an antagonist mutant of human growth hormone  
 RT J120R, in complex with its receptor at 2.9-A resolution." ;  
 RL *J. Biol. Chem.* 271:32197-32203(1996).  
 RN [25]  
 RP VARIANT KOMARSKI SYNDROME CVS-103.  
 RX MEDLINE=96150237; Pubmed=8552145; DOI=10.1056/NEJM199602153340704;  
 RA Takahashi Y., Kaji H., Okimura Y., Goji K., Abe H., Chihara K.;  
 RT "Short stature caused by a mutant growth hormone." ;  
 RL *N. Engl. J. Med.* 334:432-436(1996).  
 RN [26]  
 RP ERRATUM.  
 RA Takahashi Y., Kaji H., Okimura Y., Goji K., Abe H., Chihara K.;  
 RL *N. Engl. J. Med.* 334:1207-1207(1996).  
 RN [27]  
 RP VARIANT KOMARSKI SYNDROME GLV-138.  
 RX MEDLINE=97426478; Pubmed=9276733;

QY 496 GCACTACTCAAGAACTACGGGCTGCTACTGCTTCAGAGAGACATGACAGTCTGAG 555  
 DB 181 AlaleuLeuLysAsnTrpGlyLeuLeuTrpCySPheArgLysAspMetAspLysValGlu 200  
 QY 556 ACATTCTCGGCATCTGTCAGTCCGCTTGTGAGAGGCGACGCTGCTTC 606  
 DB 201 ThrPheLeuArgIleValGlnCysArgSerValGluGlySerCysGlyPhe 217

## RESULT 3

SOMA\_PANTR STANDARD; PRT; 217 AA.

AC 58756;  
 DT 28-FEB-2003 (Rel. 41, Created)  
 DT 28-FEB-2003 (Rel. 41, Last sequence update)  
 DT 05-JUL-2004 (Rel. 44, Last annotation update)  
 DE Somatotropin precursor (growth hormone) (GH) (GH-N) (Pituitary growth hormone) (Growth hormone 1).  
 GN Name=GH1;  
 OS Pan troglodytes (Chimpanzee).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Pan.  
 NC NCBL\_TaxID=9598;  
 RN 1)  
 RP SEQUENCE FROM N.A.  
 RA Revol A., Esquivel D., Santiago D., Barrera-Saldana H.;  
 RT "Independent duplication of the growth hormone gene in three Anthropoides lineages."  
 RL Submitted (Apr-2001) to the EMBL/Genbank/DBJ databases.  
 CC -1- FUNCTION: Plays an important role in growth control. Its major role in stimulating body growth is to stimulate the liver and other tissues to secrete IGF-1. It stimulates both the differentiation and proliferation of myoblasts. It also stimulates amino acid uptake and protein synthesis in muscle and other tissues (By similarity).  
 CC -1- SUBCELLULAR LOCATION: Secreted.  
 CC -1- SIMILARITY: Belongs to the somatotropin/prolactin family.

CC This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See <http://www.isb-sdb.ch/announce/> or send an email to [license@isb-sdb.ch](mailto:license@isb-sdb.ch)).

CC EMBL; AF374232; AAL72284.1; -  
 DR HSSP; P01241; 1HWG.  
 DR InterPro; IPR009079; 4\_helix\_cytokine.  
 DR InterPro; IPR001400; Somatotropin.  
 DR Pfam; PF00103; Hormone 1; 1.  
 DR PRINTS; PR00836; SOMATOTROPIN.  
 DR PROSITE; PS00266; SOMATOTROPIN\_1; 1.  
 DR PROSITE; PS00338; SOMATOTROPIN\_2; 1.  
 KW Hormone; Pituitary; Signal.  
 FT SIGNAL 1 26 By similarity.  
 FT CHAIN 27 217 Somatotropin.  
 FT DISULFID 79 191 By similarity.  
 FT DISULFID 208 215 By similarity.  
 SQ SEQUENCE 217 AA; 24843 MW; FEA295ED80518674 CRC64;

## Alignment Scores:

Pred. No.: 1.63e-79 Length: 217  
 Score: 1018.50 Matches: 200  
 Percent Similarity: 92.17% Conservative: 0  
 Best Local Similarity: 92.17% Mismatches: 2  
 Query Match: 91.59% Indels: 15  
 DB: 1 Gaps: 1

US-09-856-796b-1 (1-609) x SOMA\_PANTR (1-217)

QY 1 ATGGCTACAGGCTCCGAGCGTCTGCTGCTTTGGCTTGGCTGCGCTGCGCTG 60  
 DB 1 MetAlaProGlySerArgTrpSerLeuLeuAlaPheGlyLeuLeuCysLeuProTrp 20

QY 61 CTTCAAGAGGAGGAGTGGCTTCCCAACATTCCTTATCCAGGCTTTTGACACGCTAGT 120  
 DB 21 LeuGlnGlnLysSerAlaPheProTrpIleProLeuSerArgLeuPheAspAlaMet 40  
 QY 121 CTCGGCGCCCATCGTCTGACACGAGTGGCTTGGACACCTTACAGAGAGTTT 217  
 DB 41 LeuArgAlaHisArgLeuHisGlnLeuAlaPheAspThrTrpGlnGlnPheGlnGln 60  
 QY 172 -----AACCCCGAGACTTCCCTGTTTC 195  
 DB 61 TyrIleProLysGlnGlnLysTyrSerPheLeuGlnAsnProLinhSerLeuCySPhe 80  
 QY 196 TCGAGTCTATTTCGACACCTTCAACAGGAGGAGAAACACACAAATCAACTTAGAG 255  
 DB 81 SerGlnSerIleProThrProSerAsnArgGlnGlnThrGlnGlnLysSerAsnLeuGln 100  
 QY 256 CTGCTCCGATCTCCCTGCTGCTATCCATGCTGCTGCTGAGCCGCTGACATTCCTCAG 315  
 DB 101 LeuLeuArgIleSerLeuLeuLeuIleGlnSerTrpLeuGlnProValGlnPheLeuArg 120  
 QY 316 AGTCTCTGCGCCACAGCGCTGCTGCTACGGGCGCTTGCAGACAGCTATGACCTCTA 375  
 DB 121 SerValPheAlaAsnSerLeuValTyrGlyAlaSerAspSerAsnValTyrAspLeu 140  
 QY 376 AAGACCTTAGAGAGAGACATCCAAAGCTGATGGAGGAGCTGGAGAGTGCAGCCCGG 435  
 DB 141 LysAspLeuGlnGlnGlnLysIleGlnThrLeuMetGlyArgLeuGlnAspLysSerProArg 160  
 QY 436 ACTGGGCAATCTTCAAGACAGACCTTACAGCAAGTTGACACAACTCACACAGTAGAC 495  
 DB 161 ThrGlyGlnIlePheLysGlnThrTyrSerLysPheAspThrAsnSerHisAsnAspArg 180  
 QY 496 GCACTACTCAAGAACTACGGGCTGCTACTGCTTCAGAGAGACATGACAGTCTGAG 555  
 DB 181 AlaleuLeuLysAsnTrpGlyLeuLeuTrpCySPheArgLysAspMetAspLysValGlu 200

## RESULT 4

Q61YFO PRELIMINARY; PRT; 217 AA.

AC 061YFO;  
 DT 05-JUL-2004 (TRENBLrel. 27, Created)  
 DT 05-JUL-2004 (TRENBLrel. 27, Last sequence update)  
 DT 05-JUL-2004 (TRENBLrel. 27, Last annotation update)  
 DE Growth hormone 1 variant 2.  
 GN Name=GH1;  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
 NC NCBL\_TaxID=9606;  
 RN 1)  
 RP SEQUENCE FROM N.A.  
 RA Jorge A.A.U., Arnold I.J.P., Mendonca B.B.;  
 RL Submitted (Apr-2004) to the EMBL/Genbank/DBJ databases.  
 DR EMBL; AY613432; AAT11509.1; -  
 DR HSSP; P01241; 1AXI.  
 DR GO; GO:0005576; C:extracellular; IEA.  
 DR GO; GO:0005179; F:hormone activity; IEA.  
 DR InterPro; IPR009079; 4\_helix\_cytokine.  
 DR InterPro; IPR001400; Somatotropin.  
 DR Pfam; PF00103; Hormone 1; 1.  
 DR PRINTS; PR00836; SOMATOTROPIN.  
 DR PROSITE; PS00266; SOMATOTROPIN\_1; 1.  
 DR PROSITE; PS00338; SOMATOTROPIN\_2; 1.  
 SQ SEQUENCE 217 AA; 24946 MW; 72D079DF52BDB51A CRC64;

## Alignment Scores:

Pred. No.: 2.43e-79 Length: 217  
 Score: 1016.50 Matches: 200





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Db      101 LeuLeuArgIleSerLeuLeuLeuIleGlnSerThrPleuGluProValGlnPheLeuArg 120
QY      316 AGTGTCTTCGCAACAGCGCTGTACGGCGCTCTGACAGCAACGCTTAAGACCTCTTA 375
Db      121 SerValPheAlaIaAnSerLeuValTyrGlyThrSerTyrSerAspValTyrAspLeuLeu 140
QY      376 AAGGACCTAAGGAAAGGATCTCAAAACGCTGATGGGAGGCTGGAAAGATGGACGCCCGG 435
Db      141 LysAspLeuGluGluGlyIleGlnThrLeuMetGlyArgLeuGluAspIleSerSerArg 160
QY      436 ACTGGGAGAGATCTTCAAGCAGACGCTACAGCAAGTTGCACAAACCTACACAGACATGAC 495
Db      161 ThrGlyGlnIlePheLeuGlnThrTyrSerLysPheAspThrAsnSerHisAsnAsp 180
QY      496 GCACTACTCAAGAACTACGGGCTGCTACTACTGCTTACAGAAAGACATGACAGAGTGCAG 555
Db      181 AlaleuLeuLysAsnTyrGlyLeuLeuTyrCysPheArgLysAspMetAspLysIleGlu 200
QY      556 ACATCTCGCGCATCGTGCAGTGCAGTGCCTCTGTGAGAGGGCAGCTGTGCTTC 606
Db      201 ThrPheLeuArgIleValGlnCysArgSerValGluGlySerCysGlyPhe 217

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## RESULT 6

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ID      014643 PRELIMINARY; PRT; 202 AA.
AC      014643;
DT      01-JAN-1998 (TREMBLrel. 05, Created)
DT      01-JUN-1998 (TREMBLrel. 05, Last sequence update)
DT      01-MAR-2004 (TREMBLrel. 26, Last annotation update)
DE      Placental growth hormone 20kDa isoform precursor.
GN      Name=hGH-V;
OS      Homo sapiens (Human).
OC      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC      Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OX      NCBI_TaxID=9606;
RN      [1]
RP      SEQUENCE FROM N.A.
RC      TISSUE=Full-term placenta;
RX      MEDLINE=98373737; PubMed=9709963; DOI=10.1210/jc.83.8.2878;
RA      Boguszewski C.L., Svensson P.A., Jansson T., Clark R.,
RA      Carlsson L.M.S., Carlsson B.;
RT      "Cloning of two novel growth hormone transcripts expressed in human
RT      placenta.";
RL      J. Clin. Endocrinol. Metab. 83:2878-2885(1998).
DR      EMBL; AF006060; AAB71828.1; -.
DR      HSSP; P01241; 1A22.
DR      CO; GO:0005576; C:extracellular; IEA.
DR      GO; GO:0005179; F:hormone activity; IEA.
DR      InterPro; IPR009079; 4_helix_cytokine.
DR      InterPro; IPR001400; Somatotropin.
DR      Pfam; PF00103; Hormone_1; 1.
DR      PRINTS; PR00836; SOMATOTROPIN.
DR      PROSITE; PS00266; SOMATOTROPIN_1; 1.
DR      PROSITE; PS00338; SOMATOTROPIN_2; 1.
KW      Signal.
FT      SIGNAL.
SQ      SEQUENCE 202 AA; 23128 MW; 38B64D01A9197C6 CRC64;

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## Alignment Scores:

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Pred. No.:      3.4e-74      Length:      202
Score:          957.00      Matches:      187
Percent Similarity: 94.55%      Conservative: 4
Best Local Similarity: 92.57%      Mismatches: 11
Query Match:    86.06%      Indels:      0
DB:             2          Gaps:      0

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US-09-856-796B-1 (1-609) x 014643 (1-202)

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QY      1 ATGGCTAAGAGGCTCCGGACGTCCTCGGCTTTGGCTGCTGCTGACCCCTGG 60
Db      1 MetAlaAlaGlySerArgThrSerLeuLeuAlaPheGlyLeuLeuLysLeuSerTyr 20

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QY      61 CTTCAGAGGAGGAGTGCCTTCCCAACCATTCCTTATCCAGGCTTTTGACAAAGCTAGT 120
Db      21 LeuGlnGluGlySerAlaPheProThrIleProLeuSerArgLeuPheAspAsnIleMet 40
QY      121 CTCGGGCGCCATCGTGTGACAGCAGTGGCTTTGACACCTACACAGAGTTTAAACCCCGAG 180
Db      41 LeuArgAlaArgArgLeuTyrGlnLeuAlaTyrAspThrTyrGlnIlePheAsnProGln 60
QY      181 ACTCCCTCTGTTTCTCAGAGTCTATTCGACACACCTCCAAACAGGAGAAACACACAG 240
Db      61 ThrSerLeuCysPheSerGlnSerIleProThrProSerAsnArgValIleThrGlnGln 80
QY      241 AATCCAACTGAGCTGCTCCGATCCCTGCTGCTATCCAGTGCAGTGCAGGCC 300
Db      81 LysSerAsnLeuLeuLeuLeuArgIleSerLeuLeuLeuIleGlnSerThrPleuGluPro 100
QY      301 GTTCAGTTCCTCAGAGTGTCTTCGCCAACAGCCTGTGTACGGCGCTCTGACAGCAAC 360
Db      101 ValGlnLeuLeuArgSerValPheAlaAsnSerLeuValTyrGlyLysAspSerAsn 120
QY      361 GTCTATGACCTCTTAAGACCTAAGAGAGGATCCAAACGCTGATGGGAGAGCTGAA 420
Db      121 ValTyrArgHisLeuLysAspLeuGluGlyIleGlnThrLeuMetThrArgLeuGln 140
QY      421 GATGGACGCCCGGAGCTGGGACGATCTTCAAGACACCTACAGCAAGTTCCACAAAC 480
Db      141 AspGlySerProArgThrGlyGlnIlePheAsnGlnSerTyrSerLysPheAspThrLys 160
QY      481 TCACACAGATGACGACATCTACAGAACTACGGGCTGCTACTGCTTACAGGAAGAG 540
Db      161 SerHisAsnAspAspAlaLeuLeuLysAsnTyrGlyLeuLeuTyrCysPheArgLysAsp 180
QY      541 ATGACAGAGTCCAGACATTCCTGCCATCGTGCAGTGCAGTGCCTGTGAGAGGACAGCTGT 600
Db      181 MetAspLysValGlnThrPheLeuArgIleValGlnCysArgSerValGluGlySerCys 200
QY      601 GGCTTC 606
Db      201 GlyPhe 202

```

## RESULT 7

```

ID      SOM2_PANTR STANDARD; PRT; 217 AA.
AC      P58757;
DT      28-FEB-2003 (Rel. 41, Last sequence update)
DT      05-JUL-2004 (Rel. 44, Last annotation update)
DE      Growth hormone variant precursor (GH-V) (Placenta-specific growth
DE      hormone) (Growth hormone 2).
GN      Name=GH2;
OS      Pan troglodytes (Chimpanzee).
OC      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC      Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Pan.
OX      NCBI_TaxID=9598;
RN      [1]
RP      SEQUENCE FROM N.A.
RA      Revol A., Bernalvel D., Santiago D., Barrera-Saldana H.;
RT      "Independent duplication of the growth hormone gene in three
RT      Anthropoid lineages.";
RL      Submitted (APR-2003) to the EMBL/GenBank/DBJ databases.

```

-1- FUNCTION: Plays an important role in growth control. Its major role in stimulating body growth is to stimulate the liver and other tissues to secrete IGF-1. It stimulates both the differentiation and proliferation of myoblasts. It also stimulates amino acid uptake and protein synthesis in muscle and other tissues.

-1- SUBCELLULAR LOCATION: Secreted.

-1- TISSUE SPECIFICITY: Expressed in the placenta.

-1- SIMILARITY: Belongs to the somatotropin/prolactin family.

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QY 436 ACTGGGCGATCTTTCAGACGAGCTTACAGCAAGTTGACACAACTCAGACAGATGAC 495  
DB 161 ThClYglnIlePheAsnGlnSerYserYsPheAspThlYserIshAsnAsp 180  
QY 496 GCACCTACCAAGACTACGGGCTGCTTACTTCTTACAGAGACATGACAGAGTGCAG 555  
DB 181 AlAeuLeuYsaAnTyGlyLeuLeuTyrcYsPheArgYlAspMetAspYsValGlu 200  
QY 556 ACATTCTGCGCATGTCAGTCAGCGCTCTGTGAGGGAGGAGTGTGGCTTC 606  
DB 201 ThPheLeuArgIleValGlnCysArgSerValGlnYserCysGlyPhe 217  
RESULT 9  
SOM2\_HUMAN STANDARD; PRT; 217 AA.  
ID P01242; P09587;  
DT 21-UTR-1986 (Rel. 01, Created)  
DT 28-FEB-2003 (Rel. 41, Last sequence update)  
DT 05-JUL-2004 (Rel. 44, Last annotation update)  
DE Growth hormone variant precursor (GH-V) (Placenta-specific growth  
hormone) (Growth hormone 2).  
GN Name=GH2;  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
OX NCBI\_Taxid=9606;  
RN [1]  
RP SEQUENCE FROM N.A. (ISOFORM 1).  
RX MEDLINE=83182010; PubMed=7169009;  
RA Seeburg P.H.;  
RT "The human growth hormone gene family: nucleotide sequences show  
recent divergence and predict a new polypeptide hormone.";  
RL DNA 1:239-249(1982).  
RN [2]  
RP SEQUENCE FROM N.A. (ISOFORMS 1 AND 2).  
RX MEDLINE=88243769; PubMed=3379057;  
RA Cooke N.E., Ray J., Emery J.G., Liehaber S.A.;  
RT "Two distinct species of human growth hormone-variant mRNA in the  
human placenta predict the expression of novel growth hormone  
proteins.";  
RL J. Biol. Chem. 263:9001-9006(1988).  
RN [3]  
RP SEQUENCE FROM N.A. (ISOFORM 1).  
RX MEDLINE=89024984; PubMed=2460050;  
RA Igout A., Scippo M.L., Franckenne F., Hennen G.;  
RT "Cloning and nucleotide sequence of placental hGH-V cDNA.";  
RL Arch. Int. Physiol. Biochim. 96:63-67(1988).  
RN [4]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=89307277; PubMed=2744760;  
RA Chen E.Y., Liao Y.C., Smith D.H., Barrera-Saldana H.A., Gelinas R.E.,  
RA Seeburg P.H.;  
RT "The human growth hormone locus: nucleotide sequence, biology, and  
evolution.";  
RL Genomics 4:479-497(1989).  
RN [5]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899; 99  
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G., Klausner  
R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D., Altschul  
S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K., Hopkins R.F.,  
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L., Stapleton  
M., Soares M.B., Bonaldo M.F., Casavant T.L., Schetz T.E., Brownstein  
M.J., Ustin T.B., Toshiyuki S., Carninci P., Prange C., Raha S.S.,  
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,  
RA Villalón D.K., Muzny K.C., Hale S., Garcia A.M., Gay L.J., Hultyk S.W.,  
RA Fahney J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,  
RA Whitting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,  
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,

RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield  
Y.S.N., Krzywinski M.I., Skalska U., Smalins D.E., Schenck A., Schein  
J.E., Jones S.J.M., Marra M.A.; "Generation and initial analysis of  
more than 15,000 full-length human and mouse cDNA sequences.";  
Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).  
RN [6]  
RP REVISION.  
RX MEDLINE=99321812; PubMed=10393484; DOI=10.1159/000053128;  
RA Baumann G.;  
RT "Growth hormone heterogeneity in human pituitary and plasma.";  
Horm. Res. 51 Suppl. 1:2-6(1999).  
CC -1- FUNCTION: Plays an important role in growth control. Its major  
role in stimulating body growth is to stimulate the liver and other  
tissues to secrete IGF-1. It stimulates both the differentiation and  
proliferation of myoblasts. It also stimulates amino acid uptake and  
protein synthesis in muscle and other tissues.  
CC -1- SUBUNIT: Monomer, dimer, trimer, tetramer and pentamer, disulfide-  
linked or non-covalently associated, in homopolymetric and hetero-  
polymetric combinations. Can also form a complex either with GHBP or  
with the alpha2-macroglobulin complex.  
CC -1- SUBCELLULAR LOCATION: Secreted.  
CC -1- ALTERNATIVE PRODUCTS:  
Event=Alternative splicing; Named isoforms=2;  
Name=1; Synonyms=GH-V1;  
IsoId=P01242-1; Sequence=Displayed;  
Name=2; Synonyms=GH-V2;  
IsoId=P01242-2; Sequence=VSP\_006203;  
Note=No experimental confirmation available;  
-1- TISSUE SPECIFICITY: Expressed in the placenta.  
CC -1- SIMILARITY: Belongs to the somatotropin/prolactin family.  
CC  
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or send an email to [license@ebi.ac.uk](mailto:license@ebi.ac.uk)).  
CC  
DR EMBL; X00470; AAA98619.1; -  
DR EMBL; J03756; AAB59547.1; -  
DR EMBL; J03756; AAB59548.1; -  
DR EMBL; M38451; AAA35891.1; -  
DR EMBL; J03071; AAA52552.1; -  
DR EMBL; BC020760; AAH20760.1; -  
DR PIR; A28072; STHUV2.  
DR PIR; D32435; STHUV.  
DR HSSP; P01241; 1A22.  
DR Genew; HGNC:4262; GH2.  
DR H-InVDB; HIX0014077; -  
DR MIM; 139240; -  
DR GO; GO:0005179; F:hormone activity; TAS.  
DR InterPro; IPR009079; 4\_helix\_cytokine.  
DR InterPro; IPR001400; Somatotropin.  
DR Pfam; PF00103; Hormone 1; 1.  
DR PRINTS; PR00836; SOMATOTROPIN.  
DR PROSITE; PS00266; SOMATOTROPIN\_1; 1.  
DR PROSITE; PS00338; SOMATOTROPIN\_2; 1.  
KW Alternative splicing; Glycoprotein; Hormone; Placenta; Polymorphism;  
KW Signal.  
FT CHAIN 1 26  
FT SIGNAL 27 217  
FT DISULFID 79 191  
FT DISULFID 208 215  
FT CARBOHYD 166 166  
FT VARSPLIC 153 217  
FT  
FT Growth hormone variant.  
FT By similarity.  
FT By similarity.  
FT N-linked (GlcNAc...) (potential).  
FT RLEDSGPRTGQIFNOSYKPRKSHNDLAKNYGLYCFR  
FT KMDKRETERLRIQCSVSGSGCF -> VRAVGLNPGAP  
FT LNSRDVGRHCCPLFSSQALTOENSPSPFVNPGLSLQ  
FT PGEGGKMMNRGRCQPSAMPDLFLFLHFAEAGRWQPPDMA  
FT DLOSVLQOV (in isoform 2).  
FT /FTid=VSP\_006203.



ID	Q8WNE0	PRELIMINARY;	PRT;	217 AA.
AC	Q8WNE0;			
DT	01-MAR-2002 (TREMBLrel. 20, Created)			
DT	01-MAR-2002 (TREMBLrel. 20, Last sequence update)			
DT	01-MAR-2004 (TREMBLrel. 26, Last annotation update)			
DE	Growth hormone.			
GN	Name=GH-N;			
OS	Ateles geoffroyi (Black-handed spider monkey).			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Primates; Platyrrhini; Cebidae; Ateleinae; Ateles			
OX	NCBI_TaxID=9509;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RA	Revol A., Esquivel D., Santiago D., Barrera-Saldana H.;			
RL	Submitted (Apr-2001) to the EMBL/Genbank/DBJ databases.			
DR	EMBL; AF374234; AAL72286.1; -			
DR	HSSP; P01241; 1A2.			
DR	GO: GO:0005576; C:extracellular; IEA.			
DR	GO: GO:0005179; F:hormone activity; IEA.			
DR	Pfam; PF00103; Hormone_1; 1.			
DR	PRINTS; PR00836; SOMATOTROPIN.			
DR	PROSITE; PS00266; SOMATOTROPIN_1; 1.			
DR	PROSITE; PS00338; SOMATOTROPIN_2; 1.			
SO	SEQUENCE 217 AA; 24894 MW; 4258239FP41EBA56 CRC64;			

Alignment Scores:	
Pred. No.:	5 42e-70
Score:	908.50
Percent Similarity:	87.10%
Best Local Similarity:	82.03%
Query Match:	81.70%
DB:	2
US-09-856-796B-1 (1-609) × Q8MNE0 (1-217)	
	Length: 217
	Matches: 178
	Conservative: 11
	Mismatches: 13
	Indels: 15
	Gaps: 1

Db 1 MetAlaAlaGlySerArgThrSerLeuLeuAlaPheThrLeuLeuCybLeuProGln 20

QY 61 CTTCAGAGGGGAGTGCCTTCCCAACATTTCCCTTATCCAGAGGCTTTTGGACAACGCTAGT 122

Db 21 LeuGlnGlnAlaGlyAlaPheProThrIleProLeuSerArgLeuAlaPheAlaMet 40

QY 121 CTCGGCGGCCCATCGTCTGCAGCAGAGCTGGCTTTGACACCTACCAAGAGATT----- 171

Db 41 LeuArgAlaHisArgLeuHisGlnLeuAlaPheAspThrTyrGlnGlnPheGlnGlnAla 60

QY 172 -----AACCCCGAGCCTTCCCTCTGTTC 195

Db 61 TyrIleProIysGlnGlnIleTyrSerPheLeuGlnAlaAsnProGlnThrSerLeuCybPhe 80

QY 196 TCAGAGTCTATTTCGAGCAACCCCTCCCAACAGGAGGAAACCAACAATAATCAACTAGAG 255

Db 81 SerGlnSerIleProThrProAlaSerIleTyrIysGlnThrGlnGlnIlySerAsnLeuGln 100

QY 256 CTGCTCCGCATCTCCCTGCTGTATTCAGTGTGGCTGGAGCCCTGCAGTTCCTCAGG 315

Db 101 LeuLeuArgIleSerLeuLeuLeuIleGlnSerTrpPheGlnProValGlnPheLeuArg 120

QY 316 AGTGTCTTTCGCCAACAGCCTGTGTAGCGCGCTCTGACAGCAACGTCATAGACCTCCCTTA 375

Db 121 SerValPheAlaAsnSerLeuLeuTyrGlnIleValSerAspSerAspAlaTyrGlnTyrLeu 140

QY 376 AAGGACCTTAGAGAGAGGATCCAAACGCTGATGTGGAGGAGCTGAAAGATGGACGCCCGGG 435

Db 141 LysAspPheGlnGlnGlnIleGlnIleThrLeuMetGlyArgLeuGlnIlySpIysSerProGln 160

QY 436 ACTGGGCAAGATCTTCAAGACAGACCTTACAGCAAGTTGCACAAATCTCACACAGCATGAC 495

Db 161 ThrGlyGlnIlePheArgGlnThrTyrArgIysPheAspIleAsnSerGlnAsnAsnAsp 180

QY 496 GCACTACTCAAGAACTACGGGCTGCTCTTACTGCTTACAGAAAGACATGACAAAGTTCAG 555

Db 181 AlaLeuLeuLysAsnTyrGlyLeuLeuTyrCysPheArgLysAspMetAspLysValGlu 200  
Qy 556 ACATTCTGTGGCATCGTGCAGTCCGCGCTCTGTGAGAGGACAGCTGTGGCTTC 606  
Db 201 ThrPheLeuArgIleValGlnCysArgSerValGlnGlnLysCysGlyPhe 217

## RESULT 12

SOMA_SAIBB	STANDARD;	PRT;	217 AA
ID	SOMA_SAIBB		
NO	STANDARD;		

DT	28-FEB-2003 (Rel. 41, Created,
DT	28-FEB-2003 (Rel. 41, Last

DT 05-JUL-2004 (Rel. 44, Last annotation update)  
DE Somatotropin precursor (Growth hormone).

GN Name=GHI;  
OS Saimiri boliviensis boliviensis (Bolivian squ

0X NCBI TaxID:30433; Mammalia; Euteleostomi; Platyrrhini; Cebidae; Cebinae; Salimtri.

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RN      MOBL_ID=3333;
[1]
SEQUENCE FROM N.A.
RP

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RX MEDLINE=21265430; PubMed=11371582;  
RA Liu J.C., Makova K.D., Adkins R.M., Gibson S., Li W.H.;

RT "Episodic evolution of growth hormone in primates and emergence of the  
RT species specificity of human growth hormone receptor.";  
Mol Biol Evol 1997;14:1047-1054

**CC** **role in stimulating body growth is to stimulate the liver**

other tissues to secrete IGF-1. It stimulates both the differentiation and proliferation of myoblasts. It also stimulates

amino acid uptake and protein synthesis in muscle and other tissues (By similarity).

CC -1- SIMILARITY: Belongs to the somatotropin/prolactin family

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CC AAK62287.1; -.

EMBL AF339060; AAK62287.1; -.

DR

DR HSSP; P01241; 1A22.  
DR InterPro; IPR009079; 4\_helix\_cytokine.  
DR InterPro; IPR001100; 4\_helix\_cytokine.

DR PRINTS: PR00836: SOMATOTROPIN  
DR Pfam; PF00103; Hormone1; 1.  
DR interlepr0; IPR001400; somatotropin.

DR PROSITE; PS00266; SOMATOTROPIN\_1; 1  
DR PROSITE; PS00338; SOMATOTROPIN\_2; 1

	Hormone; Pituitary; Signal.	By sim
KW	1	26
FT	1	26

FT	CHAIN	27	217	Somatotropin.
FT	DISULFID	79	191	By similarity.
FT	DISULFID	308	315	By similarity.

217 AA; 24864 MW; 9515289992C5

Alignment Scores: 1.2e-69  
Pred. No.: Length:

Score:	904.50	Matches:
Percent Similarity:	86.64%	Conservat
Percent Local Similarity:	82.02%	

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best local similarity: 82.03%
Query Match: 81.34%
DB: 1
Mismatch: Mismatch
Indels: Indels
Canc: Canc

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JS-09-856-796B-1 (1-609) x SOMA.SAIBB (1-217)

1 ATGGCTACAGGCTCCCGACGTCCTCTGCTTTGGCCCTGCTCTGCTGCTGCTGG 60

1 MetAlaThrGlySerArgThrSerLeuLeuAlaPheThrLeuLeuCysLeuProGln 20

61 CTTCAAGAGGGCAGTGCCTTCCCAACCATTCCTTATCCAGGCTTTTGACAACCTAGT 120

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|||||
21 Leuylsglulalaglyalaphrothrilproleuserargleuenspamlamc 40
121 CTCGGCCGCCATGCTGTGCAACAGCTGGCTTGAACCTACAGAGTTT----- 171
41 Leuylsglulalaglyalaphrothrilproleuserargleuenspamlamc 60
172 -----AACCCGACAGCTCCCTGTTTC 195
61 Tyrlleprolysglulnlystyseryleuenglinspoglnthrseryleucysphe 80
196 TCAGAGCTATTCCGACACCTCCCAACAGGAGGAGAAACAACAAGAAATCAACCTAGAG 255
81 SerGlusertleprothrproulaserlyalysglulnlystyseryleuenglins 100
256 CTGCTCCGACATCTCCCTGCTGCTCATCTCAGTCTGCTGAGCCCGTGGAGTTCTCAG 315
101 Leuleuargliserleuileuileglnsertprhegluprovalglnleuulg 120
316 AGTGTCTTCCGCAACAGCTGCTGTATAGGGCCCTCTGACAGCAACCTATGACCTCTTA 375
121 SerValphealalanserleuerygllyalaseraspserVallyrglulryleu 140
376 AAGAGCTTAGAGGAGCATCCAAAGCTGATGGGAGGCTGGAAGATGGACGCCCGG 435
141 LysasproulglulnlylelglnthrlleuemetglulnlyspgllyserProArg 160
436 ACTGGGAGATCTTCAAGCAGACCTTACAGCAAGTTTCACACAACTACACAGATGAC 495
161 ThrGlValalalephearglnthryserlyshepshlelanserglnansasp 180
496 GCACTTACTCAAGACTACGGGCTGCTTACTGCTTCAAGAGACATGACAGAGTGGAG 555
181 AlaleuuleuylsantylrglyleuuleuylrcysphearglyaspmetaspValgln 200
556 ACATTCCTGGCGATCGTGCAGTCCGCTCTGTGAGGGGAGCTGTGGTTTC 606
201 ThrpheuularglilevalglnlycargserValglnlyserCysgllyphe 217

RESULT 13
SOMA CALJA
ID SOMA CALJA STANDARD; PRT; 217 AA.
AC O9GMB3;
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 05-JUL-2004 (Rel. 44, Last annotation update)
DE Somatotropin precursor (Growth hormone).
GN Name-GH1;
OS Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Platyrrhini; Callitrichidae; Callitrix.
OX NCBI_TaxID=9483;
RN [1]
RP SEQUENCE FROM N.A.
RA Wallis O.C., Wallis M.;
RT "Cloning and characterization of a putative growth hormone encoding
RT gene from the marmoset (Callitrix jacchus).";
RL Submitted (AU0-2000) to the EMBL/Genbank/DBD databases.
CC -1- FUNCTION: Plays an important role in growth control. Its major
CC role in stimulating body growth is to stimulate the liver and
CC other tissues to secrete IGF-1. It stimulates both the
CC differentiation and proliferation of myoblasts. It also stimulates
CC amino acid uptake and protein synthesis in muscle and other
CC tissues (by similarity).
CC -1- SUBCELLULAR LOCATION: Secreted.
CC -1- SIMILARITY: Belongs to the somatotropin/prolactin family.
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DR EMBL; AJ297563; CAC03481.1; -.
DR HSSP; P01241; 1A22.
DR InterPro; IPR009079; 4 helix cytokine.
DR InterPro; IPR001400; Somatotropin.
DR Pfam; PF00103; Hormone_1; 1.
DR PRINTS; PR00836; SOMATOTROPIN.
DR PROSITE; PS00266; SOMATOTROPIN_1; 1.
DR PROSITE; PS00338; SOMATOTROPIN_2; 1.
KW Hormone; Pituitary; Signal.
FT SIGNAL 1 26 By similarity.
FT CHAIN 27 217 Somatotropin.
FT DISULFID 79 191 By similarity.
FT DISULFID 208 215 By similarity.
SQ SEQUENCE 217 AA; 24959 MW; E102151A12CE6192 CRC64;

Alignment Scores:
Pred. No.: 7,24e-69 Length: 217
Score: 895.50 Matches: 176
Percent Similarity: 86.18% Conservative: 11
Best Local Similarity: 81.11% Mismatches: 15
Query Match: 80.53% Indels: 15
DB: 1 Gaps: 1

US-09-856-796b-1 (1-609) x SOMA_CALJA (1-217)

QY 1 ATGGCTACAGGCTCCCGAGACCTCCGCTGCTGCTTTGGCTTGCCTGCTGCTGCTG 60
DB 1 MetAlaIalaglyserprlnthrseryleuuleuulaphethrleuuleucysleuProglin 20
QY 61 CTCGAAGAGGAGGAGGCTTCCCAACCATTCCTTATCCAGGCTTTTGAACAAGCTAGT 120
DB 21 Leuularglulalaglyalaphrothrilproleuserargleuenspamlamc 40
QY 121 CTCGGCCGCCATGCTGTGCAACAGCTGGCTTGAACCTTACAGAGTTT----- 171
DB 41 Leuularglulalaglyalaphrothrilproleuserargleuenspamlamc 60
QY 172 -----AACCCGACAGCTCCCTGTTTC 195
DB 61 Tyrlleprolysglulnlystyseryleuenglinspoglnthrseryleucysphe 80
QY 196 TCAGAGCTATTCCGACACCTCCCAACAGGAGGAGAAACAACAAGAAATCAACCTAGAG 255
DB 81 SerGlusertleprothrproulaserlyalysglulnlystyseryleuenglins 100
QY 256 CTGCTCCGACATCTCCCTGCTGCTCATCTCAGTCTGCTGAGCCCGTGGAGTTCTCAG 315
DB 101 Leuleuargliserleuileuileglnsertprhegluprovalglnleuulg 120
QY 316 AGTGTCTTCCGCAACAGCTGCTGTATAGGGCCCTCTGACAGCAACCTATGACCTCTTA 375
DB 121 SerValphealalanserleuerygllyalaseraspserVallyrglulryleu 140
QY 376 AAGAGCTTAGAGGAGCATCCAAAGCTGATGGGAGGCTGGAAGATGGACGCCCGG 435
DB 141 LysasproulglulnlylelglnthrlleuemetglulnlyspgllyserProArg 160
QY 436 ACTGGGAGATCTTCAAGCAGACCTTACAGCAAGTTTCACACAACTACACAGATGAC 495
DB 161 ThrGlValalalephearglnthryserlyshepshlelanserglnansasp 180
QY 496 GCACTTACTCAAGACTACGGGCTGCTTACTGCTTCAAGAGACATGACAGAGTGGAG 555
DB 181 AlaleuuleuylsantylrglyleuuleuylrcysphearglyaspmetaspValgln 200
QY 556 ACATTCCTGGCGATCGTGCAGTCCGCTCTGTGAGGGGAGCTGTGGTTTC 606
DB 201 ThrpheuularglilevalglnlycargserValglnlyserCysgllyphe 217

RESULT 14
014644.

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ID	014644	PRELIMINARY;	PRT;	245 AA.
AC	014644;			
AD	01-JAN-1998 (TREMBLrel. 05, Created)			
DT	01-JAN-1998 (TREMBLrel. 05, Last sequence update)			
DT	01-MAR-2004 (TREMBLrel. 26, Last annotation update)			
DE	Placental growth hormone isoform hGH-V3 precursor.			
GN	Name=hGH-V;			
OS	Homo sapiens (Human).			
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.			
OX	NCBI_TaxID=9606;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RC	TISUB=full-term placenta;			
RX	MEDLINE=9837337; PubMed=9709963; DOI=10.1210/jc.83.8.2878;			
RA	Boguszewski C.L., Svensson P.A., Jansson T., Clark R.,			
RA	Carlsson L.M.S., Carlsson B.,			
RT	"Cloning of two novel growth hormone transcripts expressed in human			
RT	placenta."			
RL	J. Clin. Endocrinol. Metab. 83:2878-2885(1998).			
DR	EMBL; AF006061; AAB71829.1; -			
DR	HSSP; P01241; IAA2.			
DR	GO: GO:0005576; Cxetracellular; IEA.			
DR	GO: GO:0005179; P; hormone activity; IEA.			
DR	InterPro; IPR009079; 4_helix cytokine.			
DR	InterPro; IPR001400; Somatotropin.			
DR	Pfam; PF00103; Hormone 1; 1.			
DR	PRINTS; PR00836; SOMATOTROPIN.			
DR	PROSITE; PS00266; SOMATOTROPIN_1; 1.			
KW	Signal.			
FT	1	26	Potential.	
Q	SEQUENCE 245 AA; 27101 MW; 14CC7F8CD75D91C8 CRG4;			



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QY 172 -----AACCCAGACCTCCTCTGTTTC 195
Db 61 TyrlleuLysgluGlnlySerPheleuGlnasnProGlnThrSerleuLysPhe 80
QY 196 TCAGAGTCATTCGACACCCCTCCAAACGGAGGAAACACACAGAAATCCAACTAGAG 255
Db 81 SerGluSerlleProThrProSerasnMetGluGlnThrGlnGlnLysSerasnleuGln 100
QY 256 CTGCTCCGCGATCTCCCTGCTGCTCATTCAGTCGTGGCTGAGCCCGTGCAGTTCTCAGG 315
Db 101 leuLeuArglleSerleuLeuLeuileGlnSerTlrPheGlnProValargPheleuarg 120
QY 316 AGTGCTTCGCGCAACAGCCTGAGTGTACGGCGCTTGACAGCAACGCTATGACTCTTA 375
Db 121 SerMetPheAlasasnleuValTyrAspThrSerAspSerAspAspTyrHisleuLeu 140
QY 376 AAGGACTTAGAGGAGGACATCCAAACGCTGATGGGAGGCTGGAAGATGGCAGCCCGG 435
Db 141 LysAspPheuGlnGlnGlnlylleGlnThrleuMetArgargleuGlnAspGlySerArgArg 160
QY 436 ACTGGGCAAGATCTTCAGACAGACCTACAGAGTTGACACAACTCACACACAGATGAC 495
Db 161 ThrGlyGlnlleuLeuLysGlnThrTyrSerLysPheAspThrAsnSerHisasnHisasp 180
QY 496 GCACTACTCAGAACTACGGGCTGCTACTGCTTCAGAAAGGACATGACAAAGTTCGAG 555
Db 181 AlaLeuLeuLysasnTyrGlyleuLeuTyrCysPheArgLysAspMetAspLysValGln 200
QY 556 ACATTCCTGGCAGATCGTCAGATCCGCTCTGTGAGAGGAGCTGTGCTTC 606
Db 201 ThrPheLeuArglleValGlnCysArgSerValGlnGlySerCysGlyPhe 217
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